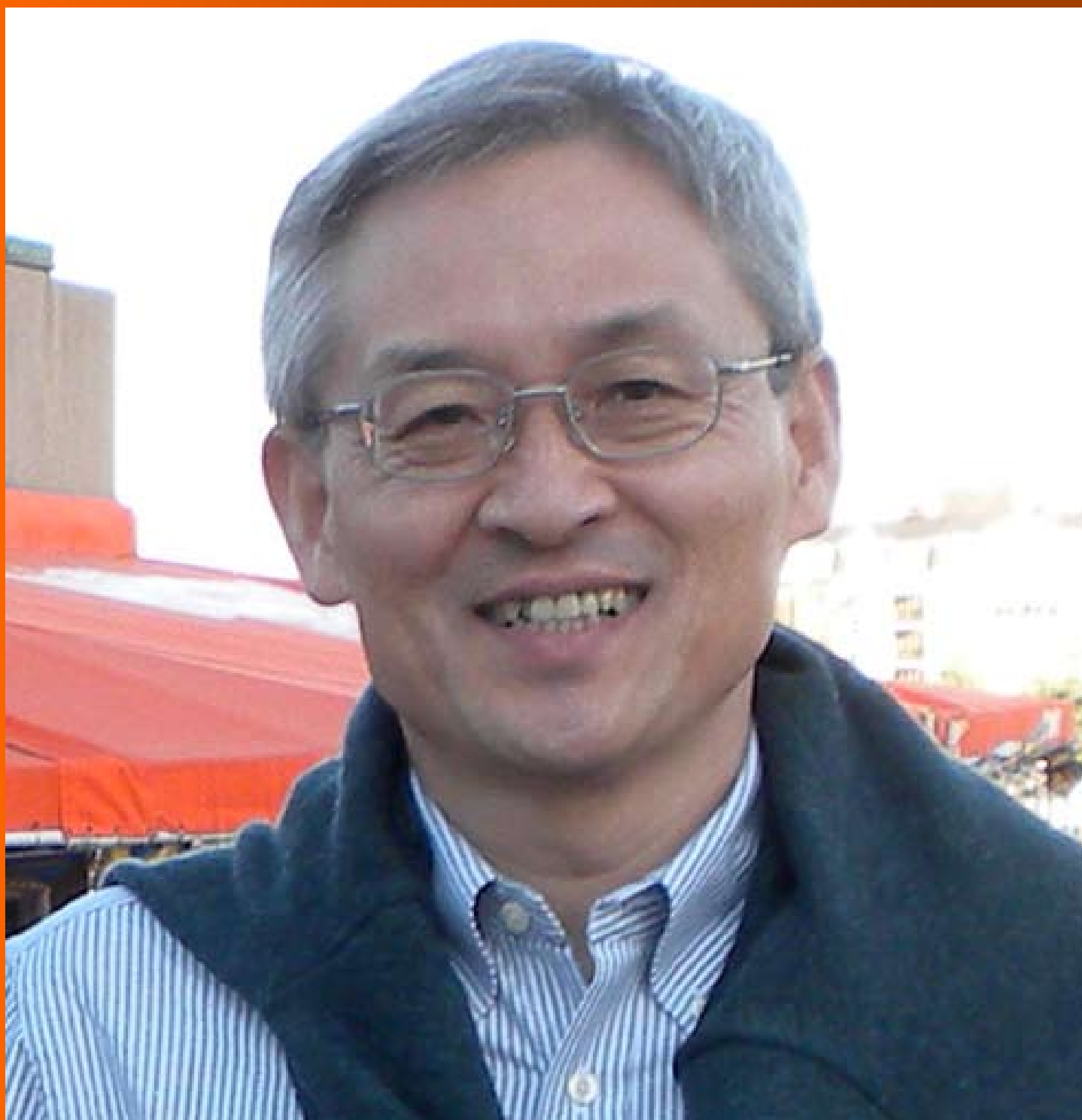


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Lysosomal acid lipase is critical for myeloid-derived suppressive cell differentiation, development, and homeostasis

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Abstract

Lysosomal acid lipase (LAL) cleaves cholesteryl esters (CE) and triglycerides (TG) to generate cholesterol and free fatty acid in lysosomes of cells. The downstream metabolic products of fatty acids are ligands for activation of peroxisome proliferator-activated receptor gamma (PPAR γ). Accumulation of CEs and TGs is resulted from lack of functional LAL in lysosomes of cells, especially in myeloid cells. One characteristic phenotype in LAL knock-out (*lal*^{-/-}) mice is systemic elevation of myeloid-derived suppressive cells (MDSCs). MDSCs infiltrate into multiple distal organs, alter T cell development, and suppress T cell proliferation and lymphokine production in *lal*^{-/-} mice, which lead to severe pathogenesis in multiple organs. The gene transcriptional profile analysis in MDSCs from the bone marrow has identified multiple defects responsible for MDSCs malformation and malfunction in *lal*^{-/-} mice, including G protein signaling, cell cycles, glycolysis metabolism, mi-

tochondrial bioenergetics, mTOR pathway etc. In a separate gene transcriptional profile analysis in the lung of *lal*^{-/-} mice, matrix metalloproteinase 12 (MMP12) and apoptosis inhibitor 6 (Api6) are highly overexpressed due to lack of ligand synthesis for PPAR γ . PPAR γ negatively regulates MMP12 and Api6. Blocking the PPAR signaling by overexpression of a dominant negative PPAR γ (dnPPAR γ) form, or overexpressing MMP12 or Api6 in myeloid or lung epithelial cells in inducible transgenic mouse models results in elevated MDSCs and inflammation-induced tumorigenesis. These studies demonstrate that LAL and its downstream effectors are critical for MDSCs development, differentiation and malfunction.

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Key words: Lysosomal acid lipase; Myeloid-derived suppressor cells; Immunosuppression; Myeloid-derived suppressive cell development; Hematopoiesis

Core tip: Neutral lipid metabolism is essential for myeloid cell proliferation and differentiation. This review summarizes the most recent discoveries that lysosomal acid lipase (LAL), an enzyme hydrolysing cholesteryl esters and triglycerides in lysosomes, plays a critical role in myeloid-derived suppressive cells (MDSCs) development, differentiation, and immune suppressive function. Both LAL knock-out and myeloid specific rescue of LAL knock-out mice are used in the studies. Doxycycline-inducible bitransgenic mouse models of LAL downstream genes are also generated to study MDSCs malformation and malfunction. The molecular pathways/mechanisms to connect LAL and MDSCs are characterized by microarray analyses of gene transcriptional profiles.

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HISTORY OF LYSOSOMAL ACID LIPASE

Lysosomal acid lipase (LAL) cleaves cholesteryl esters (CE) and triglycerides (TG) in cell lysosomes. Mutation in the LAL gene results in Wolman disease (WD) of early infantile onset, and cholesteryl ester storage disease (CESD) of late onset. WD was first described by Dr. Wolman^[1] in 1956 as severe malnutrition, hepatosplenomegaly, calcified adrenal glands, and death of children within the first few months of life. Affected WD infants display massive accumulations of CE and TG in the lysosomes of hepatocytes and Kupffer cells, as well as in macrophages throughout the viscera, which lead to liver failure, severe hepatosplenomegaly, steatorrhea, pulmonary fibrosis^[2,3], and adrenal calcification and insufficiency^[4,5]. Lipid engorged macrophages in intestinal villi lead to severe malabsorption and cachexia^[2,4]. The average life span of WD is 3.5 mo^[6]. CESD was initially described by Fredrickson, Schiff, Langeron, and Infante and their colleagues in 1967^[7-10] and named by Partin and Schubert based on phenotype that exhibited hepatomegaly with increased hepatic levels of cholesteryl esters in 1969. CESD can be a more indolent progressive disease, which shows microvesicular steatosis leading to fibrosis and cirrhosis in the liver, increases atherosclerosis and premature demise^[11-13]. Wolman disease and CESD result from allelic mutations at the LAL locus on human chromosome 10q23.2-q23.3 and are autosomal recessive traits. The gene spans 45 kb, has 10 exons, and contains no unusual structures, except for a large intron 3. The *LIPA* mutations found in Wolman disease include deletions and insertions that lead to premature stop codons and the consequent loss of LAL protein and activity^[14]. The mutations found in CESD are usually missense mutations, either heteroallelic or homoallelic with another mutant *LIPA* gene^[14].

Recently, some evidence started to emerge, showing altered mononuclear phagocyte differentiation [increased CD14⁺CD16⁺ and CD14⁺CD33⁺ cells, subsets of human myeloid-derived suppressive cells, or myeloid-derived suppressive cells (MDSCs)] in humans that were heterozygote carriers of LAL mutations^[15]. Furthermore, patients with mutations in the *LAL* gene have been reported to be associated with carcinogenesis^[16]. These clinical observations support the extensive characterization in animal models as described below.

LAL PROPERTIES

LAL is a key player in the modulation of cholesterol metabolism in all cells. On the surface membranes of various cells, there are multiple receptors that can deliver LDL-bound cholesteryl esters/triglycerides to lysosomes, but LAL is the only lipase in the lysosomes that hydrolyzes cholesteryl esters and triglycerides. Once cleaved by

LAL, the free cholesterol and fatty acids enter the cytosol from lysosome. In LAL deficiency, cholesteryl esters and triglycerides cannot be cleaved; therefore, free cholesterol and fatty acids cannot leave the lysosome^[17,18]. Cells sense this as an intracellular (cytosolic) cholesterol deficiency, and the cholesterol biosynthetic pathway is up-regulated to compensate.

Synthesized in the rough endoplasmic reticulum, LAL is a typical soluble lysosomal hydrolase, which is co-translationally glycosylated when it emerges into the endoplasmic reticulum lumen^[18,19]. Following the removal of the leader sequence (21 amino acids), LAL is decorated with oligosaccharides that are remodeled during transit through the Golgi apparatus. The N-linked oligosaccharides are remodeled from high mannosyl to complex forms, with a mannose 6-phosphate being added, which serves as the lysosomal sorting targeting signal. The mannose 6-phosphate receptor system is used to deliver the newly synthesized LAL to the lysosome. LAL is not known to require cofactors for optimal hydrolysis, and it functions as a monomer. Unmodified mature protein (378 amino acids) has a predicted molecular weight approximately 42.5 kDa. Different molecular weights have been reported for purified human LAL^[20-24]. Occupancy of the LAL N-glycosylation is essential for enzyme stability, *i.e.*, protection from rapid degradation^[25].

LAL has significant similarity to other acidic lipases, for example, lingual lipase and gastric lipases that cleave similar substrates in the stomach. However, LAL is distinct from other lipases, including hormone-sensitive lipase, pancreatic lysophospholipid lipase, lecithin cholesterol acyl transferase, lipoprotein lipase, hepatic lipase, and pancreatic lipase^[26]. All such lipases share a motif, Gly-X-Ser-X-Gly, that is an essential pentapeptide in the active site^[27,28]. This pentapeptide occurs twice in LAL at serine 99 and serine 153, and specific mutation of serine 153 identified this residue as important to catalytic activity^[23]. Like other lipases, LAL also has a catalytic triad of Ser₁₅₃, Asp₄₂₃ and His₃₅₃^[27].

GENE KNOCK-OUT PHENOTYPES AND MDSCS IN MICE

A *Lipa* knock-out mouse (*lal*^{-/-}) has been created to understand the functional roles of LAL in disease pathophysiology, lipid metabolism, and therapeutic approaches^[29,30]. The *lal*^{-/-} phenotype resembles human CESD. Its histopathologic and biochemical phenotypes are similar to human WD. The *lal*^{-/-} mice are normal appearing at birth, but develop liver enlargement by 4 wk and have a grossly enlarged abdomen with hepatosplenomegaly, lymph node enlargement, and intestinal villus infiltration by foamy macrophages by 16 wk. Massive accumulation of CE and TG and macrophage storage develops in these and other organs^[29,31-34]. Enzyme therapy has been studied in this model using human recombinant LAL (rhLAL) produced in several different eukaryotic systems^[24,35,36]. These studies clearly show the potential for correction of

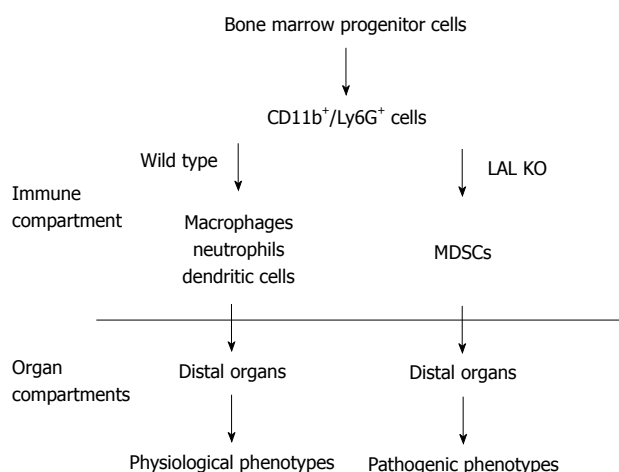


Figure 1 The functional role of Lysosomal acid lipase in myeloid lineage cells. In the wild type mice, the CD11b⁺Ly6G⁺ cells are myeloid lineage precursors for monocytes/macrophages, neutrophils, and dendritic cells, which participate in the normal physiological functions of the distal organs (e.g., lung, liver, etc.), such as clearance of invading pathogens. The lysosomal acid lipase (LAL) activity is essential for normal myeloid lineage cell development, differentiation and function. LAL deficiency leads to neutral lipid accumulation in myeloid cells and blocks CD11b⁺Ly6G⁺ cells from further differentiation into mature myeloid lineage cells. The accumulated CD11b⁺Ly6G⁺ cells possess various malfunctions that participate in the pathogenic conditions in the residing organs. MDSCs: Myeloid-derived suppressive cells.

the manifestations if enzyme therapy is begun early in the course of the disease^[36,37].

Many phenotypes of seemingly unrelated diseases in various organs co-exist in *lal*^{-/-} mice. Therefore, these diseases must share common cellular and molecular mechanisms that link these pathological processes. Extensive characterization of *lal*^{-/-} mice shows that elevation of systemic MDSCs is a major manifestation in association with most of the pathogenic conditions (e.g., > 70% in the bone marrow and > 40% in the blood), suggesting that MDSCs play a central role in mediating LAL deficiency-induced pathogenic progression^[29,31-34,36,38-41]. MDSCs was originally identified in tumor pathogenesis^[42]. Recent studies have linked this cell population to many other chronic inflammatory diseases^[43-50]. MDSCs are a mixture of myeloid cells that express CD11b and Gr-1 antigens in mice. In certain disease conditions (cancer), MDSCs are categorized into granulocytic (CD11b⁺, Ly6G⁺) and monocytic (CD11b⁺Ly6C⁺) MDSC^[51]. Interestingly, most gated *lal*^{-/-} CD11b⁺ cells show Ly6C⁺ and Ly6G⁺ double positive, making them CD11b⁺Ly6C⁺Ly6G⁺ cells^[34]. Normally, healthy immature myeloid lineage cells differentiate into dendritic cells (DCs), macrophages, or granulocytes in response to environmental changes. However, this process is blocked by LAL deficiency, leading to accumulation and expansion of MDSCs with immune suppressive function^[51-53]. This is similar to what has been observed in the tumor environment^[54]. It is conceivable that through paracrine and autocrine mechanisms, abnormally elevated MDSCs generate and secrete growth factors, chemokines and cytokines to influence cell differentiation, cell proliferation, cell apoptosis and gene expression in residing or-

gan tissues, contributing to the physiological progression of various diseases. Direct cell-cell contact by MDSCs and other cells through the juxtacrine mechanism also contributes to this pathogenic process.

The functional roles of LAL in myeloid cells have been specifically evaluated by creating a myeloid-specific doxycycline-inducible c-fms-rtTA/(tetO)⁷-CMV-hLAL; *lal*^{-/-} triple mouse model, in which human LAL is expressed in myeloid cells under the control of the 7.2 kb c-fms promoter/intron2 regulatory sequence in *lal*^{-/-} mice^[32,34,55]. The hLAL expression in myeloid lineage cells in this triple mouse model significantly reduced systemic MDSCs accumulation^[34], reversed aberrant gene expression, and ameliorated pathogenic phenotypes^[32]. Therefore, the normal biological function of myeloid cells requires normal neutral lipid metabolism (Figure 1).

MDSCS DIFFERENTIATION AND DEVELOPMENT

The myeloid lineage cells undergo the sequentially differentiated and proliferated from hematopoietic stem cells through an increasingly lineage-restricted intermediate progenitors including common myeloid progenitors (CMPs) and granulocyte-macrophage progenitors (GMPs) in the bone marrow^[56,57]. The number and frequency of primitive LSK (Lin⁻/Sca-1⁺/c-kit⁺), CMP, and GMP populations in the bone marrow, systemic myeloid cell distribution are changed in *lal*^{-/-} mice, leading to an expansion in CD11b⁺/Gr-1⁺ MDSCs^[41]. Both increased proliferation and decreased apoptosis contribute to the expansion of MDSCs in *lal*^{-/-} mice. *Lal*^{-/-} mice also display increased numbers of high proliferative potential colony-forming cells (HPP-CFC), colony-forming unit of granulocyte and macrophage progenitor cells (CFU-GM), colony-forming unit of granulocytes (CFU-G) and colony-forming unit of macrophages (CFU-M) colonies from cultured bone marrow cells. When *lal*^{-/-} bone marrow cells are transplanted into wild type mice, the donor CD11b⁺/Gr-1⁺ myeloid cells in the blood, spleen, lung and bone marrow of recipient mice are increased, confirming that the MDSCs increase is primarily due to the intrinsic defect in myeloid lineage progenitor cells. In addition to the intrinsic progenitor problem, the environment in *lal*^{-/-} mice also contributes to myeloid cell hyper-expansion, since the donor CD11b⁺/Gr-1⁺ myeloid cell population in *lal*^{-/-} recipient mice that are transplanted with wild type bone marrow cells is expanded. Therefore, the *lal*^{-/-} environment does not normally support hematopoiesis. Deregulated bone marrow progenitor cell differentiation is a primary cause for expansion of *lal*^{-/-} MDSCs, which is attributed to both cell-autonomous and environmental factors. Taken together, LAL expression in myeloid lineage cells is critical to maintain hematopoiesis and myelopoiesis. After MDSCs infiltration into distal organs, at least two mechanisms can explain how the cell-autonomous defect and environmental factors influence each other. Firstly, MDSCs and other regional

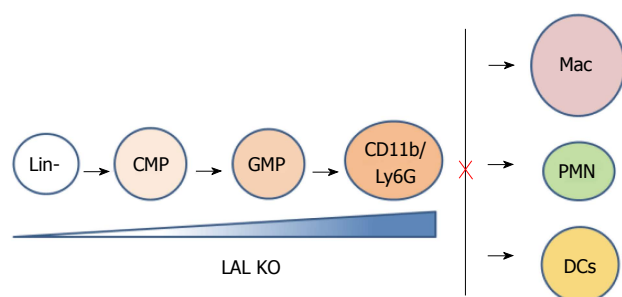


Figure 2 Lysosomal acid lipase is required for normal myeloid lineage cell development and differentiation. Lysosomal acid lipase (LAL) deficiency leads to increased myeloid-derived suppressive cells differentiation from Lin⁺ progenitor cells in the bone marrow, and decreased differentiation to mature macrophages, neutrophils, and dendritic cells in other compartments. Lin⁺: Lineage negative progenitor; CMP: Common myeloid progenitor; GMP: Granulocyte-macrophage progenitor; Mac: Macrophage; PMN: Polymorphonuclear cell, or neutrophil; DC: Dendritic cell.

cells in distal organs influence each other by the paracrine mechanism as both sides secrete cytokines and chemokines. Secondly, MDSCs and other cells can influence each other by direct contact (juxtacrine mechanism). Starting at the GMP stage, hLAL expression in myeloid cells reverses abnormal myeloid development in the bone marrow, and reduces systemic expansion of MDSCs in c-fms-rtTA/(tetO)⁷-CMV-hLAL; *lal*^{-/-} triple mice. In addition, differentiation from Lin⁺ progenitor cells to CD11b⁺GR-1⁺ cells is abnormally increased in *lal*^{-/-} mice (Figure 2). This further supports that the cell-autonomous effect of MDSCs expansion in *lal*^{-/-} mice. Myeloid hLAL expression in c-fms-rtTA/(tetO)⁷-CMV-hLAL; *lal*^{-/-} triple mice successfully reverses this abnormality^[32]. The environmental effects on MDSCs malformation are further supported by an observation that when the Stat3 pathway is overly activated in lung epithelial cells^[58], secretion of Stat3-induced pro-inflammatory cytokines in epithelial cells reversed mature myeloid lineage cells to MDSCs^[59].

MDSCS IMMUNOSUPPRESSION

In contrast to myeloid lineage cells, T cells are systemically decreased in *lal*^{-/-} mice. *Lal*^{-/-} T cells behave abnormally. In response to stimulation of anti-CD3 plus anti-CD28 antibodies, or phorbol-12-myristate-13-acetate (agonist to activate PKC) and ionomycin (calcium ionophore), there is severely diminished T cell proliferation, decreased CD69 expression, and decreased expression of T cell lymphokines. LAL deficiency does not drive effector T cells into either Th1 or Th2 status^[33]. The thymus is the most important organ for T cell development, which is divided into different developmental stages that are marked by CD4⁺CD8⁻ double negative (DN) 1 to 4 stages, CD4⁺CD8⁺ double positive (DP) stage and CD4⁺ or CD8⁺ single positive (SP) stage. The earliest stage for thymocyte paucity appears at the DN4 (CD25⁺CD44⁺) stage in the *lal*^{-/-} thymus. After this developmental point, thymocytes are declining at all stages, suggesting that

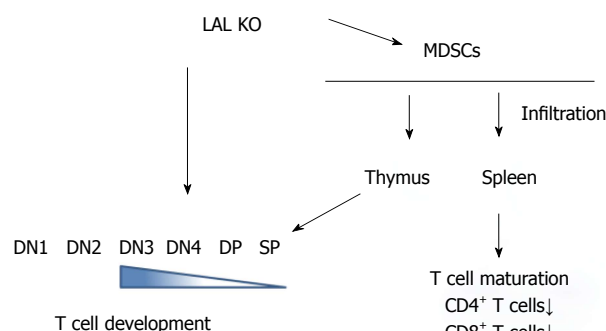


Figure 3 Lysosomal acid lipase is required for normal T cell development and differentiation. Lysosomal acid lipase (LAL) deficiency can cause the intrinsic defect in T cell development, starting at the double negative 3 (DN3) stage. In addition, myeloid-derived suppressive cells infiltrate into the thymus and spleen, resulting in blockage of normal T cell development, differentiation, and maturation. DN: CD4 and CD8 double negative; DP: CD4 and CD8 double positive; SP: CD4 or CD8 single positive.

the blockage of T cell development initially occurs at the DN3 to DN4 transition (Figure 3)^[33]. Decrease of T cell development and maturation was also observed in *lal*^{-/-} mice due to the defects in lymphoid progenitors in the bone marrow chimeras study. This notion has been supported by the bone marrow profile analysis, in which common lymphoid progenitor development is blocked in the bone marrow of *lal*^{-/-} mice^[33,41].

In addition to the above intrinsic defect, extensive analyses have revealed a second mechanism that contributes to systemic reduction of T cell populations. Strikingly, LAL deficiency dramatically increases MDSCs expansion and infiltration in the thymus and the spleen of *lal*^{-/-} mice, leading to neutral lipid accumulation and abnormal organization of the thymus and spleen^[33]. Infiltration of MDSCs in these important T cell organs affects T cell development, differentiation and maturation. Functional analyses have shown that MDSCs from *lal*^{-/-} mice strongly inhibit proliferation and function of T cells (Figure 3)^[34,40,41].

Direct connection between LAL in MDSCs and T cell abnormalities comes from the c-fms-rtTA/(tetO)⁷-CMV-hLAL;*lal*^{-/-} triple mouse study. MDSCs expansion and infiltration into the thymus and spleen are reduced in this mouse model. This leads to restoration of T cell proliferation in the spleen and normal T cell development in the thymus^[34]. Stat3 and NFκB p65 signaling play a critical role in *lal*^{-/-} MDSCs immune suppressive function^[34]. The above observations are further proved by an MDSCs depletion study, in which anti-Gr-1 antibody treatment recovers T cell numbers in *lal*^{-/-} mice^[34]. *lal*^{-/-} MDSCs also inhibits T cell lymphokine production, which is resulted from inactivation of the pZAP-70/Syk intracellular signaling, loss of expression of TCR ξ chain and CD69, a failure to respond to TCR stimulation^[33]. These defects can also be reversed by myeloid hLAL expression^[34]. Lastly, Treg cells inhibit CD4⁺ T cell lymphokine production and proliferation^[60]. LAL deficiency substantially increases CD4⁺FoxP3⁺ Treg cells in *lal*^{-/-} mice^[33].

GENE PROFILES IN LAL DEFICIENCY-INDUCED MDSCS

Since LAL controls homeostasis and development of MDSCs, which have profound pathogenic impact on various disease development, it is essential to identify the intrinsic defects that are involved in the MDSCs homeostasis and function for future targeting. In a comprehensive gene transcriptional profile study by Affymetrix GeneChip microarray analysis, multiple pathways have been revealed in *lal*^{-/-} bone marrow MDSCs. Below are lists of some major (but not limited) changed pathways in *lal*^{-/-} MDSCs.

Genes of G-protein superfamily

Expression changes of both large and small GTPases have been detected in *lal*^{-/-} MDSCs, which have diverse functions in cells^[61,62]. They include: (1) Rab GTPases, which control vesicle formation, receptor internalization, and trafficking to the nucleus, lysosome and plasma membrane. Rab GTPases regulate cellular proliferation, apoptosis and migration by integrating signaling pathways; (2) Rho GTPases, which organize actin cytoskeleton, cell adhesion and cell motility^[63]; and (3) Ras GTPases mediate cell-cycle entry, cell growth, cell survival, cell growth and cellular metabolism by phosphorylating transcription factors through activation of the Raf/Mek/Erk pathway. Activation of Erk and p38 phosphorylation has been observed in *lal*^{-/-} MDSCs^[41].

Histone cluster genes and cell cycle genes

Cell cycle regulating genes are upregulated in *lal*^{-/-} MDSCs. They include: (1) Histone-variants cluster genes, which favor the epigenetic microenvironment change to promote MDSCs expansion. Histone-variants exchange also contributes to formation of centromeric and telomeric chromatin during cell cycles. Indeed, G1/M phases of *lal*^{-/-} MDSCs are increased in a cell cycle analysis^[64]; (2) Cell cycle related genes^[65], including Cdk1, Cdk2, Cdk5, Cdk9, and all Cdk regulatory cyclins (A, B, D, E-type), suggesting constitutive mitogenic signaling and defective responses to anti-mitogenic signals; and (3) Ubiquitination and proteasome enzymes/protein factors, which direct proteins to proteolysis within proteasome for recycling^[66].

Metabolism and bioenergetics

Bioenergetic and metabolic genes are abnormally upregulated in *lal*^{-/-} MDSCs, which control mitochondrial oxidative phosphorylation and energy (ATP production) for cellular activities. These include: (1) lactate dehydrogenase A and B, which produce large quantities of secreted lactate, suggesting that *lal*^{-/-} MDSCs use an aerobic glycolysis; (2) nitric oxide/reactive oxygen species (ROS) production genes, glutathione peroxidase/glutathione reductase genes, and glucose 6-phosphate dehydrogenase gene, which are involved in production of ROS. The concentration of ROS is significantly increased in *lal*^{-/-}

MDSCs; (3) enzymes and proteins in glycolysis and citric acid cycles; and (4) respiratory chain proteins (NADH dehydrogenases, cytochrome proteins, ATPases and mitochondrial ribosomal proteins).

The mTOR pathway in LAL deficiency induced MDSCs

PI3K/thymoma viral proto-oncogene (AKT)/mammalian target of rapamycin (mTOR) is activated in *lal*^{-/-} MDSCs^[64]. mTOR is a lysosomal membrane-bound protein, which controls apoptosis, promotes influx of glucose and amino acids into the cells, stimulates ATP production^[67], contributes to cell growth, cell cycle entry, cell survival, and cell motility^[68,69]. Lack of the LAL activity changes lipid composition and dynamics on the lysosomal membrane that potentially influence endomembrane trafficking and stimulate the mTOR activity, which in turn coordinates the cellular metabolism^[64,69,70]. It has been demonstrated that mTOR plays a critical role in modulating cellular immune functions^[71,72], activation of the mTOR pathway contributes to *lal*^{-/-} MDSCs production and function^[40]. mTOR is the catalytic subunit of two distinctive complexes; mTOR complex 1 (mTORC1) and mTOR complex (mTORC2). mTORC1 contains unique regulatory associated proteins of mTOR (RAPTOR) while mTORC2 contains rapamycin-insensitive companion of mTOR (RICTOR)^[67,72-75]. Inhibition of mTOR and associated proteins (Raptor, Rictor, and Akt1) corrects *lal*^{-/-} MDSCs development, increased cell proliferation, decreased cellular apoptosis, and immune suppression in association with decreased ROS production, recovery from impairment of the mitochondrial membrane potential, increased ATP synthesis, and increased cell cycling. Potentially, the mTOR pathway can serve as a target to modulate the emergence of MDSCs in various pathophysiologic states where these cells play an immunosuppressive role (Figure 4).

The Stat3 and NFκB pathways

Although upregulation of Signal Transducer and Activator of Transcription (Stat) family members and NFκB family members are not detected by microarray analysis, phosphorylation of Stat3 and NFκB has been detected in expanded *lal*^{-/-} MDSCs^[34,41]. Activation of Stat3 directly leads to MDSCs expansion *in vivo*^[58,59].

STUDY OF LAL DOWNSTREAM GENES

The gene profile study in the lung of *lal*^{-/-} mice by Affymetrix GeneChip microarray analysis has also been performed. This is because the lung is a lipid rich organ and highly responsive to inflammation. Neutral lipids account for 10% of the composition of pulmonary surfactant that protects alveoli from collapse during respiratory cycles^[76]. LAL deficiency results in massive myeloid cell infiltration, hyperplasia and emphysema in the *lal*^{-/-} lung^[32,39]. Comparison between the changed gene lists of bone marrow MDSCs and the whole lung by Affymetrix GeneChip microarray analyses reveals a few overlapping

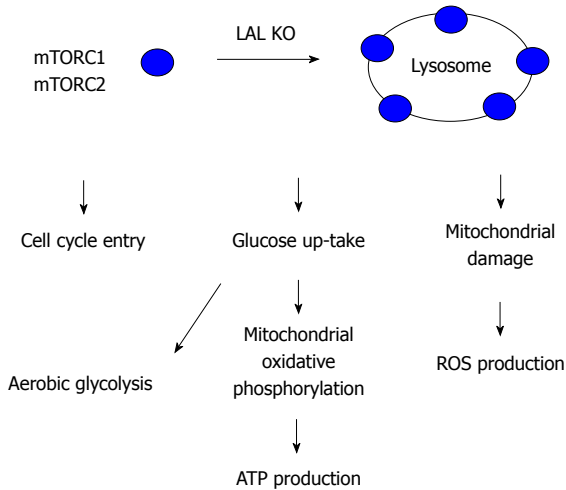
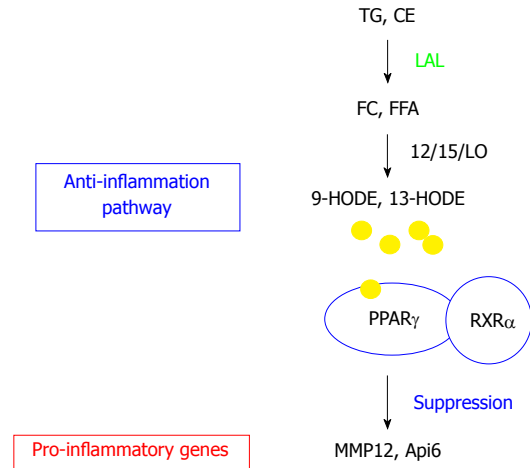


Figure 4 Lysosomal acid lipase deficiency induces overactivation of the mTOR pathway in myeloid-derived suppressive cells. Lysosomal acid lipase (LAL) is a lysosome-associated enzyme. LAL deficiency increases mTOR complexes anchoring on lysosomes and stimulates the mTOR1 activity to influence the cellular metabolism and proliferation of *lal*^{-/-} myeloid-derived suppressive cells (MDSCs). These include an increased influx of glucose through aerobic glycolysis, an increased mitochondrial oxidative phosphorylation and ATP production, an impairment of the mitochondrial membrane potential in association with increased reactive oxygen species (ROS) production, and an increased cell cycle entry in *lal*^{-/-} MDSCs.

genes. Therefore, LAL performs differential roles in different compartments. LAL exerts its biological effects through its downstream genes. In order to fully understand the LAL functions, it is necessary and essential to characterize its downstream genes. From the whole lung gene list, the two most up-regulated genes matrix metal proteinase 12 (MMP12) and apoptosis inhibitor 6 (Api6) are characterized extensively. The functional role of LAL downstream effector peroxisome proliferator-activated receptor gamma (PPAR γ) has also been studied in depth. Figure 5 shows the relationship between LAL and its downstream effectors.

PPAR γ

Involvement of the receptor network in the metabolic programming of myeloid lineage cells is essential to the innate immune system^[77,78]. PPAR γ is of high interest for several reasons. Firstly, the metabolites of LAL hydrolysis, 9-hydroxyoctadecanoic acids (9-HODE) or 13-HODE from linoleic acid, serve as ligands for PPAR γ . Upon binding to the ligands, PPAR interacts with the retinoid X receptor (RXR) to form the PPAR γ /RXR dimer on target genes. Secondly, PPAR γ plays an important role in anti-inflammation of various tissues^[77,79,80]. It has been shown that PPAR γ agonists suppress gene expression of inflammatory cytokines^[79]. In the *lal*^{-/-} lung, these pro-inflammatory cytokines are up-regulated (Figure 5)^[39]. Therefore, LAL deficiency causes inactivation of PPAR γ by depleting ligand production. Using the lung as a model system, reintroduction of LAL downstream metabolic derivative 9-HODE (a natural occurring ligand for PPAR γ) and a synthetic ligand compound ciglitazone for PPAR γ improves the inflammatory status and pathogen-



TGF- β , IL-1 β , MCP-1, IL-6, TNF- α , G-CSF, GM-CSF, NOS, NF- κ B, KC (CXCL1), EP2, MMP9, PEG2

Figure 5 Lysosomal acid lipase and its downstream effector genes. Lysosomal acid lipase (LAL) cleaves cholesteryl esters (CE) and triglycerides (TG) to produce free cholesterol (FC) and fatty acids (FFA) in lysosomes of cells. The lipid derivatives (9-HODE, 13-HODE) of FFA serve as ligands for PPAR γ in coupling with retinoid X receptor α (RXR α), which suppresses gene expression of a variety of pro-inflammatory cytokines. The LAL/PPAR γ axis serves as an anti-inflammatory pathway. LAL deficiency blocks this metabolic pathway to provoke up-regulation of pro-inflammatory cytokines (e.g., Api6, MMP12). TGF: Transforming growth factor beta; IL: Interleukin; MCP: Monocyte chemotactic protein; TNF: Tumor necrosis factor; NF: Nuclear factor.

esis in the *lal*^{-/-} lung. Therefore, the ligands/PPAR γ axis controls inflammation-triggered elevated gene expression and pathogenesis in the *lal*^{-/-} mice^[31].

To directly evaluate functional role of LAL downstream effector PPAR γ in myeloid cells, dominant negative PPAR γ (dnPPAR γ) is overexpressed in a myeloid-specific c-fms-rtTA/(TetO) γ -CMV-dnPPAR γ bitransgenic mouse model^[81]. In this bitransgenic system, total numbers and frequencies of LK, LSK, CMP and GMP progenitor cells in the bone marrow are abnormally elevated. DnPPAR γ overexpression leads to up-regulation of IL-1 β , IL-6 and TNF α in the blood plasma. MDSCs from this bitransgenic mouse model inhibit the proliferation and lymphokine production of wild type CD4⁺ T cells *in vitro*. Both CD4⁺ and CD8⁺ T cell populations are decreased in doxycycline-induced dnPPAR γ expressed mice. Bone marrow transplantation reveals that a myeloid autonomous defect is responsible for MDSC expansion, immunosuppression and tumorigenesis in this myeloid-specifically expressed dnPPAR γ bitransgenic mice. Multiple forms of carcinoma and sarcoma in various organs (the lung, liver, spleen and lymph nodes) are observed in this mouse model. Therefore, the LAL/hormonal ligands/PPAR γ axis is critical to control inflammation and the induction of various tumors. Disruption of this pathway in myeloid cells, either by blocking ligand synthesis (as in *lal*^{-/-} mice), or inhibition of PPAR γ (as in c-fms-rtTA/(TetO) γ -CMV-dnPPAR γ bitransgenic mice) can initiate up-regulation of inflammatory molecules which cause hematopoietic progenitors skewing towards myeloid lineage expansion to form MDSCs.

Matrix metalloproteinases12

Zinc-dependent MMPs act as modulators for inflammation and innate immunity by activating, deactivating or modifying the activities of signaling cytokines, chemokines and receptors through proteolytic and nonproteolytic functions^[82-84]. Among MMPs, MMP12 is a 22-kDa secretory proteinase that is predominantly expressed in macrophages as previously reported^[85]. MMP12 degrades extracellular matrix components, such as type IV collagen, fibronectin, laminin, gelatin, vitronectin, entactin, heparin, and chondroitin sulphates, to facilitate tissue remodeling^[86]. The expression of MMP12 in macrophages is induced in the lung of cigarette smokers^[87]. Inactivation of the MMP12 gene in knock-out mice demonstrates a critical role of MMP12 in smoking-induced chronic obstructive pulmonary disease (COPD)^[88], a disease highly related to lung cancer. From clinical studies, MMP12 correlates with early cancer-related deaths in non-small cell lung cancer (NSCLC), especially with those associated with tobacco cigarette smoke exposure^[89,90]. In the *lal*^{-/-} lung, MMP-12 is the highest upregulated gene^[31]. In the *lal*^{-/-} lung, both macrophages and lung epithelial alveolar type II (AT II) cells are responsible for MMP-12 increase^[31,91,92]. Both myeloid-specific and lung epithelial-specific MMP12 bitransgenic mouse models have been created to study the functional roles of this LAL/PPAR γ downstream molecule.

In the myeloid-specific c-fms-rtTA/(TetO) γ -CMV-MMP12 bitransgenic mouse model, induction of MMP12 abnormally elevates numbers and frequencies of CMP and GMP populations in the bone marrow, similar to that observed in *lal*^{-/-} mice. Addition of activated MMP12 is able to stimulate wild type Lin⁻ progenitor cells to differentiate into the MDSC population, suggesting that MMP12 directly exerts its effect on hematopoietic progenitor cells. The MDSCs are systemically increased in multiple organs of MMP12 bitransgenic mice. MDSCs from MMP12-overexpressed bitransgenic mice suppress T cell proliferation and function. MMP12 directly stimulates differentiation of CD11b⁺Gr-1⁺ cells from Lin⁻ progenitor cells. In the lung, the concentration of IL-6 is increased, which aberrantly activates oncogenic Stat3 and increases expression of Stat3 downstream genes in epithelial tumor progenitor cells. As a result, spontaneous emphysema and lung adenocarcinoma are sequentially developed in MMP12-overexpressive bitransgenic mice, suggesting a critical role of MMP12 in the transition from emphysema to lung cancer.

In epithelial-specific CCSP-rtTA/(TetO) γ -CMV-MMP12 bitransgenic mice, MMP12 overexpression induces regional MDSCs infiltration and increases epithelial growth. Again, spontaneous emphysema and bronchioalveolar adenocarcinoma are developed sequentially. Importantly, MMP12 upregulation is highly associated with COPD and lung cancer in human patients. Together, these studies support that LAL/PPAR γ downstream MMP12 plays a critical role in emphysema to lung cancer transition that is facilitated by inflammation.

Clinically, it has been reported that there is a pathophysiological connection between emphysema/COPD and lung cancers^[93,94].

Apoptosis inhibitor 6

Apoptosis inhibitor 6 (Api6) belongs to the macrophage scavenger receptor cysteine-rich domain superfamily (SRCR-SF)^[95,96]. Api6 expression is the second highest induced gene in the *lal*^{-/-} lung. Api6 is regulated by LAL metabolic derivatives (*e.g.*, 9-HODE) and PPAR γ ^[31]. In a myeloid-specific c-fms-rtTA/(TetO) γ -CMV-Api6 bitransgenic mouse model, many phenotypes are similar to those observed in *lal*^{-/-} mice. Overexpression of Api6 abnormally elevates MDSCs in the bone marrow, blood and lung with increased cell proliferation and decreased apoptotic activities. Api6 overexpression activates Stat3, Erk1/2 and p38 in myeloid lineage cells. Persistent inflammation in myeloid-specific Api6 bitransgenic mice causes lung adenocarcinoma^[97].

Pathogenic overexpression of Api6 is also observed in *lal*^{-/-} AT II cells. In an epithelial-specific CCSP-rtTA/(TetO) γ -CMV-Api6 bitransgenic mice, Api6 overexpression in AT II cells increases pro-inflammatory cytokine/chemokine levels in bronchoalveolar lavage fluid and serum, activates oncogenic signaling and inhibits apoptosis, promotes expansion of MDSCs in lung and blood but not in the bone marrow or spleen. Lung MDSCs from this bitransgenic mouse model suppress T cell proliferation and function, which results in occurrence of emphysema and adenocarcinoma.

CONCLUSION

MDSCs play vital roles in various inflammation-induced chronic diseases. Elimination or reduction of MDSCs populations can slow down disease formation and progression. It is important to identify the molecular pathways in order to effectively block MDSCs homeostasis and function. Extensive studies outlined in this review have shown that the role of LAL in controlling neutral lipid metabolism is a key player in MDSCs development, homeostasis and function, therefore, providing a new avenue to develop therapeutic or immunologic approaches for clinical application. Through studies of the LAL function, defective gene expression patterns have been mapped in *lal*^{-/-} MDSCs. These provide novel targets for controlling MDSCs and associated diseases by designing small molecule inhibitors. Clinically, small molecule inhibitors for c-kit have been tested to target MDSCs^[98]. Using the gene profile list from LAL deficiency-induced MDSCs, more small molecule inhibitors can and will be identified to inhibit MDSCs pathogenic functions in various disease conditions.

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Gut immune response in the presence of hepatitis C virus infection

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Abstract

Hepatitis C virus (HCV) is an important etiologic agent of hepatitis and a major cause of chronic liver infection that often leads to cirrhosis, fibrosis and hepatocellular carcinoma. Although, HCV is a hepatotropic virus, there is strong evidence that HCV could replicate extra-hepatic in the gastrointestinal tissue which could serve as a reservoir for HCV. The outcome of HCV infection depends mainly on the host innate and adaptive immune responses. Innate immunity against HCV includes mainly nuclear factor cells and activation of IFN-related genes. There is an immunologic link between the gut and the liver through a population of T-cells that are capable of homing to both the liver and gut *via* the portal circulation. However, little is known on the role of Gut immune response in HCV. In this review we discussed the immune regulation of Gut immune cells and its association with HCV pathogenesis, various outcomes of anti-HCV therapy, viral persistence and degree of liver inflammation. Additionally, we investigated the relationship between Gut immune responses to HCV and IL28B

genotypes, which were identified as a strong predictor for HCV pathogenesis and treatment outcome after acute infection.

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Key words: Hepatitis C virus; Colonic T_{reg}; Mucosal; Immune regulation; Liver inflammation; Interleukin-28B

Core tip: Chronic hepatitis C (CHC) is a global worldwide health problem with approximately 200 million people worldwide infected with hepatitis C virus (HCV). It is also a major cause of chronic liver infection that often leads to chronic hepatitis which may progress to cirrhosis, fibrosis and finally hepatocellular carcinoma. In CHC, immune responses play an important role in HCV pathogenesis and responses to therapy. Intra-hepatic immune responses to HCV are highly regulated. There is a clear relationship between hepatic immune responses and mucosal immune response in the gut. Additionally, genetic immunological markers have been proposed to predict response to HCV treatment, and outcome of infection.

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INTRODUCTION

Hepatitis C virus (HCV) was first identified by Harvey Alter in 1978 and named non-A, non-B hepatitis^[1], and cloned by Houghton in 1986^[2]. HCV is a single-stranded, positive sense RNA virus belonging to *Hepacivirus* group in the family *Flaviviridae*^[3]. There are 6 HCV genotypes. Due to the low fidelity and lack of proofreading of HCV

polymerase enzymes used for viral genome amplification, multiple mutations occur within a genotype to produce quasi-species^[4,5].

Chronic hepatitis C infection (CHC) is a global worldwide health care problem with an increasing burden year-by-year^[6-8]. The World Health Organization estimates that approximately 200 million people worldwide are infected with HCV^[9]. It is also a major cause of chronic liver infection that often leads to chronic hepatitis which may progress to cirrhosis, fibrosis and finally hepatocellular carcinoma^[3,10].

HCV is one of the most important etiologic agents of post transfusion hepatitis. HCV is usually spread by sharing infected needles with a carrier, from receiving infected blood, and from accidental exposure to infected blood. Some people acquire the infection through non parenteral means that have not been fully defined, but include sexual transmission in persons with high risk behaviors^[11]. It is not reported that HCV can spread orally by food, water, breast feeding, or by normal social contact as sneezing, coughing, hugging, sharing eating utensils or drinking glasses^[12]. Mother-to-baby transmission is rare and needs a high viremia as found in HIV co-infection^[13].

HCV VIROLOGY

HCV is a single stranded RNA virus which produces negative strand RNA as a replicative intermediate. The HCV genome is about 9.6 kb in length. During HCV replication cycle, one large precursor protein is synthesized from an open reading frame then cleaved to produce 10 proteins including three structural proteins which are Core, two envelope proteins (E1 and E2)^[3], and P7 which results from cleavage of E2 protein^[14]. The other six proteins that are not in the viral particle called non-structural proteins (NS) including NS2, NS3, NS4A, NS4B, NS5A, and NS5B^[3]. Non-structural (NS) proteins are not found in the virion, therefore, presence of NS proteins inside cells suggests that HCV replication occurred in those cells^[3]. Replication of HCV involves converting the viral genomic positive strand into a negative strand, and then back to the genomic strand. Thus, the presence of the negative strand strongly suggests that replication^[15].

HCV REPLICATION

HCV is primarily a hepatotropic virus^[15]. However, a broad spectrum of extra-hepatic manifestations may be associated with HCV infection, including mixed cryoglobulinemia, non-Hodgkin's lymphoma, arthralgia, paresthesia, myalgia, pruritis, cutaneous vasculitis, glomerulonephritis, neuropathy and lymphoproliferative disorders^[16,17].

HCV was believed to infect only hepatocytes^[3]. However, recent studies have reported HCV infection of other cell types^[15,18-21]. In fact, viral replication has been reported in B cells, T cells, monocytes, macrophages, and

macrophage-like cells such as Kupffer cells, dendritic cells (DCs), renal cells, thyroid cells, and gastric cells. There is mounting evidence that these cells could represent replicative compartments for the virus^[3,22,23]. In addition, it has been proposed that peripheral blood monocytes (PBMC) could be the source of recurrent HCV infection after liver transplantation^[24]. Despite these reports, extra-hepatic replication of HCV is still controversial by some investigators. However, the importance of extra-hepatic HCV replication in HCV pathogenesis is clear. Extra-hepatic compartments might serve as reservoirs for HCV, and hence HCV persistence, reactivation after antiviral therapy and also may contribute to the HCV extra-hepatic manifestations^[24].

HCV IN THE GUT

There is a molecular evidence that HCV may infect and replicate in oral mucosa and gastric cells^[23]. Moreover, HCV seems to be involved in development of B-cell non-Hodgkin's lymphoma of the gastric mucosa^[25]. Miglioresi *et al*^[26], reported that Gut mucosa may serve as possible reservoir for HCV relapse after viral clearance. They analyzed HCV gastric localization in 15 patients and compared their levels of viremia with the status of HCV in gastric biopsy specimens and PBMCs. In that study, all 15 patients with positive viremia were positive for HCV RNA on Gut tissue and PBMCs. In 2 patients, HCV RNA was positive on serum, negative at Gut biopsy but their PBMCs were positive. Two patients with negative viremia and PBMCs after antiviral treatment were positive for HCV RNA on gastric sample and eventually relapsed (after 6 and 18 wk). The finding of a positive hidden compartment for HCV and simultaneous negative viremia had previously reported in HCV infected liver without detectable viremia^[27]. Replication of HCV in gastrointestinal tissue represents a continuous new source as an extra-hepatic reservoir of viral particles for re-infection of hepatocytes^[26].

IMMUNE RESPONSE TO HCV

Systemic immune responses

The immune response against HCV involves innate and adaptive immunity^[9]. Innate immunity against HCV is mediated by several innate immune effector cells such as NK cells, and activation of the interferons-stimulated genes (ISGs) response^[28]. Recent studies have revealed that the *IL28B* gene locus, which codes for a type III interferon is a critical locus for outcome after acute infection^[29], and response to therapy^[29,30]. However, HCV may develop several strategies to overcome these responses. For example, viral NS3 and NS4a protease can cause disruption of important components of type I interferon activation cascade through inactivation of several ISGs^[31,32].

Adaptive immunity against HCV is mediated by both humoral and cellular immune responses. Most HCV-

infected individuals develop antibodies against HCV, regardless of the outcome of infection. Few of these antibodies can neutralize viral particles and may limit viral spread^[33]. However, neutralizing antibodies have a limited role in most of the infected patients due to the high replication and mutation rate of HCV^[34]. In fact, HCV clearance had been observed in some patients in the absence of neutralising antibodies^[35]. Therefore, despite the potential protective role of innate and humoral immunity in the outcome of infection, it is clear that protection and viral clearance depend primarily on cellular adaptive immune responses through a complex interplay between CD4⁺ and CD8⁺ T-cell responses^[9]. Unfortunately, in some patients, cellular immune responses are inadequate and fail to clear the infection with a subsequent viral persistence^[9]. Fully functional virus-specific CD4⁺T-cell responses are detectable in patients who cleared infection^[9,36-38]. The role of HCV-specific CD4⁺T-cell was further supported by the finding of *in vivo* depletion of CD4⁺T cells from HCV-recovered chimpanzees was associated with viral persistence^[38]. Moreover, several studies have shown that HCV-specific CD8⁺T-cells derived from the peripheral blood or liver are functionally impaired and display a reduced ability to proliferate or secrete anti-viral cytokines such as IFN- γ ^[39-41]. The mechanisms contributing to CD8⁺T cell exhaustion in HCV are not fully understood, however, it may be partially explained by the intrinsic regulatory pathways such as signals mediated by the inhibitory receptor PD-1^[40,42-45] and extrinsic regulatory pathways as regulatory T cells (T_{reg}) or secretion of immunoregulatory cytokines such as IL-10^[46-51]. Ultimately, the outcome of HCV infection, viral persistence or clearance, is determined by the host immune response^[9,52,53]. Additionally, sustained HCV-specific cytotoxic T cell responses in the liver have been associated with the development of hepatic immunopathology and liver necrosis which may lead to liver cirrhosis^[52,53]. The mechanisms that mediate liver inflammation and damage in CHC are not yet fully elucidated^[9,54]. One of the potential mechanisms that might modulate HCV-specific immune responses is T_{reg} cells which are a subtype of T cells that play a fundamental role in maintaining immune homeostasis and the balance between the tissue-damaging and protective effects of the immune response^[54-56]. It is characterized by the expression of a unique transcription factor Forkhead box protein P3 (FoxP3), which is highly expressed in the nucleus of T_{reg} cells and is generally accepted as the single best marker to quantify T_{reg} cells^[53,56-58]. In cases with CHC, it was reported that the frequency of T_{reg} cells were negatively correlated with the degree of necro-inflammatory scores and their frequency is higher than that in healthy individuals^[47,59,60]. Thus, T_{reg} cells appear to assist in the maintenance of chronicity by inhibition of anti-HCV immune responses and consequently attenuate the intrahepatic tissue-damaging response to infection^[49,53].

MUCOSAL (GUT) IMMUNE RESPONSE IN HCV

The mucosal immune system is considered the first line of defense that reduces the need for elimination of exogenous invading antigens by pro-inflammatory immune response^[61]. The mucosal immune system maintains homeostasis through evolution of two layers of adaptive non-inflammatory defense; the first strategy is immune exclusion by secretory IgA (and IgM) antibodies to limit epithelial contact and penetration of invading microorganisms and other potentially dangerous antigens^[61], and the second strategy is oral tolerance by development of immunosuppressive mechanisms to inhibit over-reaction against food antigens and commensal bacteria^[62]. Oral tolerance depends mainly on the induction of T_{reg} cells in mesenteric lymph nodes to which mucosal DCs carry and present food and commensal microbial antigens^[63]. Gut induced tolerance include other suppressive mechanisms to ensure that persistent food allergy is relatively rare^[64].

Some pathogens and food antigens could enter the liver via the portal circulation^[65] within 2 h of ingestion^[66] and presented on liver endothelial cells. The liver is critical in the regulation of immune responses to pathogens entering *via* portal circulation^[67]. It receives 75% of its blood supply from the portal vein, which drains the gut. Oral tolerance is usually lost in case of a portal-systemic shunt, which allows portal blood to bypass the liver and goes directly from the gut to the systemic circulation^[67,68].

To understand the interactions between the immune responses in the Gut and the liver during HCV infection, we have to dissect the immune responses in each organ. The intestinal immune system can be divided into inductive and effector sites based upon their anatomical and functional properties^[61,63]. Inductive sites include the gut-associated lymphoid tissues (GALT) such as Peyer's patches (PP) and isolated lymphoid follicles and the mesenteric lymph nodes (mLNs). The GALT contains a wide variety of cells, such as Microfold (M) cells, DCs, intraepithelial lymphocytes (IEL), macrophages and T_{reg} cells^[61]. The main effector sites of the intestinal immune system are the lamina propria (LP) and epithelium, which harbor large populations of activated T cells and antibody-secreting plasma cells. The LP may also contribute to the induction of tolerance. It is a site of antigen uptake and loading of the migratory DCs that encounter naïve T cells in the mLNs^[61]. Antigen are up-taken by absorptive epithelial and M cells in the mucosal inductive sites or directly captured by professional APCs (including DCs, Macrophage and B lymphocytes)^[69]. M cells take up molecules and particles from the gut lumen by endocytosis or phagocytosis then sample them to the immune cells. Antigens are transported through M cells by the process of transcytosis. The cell membrane at the base of M cells is folded around lymphocytes and dendritic cells within the Peyer's patches^[69]. M cells present the antigen to conventional CD4⁺ and CD8⁺ $\alpha\beta$ T cells at the inductive site.

At the same time, epithelial cells may process and present certain antigens directly to neighboring intraepithelial T cells such as NKT cells and $\gamma\delta$ T cells which are T cells with limited repertoire diversity^[69]. Naive B and T cells enter GALT and are primed to become memory/effector B and T cells, then migrate from GALT to mesenteric blood and the liver or to the lymph nodes *via* lymph and then *via* thoracic duct to peripheral blood for subsequent extravasation at mucosal effector sites. A system of Gut-specific lymphocyte trafficking has been evolved to target lymphocyte to the area of injury or infection through vascular adhesion molecules and chemokines. Thus, the endothelial cells act as a local gatekeeper for mucosal immunity^[61]. Under normal physiological conditions enteric antigens are presented to naïve lymphocytes in the draining mesenteric lymph nodes. Lymphocytes activated by gut dendritic cells express a gut-homing phenotype characterized by expression of the chemokine receptor CCR9 and the integrin $\alpha 4\beta 7$ which direct the migration of the activated lymphocytes back to gut tissue where their respective ligands CCL25 and MAdCAM-1 are expressed^[67,70]. Lymphocytes that are primed to hepatic antigens acquire expression of adhesion molecules that direct them to traffic to the liver by interacting with molecules expressed on hepatic endothelium such as VAP-1.

EFFECTOR MECHANISMS OF THE GUT IMMUNE RESPONSES

Innate immune system in the gut includes the lining epithelium which provides barrier function, mechanical cleaning and defensins which act as chemical antimicrobial factors^[71]. The gut mucosa contains a number of other cells as part of the innate immune system, including phagocytic neutrophils and macrophages, DCs, NK cells and mast cells. These cells contribute significantly to host defense against pathogens^[22] and also initiate adaptive mucosal immune responses^[69,72].

The adaptive humoral immune defense at the gut mucosal surfaces is mainly mediated by secretory IgA (sIgA) antibody, which is the ideal antibody for functioning in mucosal secretions due to its resistance to proteases^[61]. sIgA plays a protective role against a variety of foreign antigens such as food antigens, toxins, bacteria and viruses^[72]. sIgA blocks the access of potentially allergenic molecules derived from food or drugs^[73]. Because some dietary antigen is clearly absorbed by normal subjects, the importance of sIgA antibody may lie in reducing the amount of antigen that gains access to the lamina propria^[73,74]. sIgA can neutralize biologically active antigens as bacteria, toxins, enzymes and viruses. The effectiveness of sIgA as a neutralizing antibody against viruses is shown for example in the responses to oral live-attenuated poliovirus vaccine where protection correlates with levels of secretory antibody^[75]. Additionally, sIgA is an efficient agglutinin that can prevent adherence of pathogenic bacteria to the epithelial surfaces and enhance the antibacterial efficiency of other effector immune system; sIgA has bactericidal

potential by cooperation with complement and lysozyme and also can act as opsonin. However, the role of sIgA during HCV infection is limited.

The development of IgA immune response against mucosal pathogens and soluble protein antigens is dependent on T helper cells^[76]. Mucosal T cells produce large amounts of transforming growth factor (TGF)- β , interleukin (IL)-10 and IL-4 to promote B-cell isotype class switching to IgA^[77,78]. Additionally, muco-epithelial cells, and T_{reg} cells are the major sources of TGF- β and IL-10, suggesting that cooperation between neighboring lymphocytes and epithelial cells in the mucosal microenvironment is pivotal to promote B-cell switch to IgA and differentiation into IgA-committed B cells^[69].

One of the important cellular immune defense at the gut mucosal surfaces is mainly mediated by cytotoxic T lymphocyte (CTL) responses^[69]. It is reported that mucosal CTLs are crucial for the immune clearance of pathogens in several animal models of infection with enteric viruses like Rota virus^[79] and intracellular parasites^[80]. Besides CTLs, induced IFN- γ producing CD4⁺ T cells, have been found to be important for mucosal immune defense to both viral and bacterial infections^[69].

REGULATORY MECHANISMS OF GUT IMMUNE RESPONSE AND ORAL TOLERANCE

Gut immune response is controlled by the local microenvironment, the nature of the antigen and the type of APCs. In case of foreign food proteins and non-pathogen antigens, the default pathway for mucosal DCs and other APCs is to generate Th2 and various regulatory T cell types of responses mainly T_{reg}^[81], and Th17 cells^[82] which usually leads to down-regulatory or active suppression of systemic immunity (oral tolerance). On the other hand, antigens, most pathogens harboring motifs which could bind to Toll-like receptor (TLR), and be sensed by mucosal APCs as 'danger signals' and pro-inflammatory conditions in general favor the development of stronger and broader immune responses but do not lead to oral tolerance^[81,83,84]. Oral tolerance can be achieved through different mechanisms, including anergy, activation-induced cell death and most important, the induction of regulatory T cells^[69,85]. Anergy of antigen-specific T cells has been reported after ingestion of large quantities of soluble proteins^[86], and deletion of specific T cells only after mucosal administration of massive, non-physiological antigen doses^[87]. Induction of regulatory T cells after mucosal delivery of antigens has been reported and received major attention given the potential of manipulating these regulatory cells as therapeutic agents in immune-mediated diseases^[69].

Regulatory T cells includes: (1) CD4⁺CD45RB^{low} Tr1 cells that function through the production of IL-10 to suppresses antigen-specific T cell responses and actively down-regulates a pathological immune response^[88]; (2)

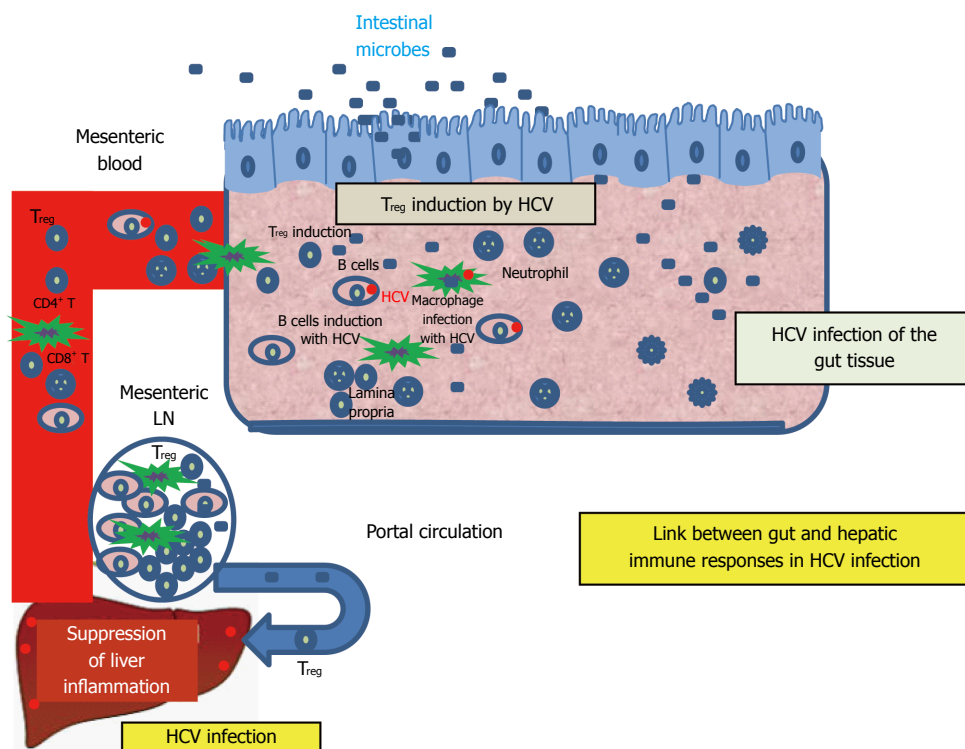


Figure 1 Link between Gut and hepatic immune responses in hepatitis C virus infection. Hepatitis C virus (HCV) replicates in the Gut B cells and macrophages and stimulates Treg cells. Colonic Treg cells migrate to the liver and inhibit immune responses to HCV infection, and inhibit liver inflammation and fibrosis.

T_H3 cell which are $CD4^+$ or $CD8^+$ T cells producing TGF- β with various amounts of interleukin-4 and interleukin-10^[89]; and (3) T_{reg} cells, a population of naturally occurring $CD4^+CD25^+$ regulatory T cells that suppress proliferation through a cell contact-dependent mechanism^[90] followed by cell-contact-independent mechanism mediated by soluble factors such as IL-10 and TGF- β ^[91]. Induction of tolerance is a contact-dependent mechanism used by naturally occurring $CD4^+CD25^+$ T_{reg} to confer suppressive activity upon conventional antigen-specific $CD4^+$ T cells through the expression of the transcription factor Foxp3 and/or the major histocompatibility complex (MHC) class II-binding molecule LAG-3 in such cells^[69,91], and inhibit T cell activation *via* soluble mediators. $CD4^+CD25^+$ T_{reg} cells expressing the mucosal $\alpha 4\beta 7$ integrin, when co-cultured with conventional $CD4^+$ T cells, induced Tr1-like IL-10-secreting T cells with strong suppressor activity on effector T cells. While $\alpha 4\beta 1$ -positive T_{reg} induced T_H3 -like TGF- β secreting suppressor T cells^[91]. Moreover, intraepithelial $CD8^+\gamma\delta$ T cells in the small intestine have been involved in mucosal tolerance and are the first T cells to encounter pathogens that have invaded an epithelial surface^[92].

ROLE OF LIVER IN ORAL TOLERANCE

Although the liver is capable of generating vigorous immune responses to infections such as hepatitis A and hepatitis E viruses, both of which enter *via* the gut, it is also characterized by immune tolerance in several settings^[93,94]. A vigorous intrahepatic immune response

depends on activation of T cells by fully activated DCs within secondary lymphoid tissues whereas direct activation within the liver by resident APCs including endothelial cells and hepatocytes usually results in tolerance^[95]. This is logic, as it allows the liver to tolerate soluble food antigens captured by liver endothelial cells and self-antigens on hepatocytes that fail to cause damage whilst responding appropriately to infections that cause injury, inflammation and full activation of DCs^[67].

Regulatory T cells as well as NK and CD1-restricted NKT cells seem to contribute to the overall bias of hepatic immune responses toward tolerance. The tolerance microenvironment of the liver may account for the survival of liver allografts and the persistence of certain liver pathogens such as hepatitis viruses^[94].

LINK BETWEEN THE GUT AND LIVER IMMUNE RESPONSES DURING HCV INFECTION

The Gut and the liver share common embryological origins; the liver develops from the ventral floor of the foregut as the liver diverticulum from the undifferentiated gut endoderm^[96]. Subsequently, the gut is populated by lymphocyte precursors derived from the developing liver^[97] (Figure 1).

There is an immunologic link between the gut and the liver through a population of T-cells that are capable of homing to both the liver and gut *via* portal circulation^[96]. Additionally, the liver is considered an important

toleragenic organ for all of foreign proteins we are eating that are probably mediated through the T_{reg} cells, which in turn act as a link between the gut and the liver^[67,96]. Most of the infiltrating T-cells in the liver are primed cells suggesting that trafficking of memory T-cells through the liver might contribute to immune surveillance^[98]. Evidence, that supports such findings, comes from observations that the gut adhesion molecules and chemokine (such as CCL25) are also detected on liver endothelium^[99] providing a mechanism for the recruitment of mucosal lymphocytes to the liver^[100].

Evaluation of the gut immune cells for the intrinsic gut-liver immune axis of the shared lymphocytes that recirculate between the gut and liver through the portal circulation may be considered a useful image of the intrahepatic micro-environment during HCV infection. Based on this relationship, the frequency of T_{reg} cells in colonic tissue and its association with the various outcomes of anti-HCV therapy, viral persistence and degree of liver inflammation were examined in our laboratory. Our data indicated that the frequency of colonic T_{reg} in CHC patients is higher than control and our findings are in concordance with previous reports that demonstrated a higher number of FoxP3⁺ T_{reg} cells in the liver of HCV-infected patients compared to healthy control^[47,59,60]. These findings support that T_{reg} plays a prominent role in maintaining the balance between tissue damaging and protective effects of immune responses to HCV.

While attempting to limit viral replication, T-cells inadvertently play a pivotal role in limiting hepatic necro-inflammation and subsequent fibrosis^[28,101-103] by suppressing HCV-specific immune responses^[48]. In our study, we found a significant inverse correlation between the frequency of colonic T_{reg} and liver pathology indicating a role of colonic T_{reg} in controlling the chronic inflammatory response and limit liver damage in CHC infection.

There is still an open question whether T_{reg} cells are protective or harmful in CHC. The effective host anti-HCV immune response may be associated with strong inflammatory reactions and liver damage. To minimize the damage to self, the activation of the immune system also triggers anti-inflammatory pathways through T_{reg} responses. Both inflammatory and anti-inflammatory reactions are normal components of the immune response, which together, fight infections while preventing immunopathology.

TREATMENT OF HCV AND RELATIONSHIP TO IMMUNE RESPONSES

Until 2011, the standard of care for chronic hepatitis C patients was combined treatment with Peginterferon (Peg-IFN) and ribavirin (RBV). The combination of Peg-IFN and RBV induced sustained virologic response (SVR) in 40%-50% of genotype 1 and 80% or more in genotype 2 and 3 infections^[104-106]. The lack of effective regimens across all genotypes and alternative therapeutics for patients who suffered serious side effects prompted basic

science research and numerous clinical trials leading to the development of direct-acting antiviral (DAA) agents. The US Food and Drug Administration approved Telaprevir (TVR) and Boceprevir (BOC) for HCV genotype 1. They inhibit HCV nonstructural protein 3/4A (NS3/4A) serine protease, which is critical for HCV replication. TVR and BOC are approved for use in combination therapies with Peg-IFN-alpha and RBV as they improved SVR rates to 75% and 66% respectively for adult HCV genotype 1 patients with compensated liver cirrhosis^[107]. However, these DAAs incur their own set of severe side effects including anemia, rash, and hyperbilirubinemia. New drugs classified as second-wave protease inhibitors, second-generation protease inhibitors, and polymerase inhibitors are being developed and currently undergoing clinical trials^[108]. The NS5B polymerase inhibitor, sofosbuvir has been recently approved by the FDA for treatment of hepatitis C genotype 1, 2, and 3 patients^[109].

Identifying patients that are likely to achieve SVR versus those that are likely to be non-responders is crucial for disease prognosis, providing optimal therapy, avoiding side effects, and reducing costs associated with Hepatitis C therapy. Since sequencing of the human genome in 2001, advancements along with decrease costs in genotyping technologies have led to investigation of genomic markers associated with a response to Peg-IFN and RBV in patients with chronic hepatitis C. The rs12979860 SNP located on chromosome 19 upstream of the *IL-28B* gene has been identified as a significant predictor of SVR in HCV Genotype 1 chronically infected patients that underwent standard therapy^[110]. The same rs12979860 SNP has the ability to predict natural clearance of the hepatitis C virus^[30]. Genotype C/C at the rs12979860 SNP was associated with a higher likelihood of natural clearance and therapy induced clearance of hepatitis C genotype 1, while T/T genotype was the most unfavorable^[111]. Studies have confirmed that rs12979860 is the strongest predictor of SVR and can effectively predict response to IFN/RBV based therapy^[112]. The mechanisms by which the rs12979860 affects HCV pathogenesis are still unclear. However, it is well-known that the *IL-28B* gene codes for cytokine IL-28B also known as interferon (IFN) λ -3, which belongs to the type III IFN family. IFN- λ is mainly produced by macrophages and DCs in response to viral proteins and plays an important role in antiviral responses to hepatitis C^[30,113]. IFN λ receptors are predominantly expressed on hepatocytes, which may explain its ability to counteract hepatotropic viruses^[114]. Therefore, stimulation of IFN λ receptors on hepatocytes by IFN- λ secreted by DCs induces ISGs^[115] which have the ability to suppress viral replication and protein synthesis of HCV^[116]. Additionally, IFN- λ promotes differentiation of monocyte-derived dendritic cells (DCs) with high PD-L1 expression and further promoted expansion of T_{reg} cells^[117] locally and suppressed the inflammatory responses in the liver. Recent data by our laboratory (Hetta *et al*, 2014 submitted) as well as others^[118] identified a correlation between IL28B SNP rs12979860 genotype TT

s and T_{reg} frequencies. The mechanism responsible for elevated T_{reg} in patients with TT genotype may be related to the precise location of rs12979860 in the promoter region of the *IL-28B* gene. The promoter region plays an important role in gene expression, and the TT genotype might favor increased IL-28B expression in turn resulting in higher T_{reg} frequencies. In support of the relationship between IL-28B phenotypes, T_{reg} frequency, and HCV pathogenesis, recent reports found elevated T_{reg} in acute HCV as a predictor for viral persistence and CHC as well as increased levels of IFN- λ , IL-28, and IL-29 in serum in chronic HCV patients^[117].

The association between IL-28B polymorphism and SVR in genotype 2 and 3 infected patients has produced mixed results making its clinical utility less clear. For instance, one study found IL-28B polymorphism to be associated with SVR in patients infected by genotype 2/3 HCV in whom RVR was not achieved^[119]. On the other hand, in a study of hepatitis C Genotype 3 infected patients, rs12979860 SNP genotype C/C did not correlate with SVR to PEG-IFN/ribavirin therapy^[120]. The majority of studies to this point have focused on IL-28B SNPs in HCV Genotype 1, 2, and 3. The clinical utility of IL-28B testing is probably best served in HCV genotype 1 infected-patients for prediction of outcomes and to limit expenses and side effects associated with IFN-based therapy^[110].

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CD28/CTLA-4/B7 and CD40/CD40L costimulation and activation of regulatory T cells

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Abstract

Costimulatory signals are crucial for T cell activation. Attempts to block costimulatory pathways have been effective in preventing unwanted immune reactions. In particular, blocking the CD28/cytotoxic T lymphocyte antigen (CTLA)-4/B7 interaction (using CTLA-4Ig) and the CD40/CD40L interaction (using anti-CD40L antibodies) prevents T cell mediated autoimmune diseases, transplant rejection and graft vs host disease in experimental models. Moreover, CTLA-4Ig is in clinical use to treat rheumatoid arthritis (abatacept) and to prevent rejection of renal transplants (belatacept). Under certain experimental conditions, this treatment can even result in tolerance. Surprisingly, the underlying mechanisms of immune modulation are still not completely understood. We here discuss the evidence that costimulation blockade differentially affects effector T cells (Teff) and regulatory T cells (Treg). The latter are required to control inappropriate and unwanted immune responses, and their activity often contributes to tolerance induction and maintenance. Unfortunately, our knowledge on the costimulatory requirements of Treg cells is very limited. We therefore summarize the current understanding of

the costimulatory requirements of Treg cells, and elaborate on the effect of anti-CD40L antibody and CTLA-4Ig treatment on Treg cell activity. In this context, we point out that the outcome of a treatment aiming at blocking the CD28/CTLA-4/B7 costimulatory interaction can vary with dosing, timing and underlying immunopathology.

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Key words: Regulatory T cells; Tolerance; Cytotoxic T lymphocyte antigen-4Ig; Anti-CD40L; Costimulation

Core tip: Costimulation blockade (*e.g.*, CD28/B7 and CD40/CD40L blockade) has been successfully used experimentally to induce tolerance to allo- or auto-antigens. Several studies suggest that effector T cells (Teff) and regulatory T cells (Treg) have different requirements regarding costimulation. While blockade of the CD40L receptor does not affect Treg cells and targets Teff cells, the effect of blocking the CD28/cytotoxic T lymphocyte antigen (CTLA)-4/B7 interaction (with CTLA-4Ig) is more difficult to predict and depends on the type, the strength and the stage of an immune process. Importantly, manipulating these costimulatory signals can therefore shift the Treg/Teff cell balance towards dominant Treg cell activity.

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INTRODUCTION

Costimulatory interactions between T cells and antigen presenting cells (APCs), such as the CD28/B7 pathway

and the CD40/CD40L pathway, are essential for T cell activation. As a consequence, reagents that deliberately block those costimulatory signals (*e.g.*, the CTLA-4Ig fusion protein or antagonistic anti-CD40L antibodies) can be used to prevent unwanted or inappropriate T cell activation. Blocking costimulation, therefore, has been used to treat T cell mediated autoimmune diseases, transplant rejection or graft *vs* host disease (GvHD). Although anti-CD40L antibodies showed great potential in pre-clinical animal models and cytotoxic T lymphocyte antigen (CTLA)-4Ig is successfully used in clinical practice to treat rheumatoid arthritis and to prevent rejection of renal transplants, the precise mechanisms underlying their efficacy are still not fully understood. While effector T cells (Teff) clearly depend on costimulation for their activation, the costimulatory requirements of a suppressive T cell population, the regulatory T cells (Treg), are not completely clear. Several studies suggest that Treg and Teff cells have different requirements regarding costimulation. Furthermore, it has been suggested that Treg cells play an important role in the process of tolerance induction by costimulation blockade. In this review we discuss some possibilities to modulate costimulation in such a way that Teff cells are blocked but Treg cells remain active and functional. In this context, we summarize the current understanding of the costimulatory requirements of Treg cells, and elaborate on the effect of anti-CD40L antibody and CTLA-4Ig treatment on Treg cells. We point out that CTLA-4Ig has a quite complex effect on Treg cells, which should be taken into account when interfering with the CD28/CTLA-4/B7 interaction.

MECHANISMS OF PERIPHERAL TOLERANCE

Immune tolerance refers to a state of specific immune non-responsiveness of the immune system to a particular antigen or a group of antigens. Tolerance to self-antigens is a hallmark of an effectively functioning immune system and disabling tolerance to self-antigens can lead to autoimmune diseases. In a similar way, an inappropriate response to a harmless environmental antigen can result in allergies. To avoid such harmful reactions, the immune system has developed several sophisticated mechanisms to induce and maintain tolerance.

During the maturation in the thymus, T cells undergo positive and negative selection. T cells which recognize a self-antigen presented by major histocompatibility complex (MHC) molecules, can be eliminated (negative selection)^[1]. In this process, the signal strength with which the T cell receptor (TCR) recognizes its antigen determines the fate of the T cell. A strong signal and definite recognition of the auto-antigen leads to immediate deletion of the responding cell. A weak signal often leads to ignorance and migration to the periphery^[2]. This is reasonable in order to maintain a pool of variable TCRs in the periphery. However, these cells might regain self-reactivity later on. Furthermore, some T cells escape thymic selec-

tion. Under these circumstances, peripheral tolerance induction should come into action.

Peripheral tolerance is maintained by mechanisms such as anergy (which results from a lack of sufficient activation signals)^[3], deletion by apoptosis^[4,5] and control by regulatory T (Treg) cells. The role of regulatory T cells, as well as the importance of costimulation for the induction and maintenance of peripheral tolerance, will be discussed in the following section.

Costimulatory signals

Naïve T cells need two distinct signals in order to get fully activated^[6]. The first signal is transmitted through the TCR, which recognizes an antigen presented by specialized antigen-presenting cells (APCs) on MHC molecules. This signal determines the specificity of the T cell response. The second (or accessory) signal is provided by the ligation of costimulatory receptors on the cell surface^[7]. Without proper costimulation, T cells fail to become fully activated and enter a state of hypo-responsiveness (anergy)^[8]. Up to now, many costimulatory signals and pathways have been identified, among which the best characterized are the CD28/CTLA-4/B7 pathway and the CD40/CD40L pathway.

The CD28/CTLA-4/B7 interaction: Mice deficient in CD28 are unable to mount an effective immune response to foreign antigens, pathogens or allografts. The CD28 receptor is a disulfide-linked homodimer, which is constitutively expressed on T cells and is engaged by both the CD80 (B7-1) and CD86 (B7-2) molecule on activated APC^[9]. The monomeric CD86 ligand is constitutively expressed in low amounts on professional APC and up-regulated upon activation, while CD80 is expressed as a dimer on activated APC. The up-regulation of CD86 occurs rapidly after activation and reaches its maximum 18 to 24 h after stimulation, while the up-regulation of CD80 is delayed and reaches a maximum after 48 to 72 h^[10,11]. Studies with knock-out (KO) mice have shown that CD86 is more important for initiating an immune response than CD80. Otherwise the functions of the two B7 molecules are largely overlapping^[12]. Signalling *via* CD28 is mediated through the phosphatidylinositol 3-kinase-protein kinase B (PKB/Akt) and the growth factor-receptor-bound protein 2 (Grb2) pathways and promotes IL-2 production^[13] and T cell proliferation^[14] by decreasing the threshold for activation *via* the TCR^[15]. In addition, T cell survival is strengthened by up-regulation of the anti-apoptotic factor Bcl-xL^[16]. CD28 engagement also up-regulates or induces the expression of additional costimulatory receptors such as ICOS and CTLA-4^[17]. While CD28/B7 signalling is crucial for the activation of naïve T cells, previously activated cells are less dependent on costimulation. After priming and differentiation are completed, the production of effector cytokines (*e.g.*, IL-4 or IFN γ) does not require further costimulation. Only IL-2 production depends on continuous costimulatory signalling^[12].

Another receptor molecule, which binds to both B7 molecules and is structurally homologous to CD28, is the “cytotoxic T lymphocyte antigen 4” (CTLA-4) or CD152. It is up-regulated on T cells upon activation with a peak at 24–48 h after initial priming^[18]. However, its expression on the surface is not stable and the CTLA-4 molecule is continuously internalized in a clathrin dependent way, degraded in lysosomes and recycled to the cell surface^[19]. CTLA-4 binds CD80 and CD86 with a 10–20 fold higher affinity compared to CD28^[20] and consequently outcompetes CD28 mediated activation^[21]. Furthermore, CTLA-4 has an advantage in engaging to B7 molecules as it binds divalently, while CD28 binds monovalently^[22]. In contrast to CD28 signalling, the CTLA-4 pathway has a suppressive character, and CTLA-4 deficient mice develop severe lymphoproliferative disease and die 3 to 4 wk after birth^[23]. Of note, CTLA-4 KO mice deficient in B7-1 and B7-2, as well as CTLA-4 KO mice with a defective CD28 receptor are protected from this fatal disease^[24,25]. This suggests that CTLA-4 selectively regulates CD28 mediated activation. Binding of CTLA-4 to its ligands recruits phosphatases (SHP-1, SHP-2 and PP2A), which inhibit TCR phosphorylation and several other pathways such as the PKB/Akt activation as well as the phosphorylation of extracellular-signal-regulated kinases (ERK) and c-Jun N-terminal kinases (JNK)^[26]. This reduces the production of IL-2 and its receptor, inhibits T cell proliferation, and consequently results in termination of the immune response^[18,27].

Other members of the B7 and CD28 superfamilies:

Other members of the B7 superfamily, which have been studied extensively, are the inducible costimulator ligand (ICOSL, CD275, B7h or B7-PR-1), which binds to ICOS (CD278) and the programmed death ligands 1 and 2 (PD-L1 and PD-L2) which binds to programmed death 1 (PD 1). ICOS is structurally and genetically related to CD28 and up-regulated in the course of activation^[28]. ICOSL is expressed on APCs and some non-hematopoietic cells (*e.g.*, endothelial cells). Different from CD28/B7 signalling, ICOS/ICOSL interaction is not essential for T cell activation, but rather acts by fine-tuning effector T cell differentiation and cytokine production^[29]. Furthermore, ICOS is crucial for germinal centre formation and class switching in B cells^[30,31].

PD-1 is a suppressive member of the CD28 superfamily. Different from CD28 and CTLA-4, PD-1 is not expressed as a dimer and its expression is not limited to T cells. It can be found on activated T cells, but also on B cells and myeloid cells, which suggests a broader spectrum of regulation compared to CTLA-4^[32]. Ligation to PD-L1 and PD-L2, which are expressed on activated APCs, inhibits cytokine production and leads to cell cycle arrest^[33,34]. Furthermore, PD-1 signalling was found to be involved in CD8⁺ T cell differentiation and regulation^[35].

The CD40/CD40L interaction: CD40 (TNFRSF5) is a type I trans-membrane protein, which clusters upon en-

gagement to its ligand CD40L (CD154, TNFSF5, gp39, T-BAM, or TRAP)^[36]. CD40 ligation further induces the recruitment of adaptor proteins (TNF-associated factors), which then in turn trigger several possible pathways including the canonical and non-canonical nuclear factor κ B (NF κ B) signalling pathway, the mitogen activated protein kinases (MAPK), the phosphoinositide 3-kinase (PI3K) and the phospholipase C γ (PLC γ) pathways^[37]. CD40 is constitutively expressed on APC and on many other cell types including non-hematopoietic cells (*e.g.*, fibroblasts and epithelial cells)^[38]. CD40L forms a sandwich structure composed of a β -sheet, an α -helix loop and another β -sheet and is expressed as a trimeric complex on activated T cells and platelets^[39]. Under inflammatory conditions it can also be found on natural killer (NK) cells, mastocytes and eosinophils^[38]. Its expression on T cells is mainly restricted to CD4⁺ T helper (Th) cells, but there is also a small population of CD8⁺ T cells and $\gamma\delta$ T cells which can express CD40L^[36]. Furthermore, it has been shown that CD40L is expressed on CD8⁺ T cells in the presence of IL-12 and that these cells potentially represent a CD8⁺ T helper cell subset^[40,41].

Upon activation, CD40L is up-regulated as early as 5 to 15 min after stimulation and reaches a maximum after 6 to 8 h^[36]. This fast up-regulation is made possible *via* preformed CD40L (pCD40L), which is stored in lysosomal compartments and can be mobilised in response to an activation signal^[42].

The broad expression of CD40 suggests involvement in many different immune modulatory mechanisms. In this context, CD40L engagement to CD40 results in increased survival of APC^[43], production of cytokines^[44], up-regulation of B7 molecules and nitric oxide (NO) production^[45] and is critical for full maturation of dendritic cells (DC)^[46]. Furthermore, CD40 signalling is crucial for B cell activation and differentiation, antibody production, immunoglobulin-class switching and germinal centre formation^[47,48]. CD40/CD40L KO mice do not only show hyper-IgM syndrome, but also exhibit deficiency in priming of T cells^[36]. Signalling *via* CD40/CD40L results in enforcement of the CD28-B7 interaction and antigen presentation and is crucial for expansion and maturation of effector T (Teff) cells^[38,49]. Furthermore, CD40/CD40L mediated contact between CD4⁺ T helper cells and professional APC (DC) is important to enable DC to subsequently prime CD8⁺ cytotoxic T lymphocytes (CTL)^[50].

Other members of the TNF and TNFR superfamilies:

Other members of the TNF/TNFR superfamily have gained importance during the last years. Among those are the interactions between the glucocorticoid-induced tumour necrosis factor related receptor (GITR) and its ligand GITR-L, between OX40 (CD134 or TNFRSF4) and OX40 ligand (OX40L, CD252 or TNFSF4), between 4-1BB (CD137 or TNFRSF9) and 4-1BB ligand (4-1BBL or TNFSF9) and CD27 (TNFRSF7) and CD70 (TNFSF7). In general, these

TNF/TNFR superfamily members are up-regulated or induced upon activation on T cells and their ligands on APCs. Signalling *via* these pathways regulates the frequency of effector or memory cells, provides proliferation and survival signals and promotes cytokine production^[51]. The expression of OX40L, 4-1BBL and CD70 on non-immune cells (*e.g.*, endothelial cells or smooth muscle cells) further suggests a role in tissue inflammation in different disease settings^[52,53]. In addition, TNF/TNFR superfamily members are expressed on natural killer (NK) and natural killer T (NKT) cells and signalling increases their effector function^[51].

Regulatory T cells

A subset of CD4⁺ T cells has regulatory capacity. In a healthy individual they constitute about 10% of circulating CD4⁺ T cells. Treg cells play a key role in dampening of immune responses, prevention of autoimmune and allergic diseases, as well as in tolerance after transplantation^[54]. They are characterized by constitutive expression of the IL-2 receptor α -chain CD25, CTLA-4 and the forkhead transcription factor Foxp3^[55,56]. The latter one is crucial for the suppressive function of Treg cells, as ectopic expression of Foxp3 can induce regulatory function in naïve T cells^[57]. Loss of Foxp3 results in impairment of Treg cells and in autoimmune disorders in mice (Scurfy)^[58] and humans (IPEX-syndrome)^[59].

Two subgroups of Foxp3 expressing Treg cells have been identified: the so called thymus derived Treg cells (tTreg) and induced Treg cells (iTreg), which are generated in the periphery from naïve CD4⁺ T cells. *In vitro*, iTreg cells can be induced by antigenic stimulation in the presence of IL-2 and TGF- β ^[60,61]. Although the situation *in vivo* is less clear, iTreg cells are thought to be generated under non-inflammatory conditions in the presence of IL-2 and TGF- β by chronic sub-optimal antigen exposure^[62-64], *e.g.*, by recognition of an antigen on immature DC which do not provide costimulation^[65]. Furthermore, a role for retinoic acid (RA), which increases TGF- β production and favors Foxp3 polarization, has been unraveled^[66,67]. During an acute inflammation (*e.g.*, in allergic or autoimmune diseases or during the course of an infection), in the presence of high amounts of inflammatory cytokines, the generation of Teff cells is favored over Treg cell induction^[68].

Unfortunately it is not yet possible to distinguish tTreg and iTreg cells since both of them express CTLA-4, CD25 and Foxp3. Helios (a member of the Ikaros transcription factor family) and Neuropilin-1 (Nrp1) have been suggested as specific markers for tTreg cells, but controversial findings regarding their expression on tTreg *vs* iTreg cells limit their use as reliable markers^[69-72].

There are also CD4⁺ Treg cell subtypes induced in the periphery which do not express Foxp3. Among those are T regulatory cells 1 (Tr1), which can be induced from naïve CD4⁺ T cells in the presence of IL-10^[73] and T helper cells type 3 (Th3), which require TGF- β ^[74]. Up to now, it is difficult to identify those Treg cell subsets by

means of a specific surface marker. Therefore, they are predominantly defined by their cytokine profile. Tr1 cells are characterized by a high IL-10 and TGF- β production, low levels of IL-2, variable levels of IL-5 and IFN- γ and no IL-4^[73]. Th3 cells produce mainly TGF- β and variable levels of IL-10 and IL-4^[75].

Activation and expansion of Treg cells requires a TCR signal *in vitro*^[76,77] and *in vivo*^[78,79] and is consequently antigen specific. Whether or not they suppress in an antigen-specific way is still a matter of debate. A key molecule in suppression by Treg cells is CTLA-4. Mice which display a Treg-specific deficiency in CTLA-4 develop severe autoimmune diseases, and Treg cells from these mice show reduced suppressive capacity *in vitro*^[80]. In contrast to conventional T cells, Treg cells express CTLA-4 constitutively^[81] and therefore have a natural advantage over naïve T cells in terms of CD80/CD86 engagement. In addition, CTLA-4 expressed by Treg cells also has a cell-extrinsic mechanism of action. It has been demonstrated by Qureshi and coworkers that CTLA-4 engagement to the B7 molecules leads to trans-endocytosis and degradation of CD80 and CD86 on the surface of APCs^[82]. This effect can only be mediated by CTLA-4 expressed on the cell surface, but not by soluble CTLA-4. As a result, the availability of B7 receptors and consequently the CD28 mediated activation of T cells are reduced. Moreover, CTLA-4/B7 interaction might lead to “reverse signalling” in APC. In the course of CTLA-4 engagement, APC start to produce indoleamine 2,3-dioxygenase (IDO), which catalyses the degradation of tryptophan and thus creates a local inhibitory environment for T cells^[83]. This also induces the nuclear translocation of the transcription factor Foxo3^[84], which inhibits the production of IL-6 and of tumor necrosis factor alpha (TNF α) but increases the secretion of suppressive cytokines such as IL-10^[85]. Apart from mechanisms mediated by direct cell contact to APCs, Treg cells also secrete suppressive molecules such as IL-10^[86], TGF β ^[87] and IL-35^[88] and molecules which can directly kill Teff cells, such as granzyme B and perforin^[89]. Membrane-bound TGF β ^[90] or production of cyclic adenosine monophosphate (cAMP), which can be transferred to Teff cells *via* gap junctions, can suppress Teff cells *via* direct cell-cell contact^[91]. Other suppressive mechanisms involve CD39 and CD72 mediated degradation of adenosine monophosphate (AMP) and adenosine triphosphate (ATP) to adenosine^[92] or suppression by Galectin-1^[93]. Finally, Treg cells are thought to suppress Teff cells by IL-2 deprivation and subsequent apoptosis^[94]. IL-2 is crucial for Treg cell generation, induction and maintenance^[95], but, in contrast to Teff cells, Treg cells lack the ability to produce IL-2 and are consequently dependent on an external source^[96]. Since Treg cells constitutively express the high affinity receptor for IL-2 (CD25)^[55], they have an advantage over Teff cells in terms of binding IL-2. In an inflammatory setting, however, when Teff cells also up-regulate CD25, this advantage is lost. Therefore, it was suggested that suppression by IL-2 consumption is predominantly important

in steady-state conditions as a feed-back mechanism to prevent Treg cell overgrowth and not in an inflammatory setting^[97].

Since none of the above described mechanisms results in a complete absence of regulatory activity when deleted, there is most likely not one core-mechanism of suppression. In this context, Treg-specific CTLA-4 deficiency resulted in systemic autoimmune diseases^[80], but transfer of CTLA-4 deficient Treg cells could prevent experimental colitis *in vivo*^[98] and IL-10 deficient Treg cells are able to suppress auto-immunity, but cannot prevent experimental colitis^[86,99]. Thus, Treg cells can compensate for defects and adapt to environmental circumstances.

THE EFFECTS OF BLOCKING COSTIMULATORY SIGNALS

Since the “second” or “costimulatory” signal is of great importance for the activation and successful differentiation of naive T cells into fully functional Teff cells^[6], blocking these pathways presents a promising approach to treat T cell mediated autoimmune diseases (*e.g.*, rheumatoid arthritis or multiple sclerosis), transplant rejections or graft *vs* host disease (GvHD). Compared to conventional immunosuppressive drugs, costimulation blockade provides the advantage of selective inhibition of T cell responses and has the potential of inducing long-lasting antigen-specific tolerance^[100]. The most promising and best studied candidates for such manipulations are the CD28/B7 and CD40/CD40L pathways as they are both critical for T cell activation.

Blocking the CD28/B7 pathway using CTLA-4Ig

Up to now, the most promising candidate to achieve CD28/B7 costimulation blockade is the CTLA-4Ig fusion protein. It consists of the extracellular domain of the CTLA-4 molecule fused to the Fc-region of IgG. CTLA-4Ig binds both B7 molecules with the same high binding affinity as CTLA-4. The effect of CTLA-4Ig has first been demonstrated in an animal model of islet transplantation, where CTLA-4Ig treatment led to long-term acceptance of xenografts^[101]. Also in systems of allogeneic islet or cardiac transplantation or graft *vs* host disease (GvHD), CTLA-4Ig could prolong survival and reduce rejection^[102-104]. Furthermore, CTLA-4Ig is a potent immunosuppressor in animal models of autoimmunity such as experimental autoimmune encephalomyelitis (EAE)^[105], diabetes^[106] and systemic lupus erythematoses (SLE)^[107].

CTLA-4Ig has also been used effectively in clinical trials. Davies and co-worker showed that tolerizing bone marrow cells *ex vivo* in the presence of CTLA-4Ig prior to transplantation to a MHC-matched recipient reduces the incidence of acute and chronic GvHD^[108]. Furthermore, CTLA-4Ig (abatacept) treatment in combination with cyclosporin and methotrexate prevents acute GvHD after hematopoietic cell transplantation from an unrelated donor^[109]. Since 2005, CTLA-4Ig (abatacept) is approved by the FDA for the treatment of rheumatoid arthritis (RA)^[110]

and a second-generation molecule (belatacept) with higher binding affinity for B7-1 and B7-2 was approved in 2011 to prevent rejection after renal transplantation^[111].

Blocking the CD40/CD40L pathway

Antagonistic anti-CD40L monoclonal antibodies (mAb) have shown impressive effects in many animal models. Blocking CD40L prevents acute and chronic GvHD^[112]. If given at the time of transplantation, anti-CD40L treatment prolongs graft survival in a model of heart, islet, liver and limb transplantation^[113-116]. Targeting the CD40L receptor proved to be efficient in animal models of autoimmune diseases such as EAE, arthritis, SLE, colitis and arteriosclerosis^[117]. However, clinical trials with an anti-CD40L mAb (Ruplizumab) in SLE patients have led to thromboembolic side-effects and had to be halted^[118]. This effect was caused by the Fc-fragment of the antibody bound to a receptor on platelets which also express CD40L. Nonetheless, the findings in animal systems are extremely promising and, consequently, it is attempted to find alternative ways to achieve CD40L blockade. mAb with an engineered, aglycosylated or mutated Fc-part were created^[119-121]. The modifications alter the antibody in a way that Fc-receptor or complement mediated platelet aggregation and subsequent thromboembolic events are prevented. Furthermore, alternative blocking reagents such as small molecules or peptides are currently explored^[122,123].

The CD40/CD40L interaction can also be interrupted by targeting the CD40 receptor. A human antagonistic anti-CD40 antibody showed some effect in *ex vivo* studies^[124,125] and proved to be safe in a Phase I clinical trial on lymphocytic leukaemia patients^[126]. Another antagonistic anti-CD40 antibody, chimeric 5D12, was tested successfully in an EAE model in marmoset monkeys^[127]. Furthermore, we showed that 5D12 was well tolerated in a phase I clinical trial in patients with Crohn's disease^[128]. However, CD40 is expressed on many different cell types and consequently targeting this molecule might have broad and undesired effects. Additionally, most antibodies directed against CD40 are stimulatory for APC and B cells by cross-linking the trimeric receptor.

Combined blockade of the CD28/B7 and the CD40/CD40L pathway

Although CTLA-4Ig and anti-CD40L antibodies show great potential in various disease models, the combination of both is often superior. It is indeed possible that in the absence of CD40L or CD28 triggering, the T cell can still receive sufficient activation signals from other costimulatory pathways^[129,130]. Especially in animal models of solid organ transplantation, combined blockade of CD28/B7 and CD40/CD40L is required for permanent tolerance induction in mice^[131] and non-human primates^[132]. Also, in animal models of leukaemia^[133] or autoimmune diseases such as EAE^[134] and SLE^[135], the combination of CTLA-4Ig and MR1 (an anti-CD40L mAb) could more effectively reduce disease symptoms than both alone.

We made similar observations in a fully MHC mismatch model of GvHD with allogeneic bone marrow transfer. In our study, only the combined blockade of the CD28/B7 pathway (using CTLA-4Ig) and the CD40/CD40L pathway (using MR1) prevented lethal GvHD and resulted in long-lasting tolerance and the induction of stable mixed chimerism^[136].

Mechanisms of suppression by CD28/CTLA-4/B7 and CD40/CD40L blockade

The mechanisms of tolerance induction by costimulation blockade, in particular of the CD28/CTLA-4/B7 and the CD40/CD40L interaction, have extensively been studied in allo-responses such as GvHD or transplant rejection. In these settings, deprivation of necessary activation signals (CD28 and/or CD40 triggering) leads to T cell hypo-responsiveness^[8], which is followed by peripheral clonal deletion^[136,137]. Elimination of the hypo-responsive T cells is predominantly mediated by apoptosis^[138-140]. In a fully miss-matched transplantation model, the tolerising effect of combined CD28/B7 (using CTLA-4Ig) and CD40/CD40L (using MR1) blockade can be reversed by the calcineurin inhibitor cyclosporine A (CsA), which prevents apoptosis^[138]. In contrast, rapamycin (which favours apoptosis) acts synergistically with costimulation blockade. While activation induced cell death (AICD) seems not to be essential, passive cells death is crucial for the induction of tolerance under the cover of CTLA-4Ig and MR1. Heart allografts were rejected in Bcl-xL deficient mice despite costimulation blockade^[139], but Fas-deficiency was not able to break tolerance^[140]. Additionally, CTLA-4Ig has been suggested to act *via* reverse signalling to APCs and to induce IDO production, which contributes to creating a suppressive environment^[141].

THE ROLE OF TREG CELLS IN IMMUNE SUPPRESSION BY COSTIMULATION BLOCKADE

Although apoptosis of Teff cells after activation in the absence of costimulatory has been demonstrated by many research groups, complete deletion of responsive T cells takes several weeks^[137] while tolerance can already be observed shortly after treatment^[142]. In this context, it has been demonstrated by the group of Waldmann that CD4⁺ cells, which have been tolerized to allo-antigens by CD40L blockade, are not only hypo-responsive but moreover display a suppressive function^[143,144]. Therefore, it has been suggested that Treg cells, at least partially, mediate tolerance until Teff cells have been eliminated. In line with this, it has been demonstrated that tolerance induction by CD40L or B7 blockade is abrogated when Treg cells are depleted. In a study performed by Taylor and co-workers, CD4⁺ cells were tolerized to allo-antigens *ex vivo* in the presence of antagonistic anti-CD40L or anti-B7 antibodies. Transfer of these cells to animals suffering from GvHD did abrogate the disease. However,

if Treg cells were depleted prior to the transfer, GvHD was not suppressed^[145]. Also, long-term acceptance of a skin or a heart allograft under the cover of CD40L blockade could be abrogated if recipient Treg cells were depleted^[146,147]. However, Kurtz *et al.*^[148] showed that it is possible to induce mixed chimerism after allogeneic bone marrow transplantation under the cover of CD40L blockade, but they did not find evidence for an involvement of Treg in this system. In line with this, we have previously shown in a model of GvHD with allogeneic bone marrow transplantation that tolerance induction by combined CD40/CD40L and CD28/B7 blockade and the development of mixed chimerism are still possible despite the absence of donor Treg cells^[136]. In both studies T cell hypo-responsiveness and deletion were the main mechanisms by which tolerance was achieved. The importance of Treg cells for tolerance induction by costimulation blockade thus might depend on the disease model. The recipient Treg cells might be important in the setting of a solid organ transplant, while in GvHD the presence of Treg cells within the donor cell transplant might not be crucial for the outcome of the disease.

Costimulatory requirements of Treg cells

Involvement of Treg cells in tolerance induction by costimulation blockade implies that Teff cells and Treg cells have different requirements regarding costimulation. Such different requirements could result in differential modulation of Teff cells and Treg cells by costimulation blockade. Both cell types share the TCR-mediated recognition of an antigen as the first signal for activation. However, the costimulatory requirements for Treg cells are less clear than those for Teff cells (Figure 1). CD28/B7 signalling is crucial for thymic Treg cell generation and homeostasis since mice deficient in CD28 or B7 molecules have a significantly reduced number of Treg cells in the thymus as well as in the periphery^[149,150]. CD40L and glucocorticoid-induced tumour necrosis factor related receptor (GITR) signalling also play an important role during thymic development of Treg cells^[151-153]. Whether CD28 and/or CD40L costimulation is equally important for the activation or the induction of Treg cells in peripheral lymphoid organs as it is for Teff cells, however, is still a matter of debate. We have shown that blocking the B7 molecules using anti-B7-1 and anti-B7-2 antibodies in combination with an antagonistic anti-CD40 antibody resulted in human T cell hypo-responsiveness *in vitro*. This effect was associated with the induction of a T cell subset with suppressive activity, which expressed high levels of ICOS and produced IL-10^[154]. Furthermore, we have shown that the beneficial effect of combined CTLA-4Ig and MR1 treatment in a mouse model of GvHD is associated with an increase in the frequency of Foxp3⁺ Treg cells between day 6 and 30 after T cell transfer^[136]. Both findings argue for costimulation independent Treg induction and expansion. We further conducted a more detailed examination of the effect of CTLA-4Ig and MR1 on murine Treg cells *in vitro*. Here, we showed that Treg cells can proliferate

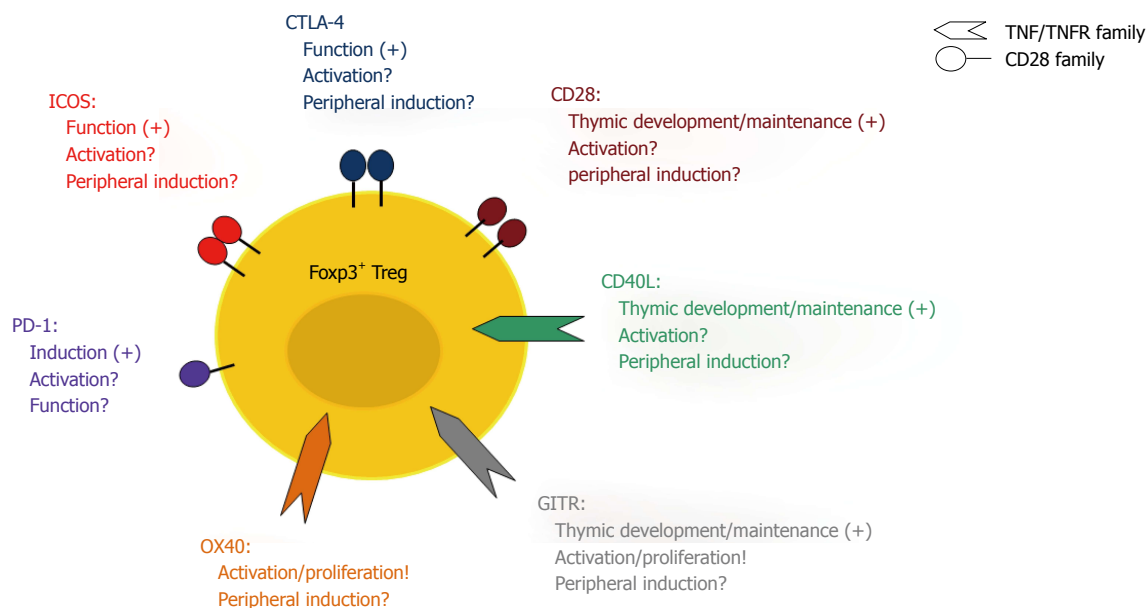


Figure 1 Costimulatory requirements of Foxp3⁺ Treg cells. Treg cells, similar to Teff cells, depend on T cell receptor (TCR)-mediated recognition of an antigen for activation (signal 1). The requirements of Treg cells regarding the second, costimulatory signal are less clear. The exact pathways and necessary signals are still a matter of debate. So far, it is well established that Treg cells depend on CD28 and CD40L for their thymic development. Also, glucocorticoid-induced tumour necrosis factor related receptor (GITR) is stabilizing Foxp3 expression during maturation in the thymus. In order to get properly activated and to proliferate, triggering of OX40 and GITR, in concert with IL-2, was reported to be crucial. The induction of iTreg cells in the periphery is promoted by PD-1 signalling. The function of Treg cells depends on cytotoxic T lymphocyte antigen (CTLA)-4 and ICOS. See text for more details and references.

and be activated if CTLA-4Ig and MR1 were added to the cultures at a dose where Teff cells are inhibited^[155]. Also other laboratories, in which the blockade of the CD28/B7 and/or the CD40/CD40L interaction was studied, have observed an increase of functional Treg cells *in vitro*^[145,156]. Furthermore, a selective non-cross-linking CD28 antagonist induced tolerance to renal and cardiac allografts in non-human primates and this was associated with an increased frequency of Foxp3⁺ Treg cells^[157]. In a mouse model of heart transplantation under the cover of an anti-CD40L mAb, Treg cell were functional and crucial to prevent rejection^[147]. Altogether, these findings suggests that Treg cells are less dependent on CD28/B7 and CD40/CD40L costimulation compared to Teff cells and can therefore still be activated and expand in the presence of CTLA-4Ig and MR1.

However, Treg cells are probably not completely independent of CD28/B7 and CD40/CD40L costimulation. In this context, we showed that the increase in the Treg cell frequency *in vitro* observed in the presence of CTLA-4Ig and MR1 is dependent on the concentration of the blocking agents. While a low dose of CTLA-4Ig and MR1, ranging between 0.125 µg/mL and 4 µg/mL, resulted in a concentration dependent increase in the frequency of Treg cells, a higher dose (between 8 µg/mL and 32 µg/mL) resulted in a concentration dependent decrease in the frequency of the Treg cells (manuscript in preparation). Thus, at a very high dose of costimulatory blocking agents, Treg cells also seem to be affected. We further explored this issue in a mouse model of GvHD. A treatment regime using 500 µg (per mouse) of CTLA-4Ig (in combination with MR1) was equally effective as a

10 times lower dose in preventing the disease. However, intermediate doses had no effect on survival. Again, the treatment with a low dose of CTLA-4Ig, but not with a high dose, was followed by an increase in Treg cell frequency (manuscript in preparation). This observation can potentially be explained assuming two separate mechanisms of action (Figure 2): treatment with a high dose blocks all the Teff cells (but also the Treg cells) and therefore prevents the disease. At a low dose, however, not all the Teff cells are blocked, but Treg cells remain activated and are able to suppress the remaining Teff cells. Intermediate doses are not effective, most likely because not all the Teff cells are blocked while at the same time Treg cells are affected and therefore not able to suppress Teff cells. It is possible that Treg cells need the same costimulatory signals as Teff cells, but have a lower threshold for activation. Another possibility is that a low dose of CTLA-4Ig and MR1 only partially blocks the Teff cells, which produce low amounts of IL-2. As Treg cells can take up IL-2 more efficiently than Teff cells due to the constitutive expression of the high affinity IL-2 receptor (CD25)^[95], the low amounts of IL-2 might be sufficient to maintain Treg cells but not enough to allow for Teff cell priming and activation. This issue will have to be examined more closely in the future. If IL-2 and not costimulation is the limiting factor for Treg cell activation, expansion of Treg cells can be facilitated by adding exogenous IL-2.

Other costimulatory pathways have been suggested to be relevant for Treg cell activation and function. Triggering GITR on Treg cells increases their proliferation and enforces their suppressive activity^[158]. Blocking the

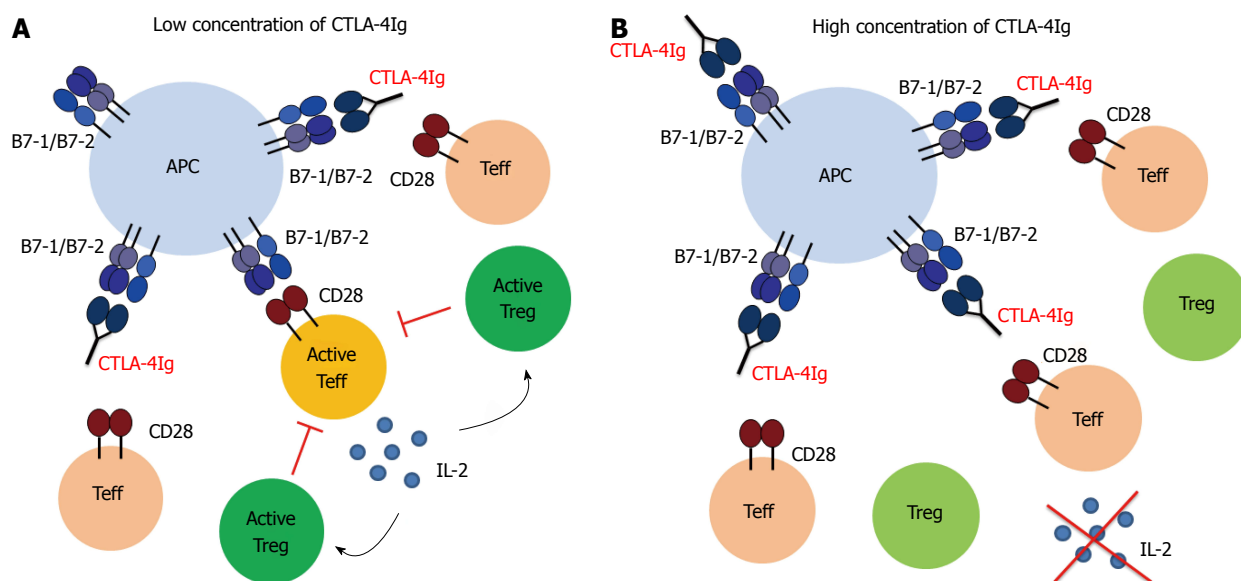


Figure 2 The potential effects of a cytotoxic T lymphocyte-associated antigen-4Ig treatment started before T cell priming. If cytotoxic T lymphocyte antigen (CTLA)-4Ig is given before T cell priming at a low dose, it reduces CD28 mediated T cell activation. Since blockade of B7 molecules is not complete, some Teff cells are still activated and produce interleukin (IL)-2. Treg cell-activation is less or not dependent on CD28 signalling and the low amounts of IL-2 produced by the Teff cells are sufficient to maintain Treg cell activation. In that way activated Treg cells further suppress the remaining Teff cells. The effect of CTLA-4Ig is in this situation based on down-regulation of Teff cells and maintenance of Treg activity (A). If CTLA-4Ig is given at a high concentration, Teff and Treg cells are equally suppressed due to missing costimulation and/or IL-2. The effect of CTLA-4Ig is in this case based on reduced Teff cell activity (B). APC: Antigen presenting cell, Teff: effector T cell, Treg: Regulatory T cell.

ICOS/ICOSL interactions in a model of ovalbumin (OVA) induced airway inflammation^[159] and EAE^[30] abrogated Treg activity *in vitro* and *in vivo*. An antagonistic anti-PD-1 antibody can prevent the induction of Treg cells from naïve CD4⁺ T cell *in vitro*, which suggests that PD-1 signalling is important in this process^[160]. Defects in or blockade of CTLA-4 leads to uncontrolled expansion of Treg cells, which suggests a cell-intrinsic effect of CTLA-4 triggering on Treg cells and an important role for CTLA-4 in regulating Treg generation in the thymus and in the periphery^[161,162]. Also, CTLA-4 regulates the TCR specificity during thymic development as over-expression of CTLA-4 leads to a self-skewed TCR repertoire whereas deficiency of CTLA-4 prevents the development of a self-skewed TCR repertoire^[163]. There is also evidence that CTLA-4 signalling is involved in the induction of Foxp3 in naïve T cells and promotes generation of iTreg cells in the periphery^[164]. In addition, CTLA-4 is a key mediator in suppression by Treg cells as described before. Recently, the OX40/OX40L pathway has come into focus with regard to Treg cell activation and proliferation. OX40 triggering acts in concert with IL-2 and leads to extensive Treg cell expansion. In the presence of IL-2, these cells are stable and show potent suppressive activity^[165].

The effect of CD40/CD40L blockade on Treg cells

A large body of evidence including our own studies suggests that Treg cells are not affected by CD40/CD40L blockade^[120,136,143-147,155]. Although Treg cells require CD40L signalling during their development in the thymus^[152,153], only about 4%-9% of Treg cells express

CD40L in the periphery^[166]. Up-regulation of CD40L in Treg cells upon activation is delayed compared to Teff cells, which express CD40L within the first 5 to 15 min after activation^[136]. This fast up-regulation is made possible through the storage of preformed CD40L (pCD40L). Treg cells, on the other hand, are incapable of storing pCD40L and consequently have to generate it *de novo*^[42,166]. Altogether this suggests that Treg cells are indeed not dependent on CD40L signalling concerning their activation. Therefore, CD40L blockade provides a promising target to modulate the balance between Treg cells and Teff cells in favour of Treg cell activity.

The effect of CTLA-4Ig on Treg cells

CTLA-4Ig has been proven to be very effective as an immunosuppressive treatment in various animal models and is successfully used in the clinic to treat rheumatoid arthritis (abatacept) and rejection after renal transplantation (belatacept)^[110,111]. However, recent findings have raised concern about the use of CTLA-4Ig in systems where Treg cells are crucial for the success of the therapy. Riella and co-workers showed that CTLA-4Ig accelerates transplant rejection in a MHC class II mismatch model, in which tolerance induction and graft survival is crucially dependent on Treg cell function^[167]. Furthermore, in a study in which rejection of a skin transplant could be prevented by expansion of Treg cells using IL-2/anti-IL-2 complexes, simultaneous administration of CTLA-4Ig could break tolerance induction^[168]. As mentioned before, we have observed a dose dependent effect of CTLA-4Ig on Treg cells (manuscript in preparation). It is possible that the amount of CTLA-4Ig applied was indeed high

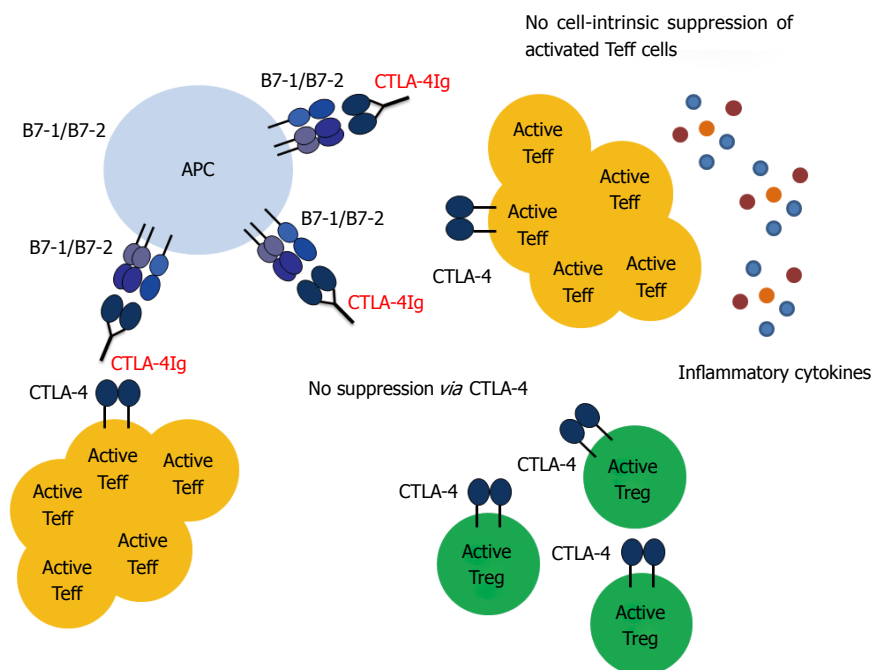


Figure 3 The potential effects of cytolytic T lymphocyte-associated antigen-4Ig treatment given after T cell priming. If cytolytic T lymphocyte antigen (CTLA)-4Ig is applied after priming when T cells are already activated, it mainly interferes with the CTLA-4/B7 interaction. This interaction is important for cell-intrinsic down-regulation of Teff cells. In the absence of this cell-intrinsic regulation, activated Teff cells proliferate more strongly and secrete more inflammatory cytokines. Furthermore, Treg cells are not able to exert their suppressive function mediated via CTLA-4. Both effects will potentially result in further increase of the T cell mediated inflammation. APC: Antigen presenting cell; Teff: Effector T cell; Treg: Regulatory T cell.

enough to interfere with the Treg cells. Especially in a model where Treg cells are crucial for the outcome of the disease, a high dose might be less effective than a low dose which spares the Treg cells.

The differential sensitivity of Treg cells vs Teff cells to CD28/CTLA-4/B7 blockade is certainly not the only problem that might arise from CTLA-4Ig treatment. Another factor that has to be considered is that CTLA-4Ig does not only interfere with the CD28/B7 signaling but also with the CTLA-4/B7 signaling (Figure 3). CTLA-4 is expressed on activated Teff cells and constitutively on Treg cells, and triggering of membrane CTLA-4 leads to suppression of the corresponding T cell^[18,20]. This holds true for Teff cells as well as for Treg cells^[169]. Since Treg cells express CTLA-4 constitutively, CTLA-4Ig administration during priming will presumably prevent CTLA-4 mediated cell-intrinsic suppression of Treg cells and will therefore enhance their activity. In addition, CTLA-4Ig engagement to the B7 ligands leads to reverse signalling to the APCs, which results in IDO production^[141]. Both mechanisms thus result in the creation of a suppressive environment. However, CTLA-4 is also a key molecule for Treg cell function^[81]. Our above mentioned data argue against interference of CTLA-4Ig with Treg cell activation, but do not exclude interference with Treg function or induction. In this context, blockade of the B7 molecules with CTLA-4Ig prevents CTLA-4 mediated trans-endocytosis and degradation of the B7 molecules by Treg cells as well as “reverse signalling” via CTLA-4/B7 signalling and IDO production. Moreover, if CTLA-4Ig is given after T cell priming, Teff cells will also have up-

regulated CTLA-4 and by blocking B7 molecules, the cell-intrinsic suppression of Teff cells might be blocked. This is not relevant in a setting of transplantation, when it is exactly known when T cell priming occurs. However, for patients with autoimmune diseases such as multiple sclerosis (MS), the situation is different. It is not possible to predict disease onset or a relapse episode and therefore it is not known when auto-reactive T cells are primed and activated. In such settings it might be dangerous to apply CTLA-4Ig treatment. Indeed, we have found in a model of experimental autoimmune encephalomyelitis (EAE), the mouse model for the human disease MS, that treatment with CTLA-4Ig after T cell priming leads to exacerbation of the disease. This is most likely due to interference with the CTLA-4/B7 mediated suppression (manuscript in preparation). Further studies will be required to examine if this exacerbation is a result of missing cell-intrinsic suppression of the Teff cells, interference with Treg cell function and *de novo* induction or both.

CONCLUSION

Based on the above discussed studies and our own results we believe that it can be possible to modulate costimulation in such a way that Teff cell activation is prevented but Treg cells can still be activated. Especially blockade of the CD40/CD40L pathway provides a promising target to manipulate the Teff/Treg cell balance in favor of Treg cell activity. However, blockade of the CD40/CD40L interaction alone is not always sufficient to guar-

antee full protection. Therefore, CD40/CD40L blockade must be combined with CTLA-4Ig in order to prevent CD28 mediated activation. Several factors have to be taken into account when using CTLA-4Ig as a treatment option. First, if CTLA-4Ig is given before T cell priming (*e.g.*, in a transplant setting), the dose of the reagent is an important factor. A high dose of CTLA-4Ig can also affect the Treg cells. Careful titration is required to find the optimal dose that blocks Teff cells but spares the Treg cells (Figure 2). This might be of great importance if Treg cells are crucial for the success of the therapy. Second, it has to be considered whether CTLA-4Ig is given before or after T cell priming. CTLA-4Ig treatment after T cell priming might be dangerous as it can interfere with CTLA-4 mediated suppression (Figure 3). This can affect cell-intrinsic suppression of the Teff cells and/or affect Treg cell function and induction. Third, knowing the pathophysiology of the disease (especially concerning involvement of Treg cells) is crucial in order to find a balance between maximal suppression of Teff cells and minimal interference with Treg cells.

It will be important to more closely study the costimulatory requirements of Treg cells and the effect of blocking those signals on their activity. This will help to improve the success of a therapy involving costimulation blockade. Especially when using CTLA-4Ig, it will be necessary to know exactly which effect the treatment has in the corresponding disease setting in order to prevent undesired effects. Furthermore, the finding that Treg cells and Teff cells respond differently to costimulation blockade can potentially be exploited in a context of Treg cells based therapy. Treg cells can be expanded *in vitro* or perhaps even *in vivo*, while the outgrowth of Teff cells is prevented under the cover of costimulation blockade.

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Immunopathogenesis of reactive arthritis: Role of the cytokines

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Abstract

Reactive arthritis (ReA), also known as sterile postinfectious arthritis, belongs to the group of related arthropathies known as spondyloarthritis (SpA). ReA can arise 1-4 wk after a gastrointestinal or genitourinary infection, but once arthritis develops, the microorganism is not found in the joint. The classical microbes associated with ReA development include Gram-negative aerobic or microaerophilic bacteria containing LPS in their outer membrane. The immunopathogenic mechanisms involved in ReA development are still unknown. A hypothesis suggested that the bacteria probably persist outside the joint, at sites such as gut mucosa or lymph nodes, and bacterial antigens might then be transported to the joints. On the other hand, an altered immune response and the unbalanced production of cytokines have been reported in subjects with ReA. Cur-

rently, there is increased evidence to suggest that both mechanisms would operate in the immunopathogenesis of ReA. In this review we highlight recent advances on the role of cytokines in the ReA. Particularly, we discuss the roles of some pro- and anti-inflammatory cytokines involved in the immunopathogenesis of ReA.

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Key words: Reactive arthritis; Cytokines; Immunopathogenesis; Infection; Interleukin-17; Interleukin-12; Interleukin-23; Interleukin-6; Tumor necrosis factor- α ; Interleukin-10

Core tip: The immunopathogenic mechanisms involved in reactive arthritis (ReA) development are still unknown. However, in the last years, increased evidence suggests that the immune response in particular certain cytokines could be involved in the pathogenesis of ReA. Currently, the use of biological agents that block the action of certain cytokines has contributed to improving the treatment of some rheumatic pathology. Understanding the role of cytokines in the pathogenesis of ReA could contribute to the development of future treatments. In this review, we highlight recent advances on the role of certain cytokines in the pathogenesis of ReA.

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INTRODUCTION

Reactive arthritis (ReA), also known as sterile postinfectious arthritis, belongs to the group of related arthropathies known as spondyloarthritis (SpA)^[1]. This group

also includes undifferentiated SpA, psoriatic arthritis (PsA), arthritis associated with inflammatory bowel disease and ankylosing spondylitis (AS). The SpA arthropathies have common several epidemiological, pathological, clinical and radiological features. ReA, as with other SpA, exhibits an absence of rheumatoid factor and has a genetic association with the molecule HLA-B27^[1-3]. ReA can arise 1-4 wk after a gastrointestinal or genitourinary infection, but once arthritis develops, the microorganism is not found in the joint^[2]. The ReA symptoms were recognized and studied in 1942 by Bauer and Engelmann, who associated these symptoms with those described in 1916 by the German physician Hans Reiter. At that time, Reiter described the clinical triad: arthritis, non-gonococcal urethritis and conjunctivitis in a German soldier after an episode of bloody diarrhea. So, Bauer and Engelmann coined the term Reiter's syndrome to describe this new pathology^[2]. However, most patients do not have the complete triad of symptoms. These observations drove Ahvonen to propose the name of ReA as the term most adapted to describe the "arthritis that happens during or after an infection in another site of the body without evidence of microorganisms in the joint"^[4]. Yet, this operational definition of ReA has led to uncertain diagnosis in different clinical settings. Thus, several attempts have been made to create classification criteria; however, lack of consensus has led to a failure to achieve any universally validated diagnostic criteria. Based on discussions at the 4th International Workshop on ReA, this term should be used only in patients with clinical features of ReA and in cases where a pathogen known to cause ReA is implicated^[5].

CLINICAL FEATURES

ReA most commonly affects young adults aged 20 to 40 years old and is rare in children^[6-8]. Both sexes are equally affected by ReA after a gastrointestinal infection, while ReA is more frequent in men when triggered by a urogenital tract infection^[3]. The presence of the HLA-B27 allele does not seem to be related to the onset of ReA; however, HLA-B27 positive patients have more severe arthritis with a tendency to progress to a chronic stage and they also have a greater chance of developing extra-articular symptoms. One hypothesis suggests that this molecule favors the cross-reaction between antigen and host, or it might be itself a target of the immune response^[9].

The symptoms of ReA typically start between 1 to 4 wk after the gastrointestinal infection. However, the triggering infection could be asymptomatic, such as *Chlamydia*-induced ReA, resulting in underdiagnosis^[2]. Clinical features of ReA are characterized by asymmetrical oligoarthritis, often in large joints of the lower extremities or in the upper extremities. A mild polyarticular form, particularly in the small joints, can also occur. Patients can have dactylitis. The typical extra-articular manifestations

are enthesitis, tendinitis and bursitis. ReA share these clinical characteristics and inflammatory back pain with other members of SpA, such as AS and PsA^[1]. Other extra-articular features include eye disease, where conjunctivitis is most prevalent, followed by acute anterior uveitis, and skin changes, such as erythema nodosum, keratoderma blennorrhagica and circinate balanitis^[3].

The clinical diagnosis is made based on the clinical symptoms. Evidence for infection triggering the arthropathy is most convincing when microbe isolation or antigen detection is successful. In this respect, fecal culture of enteric pathogens associated with ReA or the finding of *Chlamydia trachomatis* nucleic acids in urine, cervical or urethral swabs are secondary criteria used to confirm the diagnosis.

Animal models

Animal models of ReA have complemented studies in human materials. However, these animal models are limited since even when they are developed after bacterial infection as in human ReA, in some of them the route of infection was intravenous instead of oral. Table 1 shows animal models of ReA similar to the human form of the disease^[10-17]. We have described an experimental model useful for studying the pathogenesis of *Yersinia enterocolitica* (*Y. enterocolitica*) ReA. In our model, TNFRp55 deficient mice develop ReA after oral infection with *Y. enterocolitica* O: 3, the most common serotype associated with human ReA. *TNFRp55*^{-/-} mice exhibited macroscopic signs of severe and progressive arthritis with significantly higher clinical score compared with wild-type mice from d 14 to 56 after infection^[14]. Extensively, increased scores for inflammation and bone/cartilage degradation resulted when histopathological changes were analyzed in the joints. In these animals, we observed luminal disorganization of the synovial membrane, which was densely infiltrated with various types of leucocytes, sometimes concomitant with follicle formation. The articular cartilage and bone were degraded. Proliferation of synovial lining cells was also detected^[14,15]. This evidence and the data presented in Table 1 indicate ReA development in animal models that resemble this disease in humans. Nevertheless, the convergence of these models with human studies will contribute to understand the pathogenic mechanisms of ReA.

TRIGGERING BACTERIAL AND PATHOPHYSIOLOGY

The classical bacteria associated with gastrointestinal ReA are *Yersinia*, *Salmonella*, *Shigella* and *Campylobacter*, while *C. trachomatis* is by far the most common cause of ReA associated with genital infection^[3,18]. All these pathogens are Gram-negative aerobic or microaerophilic bacteria containing LPS in their outer membrane.

The immunopathogenic mechanisms involved in ReA development are still unknown. Even when bacterial

Table 1 Animal models of reactive arthritis similar to the human form of the disease

| Animal | Bacteria | Route of infection | Arthritis onset/ remission | Clinical symptoms | Cytokine involved | Ref. |
|--|--|------------------------------|-------------------------------|---|--|--|
| Lewis rats | <i>Y. enterocolitica</i> O:8 ¹ | <i>iv</i> ¹ | 1 wk/6 wk | Polyarticular arthritis, erythema | ND | Hill <i>et al</i> ^[10] |
| DBA/2 and BDF1 mice | <i>Y. enterocolitica</i> O:8 plasmid cured ¹ | <i>iv</i> ¹ | Day 31/3 wk | Polyarticular arthritis | ND | Yong <i>et al</i> ^[11] |
| SHR rats | <i>Y. enterocolitica</i> O:8 ¹ | <i>iv</i> ¹ | 1-4 wk/7-25 wk | Polyarticular arthritis, erythema, swelling and impaired movement of the joint | ND | Merilahti-Palo <i>et al</i> ^[12] |
| Swiss, BALB/ c and C3H/ HeJ mice | <i>Y. enterocolitica</i> O:3 | <i>iv</i> ¹ /Oral | 1-3 wk/2-8 mo | Monoarticular arthritis, swelling redness, deformations and conjunctivitis | ND | de los Toyos <i>et al</i> ^[13] |
| C57BL/6 <i>TNFRp55</i> ^{-/-} mice | <i>Y. enterocolitica</i> O:3 | <i>ig</i> | 2 wk/chronic until 8 wk | Polyarticular arthritis, swelling, erythema | IL-17 IFN- γ IL-6 IL-1 β | Di Genaro <i>et al</i> ^[14] Eliçabe <i>et al</i> ^[15] |
| BALB/c mice | <i>S. enteritidis</i> | <i>ig</i> | 1 wk/ND | Synovial inflammation | TNF- α IL-17 | Noto Llana <i>et al</i> ^[16] Noto Llana <i>et al</i> ^[17] |

¹Different to the human form of the disease. ND: Not determined; *iv*: Intravenous infection; *ig*: Intragastric infection; IL: Interleukin; TNF: Tumor necrosis factor.

cultures of synovial fluids are negative in ReA, bacterial antigens have been found in the joints of patients. In *Chlamydia*-induced ReA, bacterial DNA and RNA have been detected in the joint, suggesting that live *Chlamydia* are present^[19-21]. Positive reaction of antibodies specific to *Salmonella* and *Yersinia* antigens in synovial fluid cells of ReA patients suggests the presence of bacterial antigen in the joint^[22,23]. Based on these findings, some authors have suggested that the bacteria probably persist outside the joint at sites such as gut mucosa or lymph nodes, and bacterial antigens might then be transported by monocytes to the joints^[24,25]. On the other hand, an altered immune response and the unbalanced production of cytokines have been reported in subjects with ReA^[26,27]. This altered immune response benefits the bacterial persistence and disfavors the elimination of the antigen by the host.

In this review, we highlight recent advances on the role of cytokines in ReA. Particularly, we discuss the roles of pro- and anti-inflammatory cytokines, especially interleukin (IL)-17, IL-12, IL-23, IL-6, tumor necrosis factor- α (TNF- α), interferon- γ (IFN- γ) as well as IL-10 in the pathophysiology of the ReA. Finally, we discuss the latest advances in the treatment of ReA based on the use of biological agents that neutralize the functions of certain cytokines, such as TNF- α or IL-6.

ROLE OF THE CYTOKINES IN ReA

Conflicting data have been reported on the production of cytokines in ReA patients. CD4⁺ T cells mediate immunity as a balance between different lineages of T helper (Th)-1, Th2, Th3 and Th17 which secrete IFN- γ , IL-4, TGF- γ and IL-17, respectively, as the main cytokine for each profile. Some studies revealed low levels of Th1 cytokines in ReA, especially of TNF- α but also of IFN- γ in peripheral blood and synovium^[28-34]. Since Th1 cells secreting IFN- γ and TNF- α have been proposed for bac-

terial clearance, defective Th1 response may contribute to bacterial persistence. Other data suggest that a Th2 cytokine profile and Th3 response with expression of TGF- β is common in ReA^[32]. Temporal relationships of these different Th1 and Th2 cytokines or blunting of initial cytokine response might also be important in the disease manifestations and its maintenance. On the other hand, the discovery of Th17 cells and their importance in the pathogenesis of chronic inflammatory diseases suggested that these cells may have a pathogenic role in ReA. However, the available studies are not large enough to support the role of certain cytokines in the pathogenesis of ReA.

NOVEL CYTOKINES IMPLICATED IN PATHOGENESIS OF ReA

IL-17

IL-17 is a 15-20-kDa glycoprotein produced by a novel subset of Th cells, termed Th17 cells, and to a lesser extent by innate lymphoid cells, including T-cells, innate-like lymphoid cells, mast cells and neutrophils^[35]. Th17 cells are critical in the pathogenesis of the arthritis, as demonstrated in several animal models^[36-38]. Th17 differentiation, survival and expansion depend on a variety of cytokines and transcription factors that work in concert to drive the induction of increased Th17 numbers. TGF- β in synergy with IL-6 has been described as the central factor involved in generating Th17 cells in mice. It has been shown in humans that TGF- β , IL-1 β and IL-6, combined with IL-21 or IL-23, can induce Th17 differentiation^[39]. IL-17 binds to IL-17RA/IL-17RC, which is expressed by a variety of cells, such as monocytes, lymphocytes, lymphoid tissue inducer cells, epithelial cells, synoviocytes, fibroblasts and keratinocytes^[35].

Th17 cell responses and IL-17 expression provide protection against bacterial and fungal pathogens through production and induction of inflammatory cytokines

and granulopoiesis, or by the recruitment of neutrophils. However, Th17 cells producing IL-17 have been suggested as the central effector lineage involved in the pathogenicity of ReA^[40]. Thus, it has been shown that ReA patients have elevated levels of IL-17 in synovial fluid and that this cytokine contributes to the development of joint inflammation^[40,41]. Furthermore, high expression of IL-17 was found in the synovial fluid of patients with SpA and an increased number of circulating memory Th17 cells has been recently reported in these patients^[42,43]. Moreover, in patients with *C. trachomatis*-induced ReA, increased percentages of IL-17-positive CD4⁺ T cells^[44] and higher IL-17 concentrations were detected in synovial fluid^[45].

Recent works suggest that *Salmonella*-induced ReA in mice dependent on CD4⁺ T cells secreting IL-17^[17]. Interestingly, these authors observed that the expression of IL-17 in the large intestine and in mesenteric lymph nodes (MLN) resembles that of popliteal and inguinal lymph nodes (ILN)^[17]. Accordingly, previous results from our laboratory demonstrated that IL-17 plays a major role in *Yersinia*-induced ReA^[15]. Furthermore, we detected a strong correlation among IL-17 levels in MLNs, ILNs and joints from *TNFRp55*^{-/-} mice with arthritis, supporting a link between the intestinal mucosa and the articular immune response. In addition, we observed that neutralization of IL-17 resulted in the abrogation of synovitis^[15]. In line with these results, other authors have reported recently that modulating intestinal IL-23/IL-17 expression by consumption of *Lactobacillus casei* prior to *Salmonella* infection in mice abolishes intestinal and joint inflammation^[46].

These data in animal models and patients support the hypothesis that Th17 cells may be involved in ReA pathogenesis. However, there are few reports for understanding and elucidating the true role of IL-17 in the pathogenesis of ReA.

IL-12 and IL-23

IL-12 and IL-23 are heterodimeric cytokines that share subunits and have important roles in autoimmunity. These IL-12 family cytokines share some biological characteristics but have functional differences. IL-12 is composed of two covalently linked subunits, IL-12p35 and IL-12p40, while IL-23 is composed of two covalently linked subunits, IL-23p19, which is distantly related to IL-12p35, and the IL-12p40 subunit^[47,48]. Furthermore, the receptors of IL-23 and IL-12 are also heterodimers that share the receptor 1 chain and have unique 2 chains^[49]. IL-12 is released by antigen presenting cells such as dendritic cells (DCs) and monocytes/macrophages in response to bacterial products and immune signals. Furthermore, IL-12 is the main stimulator of IFN- γ production by inducing development of Th1 responses^[49,50]. In addition, IL-23 is produced by macrophages and activated DCs and plays a crucial role in the generation of the Th17 cells. Since IL-12 has the ability to orchestrate the Th1 response, this cytokine plays a crucial role in the protective immunity

against many pathogens associated with ReA. Thus, the low concentrations of IL-12 have been linked to the bacterial persistence hypothesis and then to the pathogenesis of ReA^[28]. On the other hand, data on IL-23 concentrations in synovial fluid or serum of patients with ReA are limited, but high levels of IL-17 found in synovial fluids and sera of patients with ReA may reflect IL-23 activity. Moreover, abnormality of IL-12p40 gene expression in humans has been reported and IL-12 deficiency has been detected in patients with ReA^[51,52]. Yin *et al.*^[28] found that the balance of anti-inflammatory cytokines (IL-10) and IL-12 in the synovial fluid is also important. This may contribute to the decreased clearance of the bacteria or their components from the joint and lead to ReA^[28]. In relation to these findings, a recent study has shown that monocyte-derived macrophages from subjects with a history of ReA show low IL-12 and IL-23 production^[53]. Conversely, some authors have reported that IL-12/23p40 levels in synovial fluids of patients with ReA and other SpA are higher compared to synovial fluids of patients with osteoarthritis (OA) used as control^[41,54].

Interestingly, we demonstrated that the p40-deficient mice develop acute ReA after oral infection with *Y. enterocolitica*, suggesting that IL-12 or IL-23 could exert a protective effect on the development of ReA^[55]. However, we have observed elevated levels of p40 in regional lymph nodes to joints of *TNFRp55*^{-/-} mice with *Yersinia*-induced ReA. This effect has been accompanied by high levels of IFN- γ and IL-17 in affected joints^[15]. These results are in accordance with the concept that the IL-12/IL-23 pathway plays a dual role protecting from infection and eliciting tissue damage, and support future study to determine whether IL-12/23p40 could be a possible target for ReA treatment.

IL-6

IL-6 is a pleiotropic cytokine that is involved in numerous biological processes. The pleiotropy and redundancy of IL-6 functions have been identified by characterizing a unique receptor system comprising two functional proteins: a receptor specific for IL-6 (IL-6R)^[56] and gp130, the common signal transducer of cytokines related to IL-6, including the IL-12 family cytokines IL-27 and IL-35^[57,58]. In the early phase of infectious inflammation, IL-6 is produced by monocytes and macrophages immediately after the stimulation with distinct pathogen-associated molecular patterns. In noninfectious inflammation, damage-associated molecular patterns from damaged or dying cells stimulate monocytes and macrophages to produce IL-6. The pathogenic role of IL-6 in rheumatic diseases like rheumatoid arthritis (RA) has been well established. The critical role for IL-6 in the pathogenesis of RA is provided by clinical trials, in which tocilizumab, a humanized mAb specific for IL-6R, has been shown to suppress disease activity and erosive progression in patients with RA^[59]. In ReA, elevated IL-6 concentrations in the plasma and sera of the patients has been reported^[60,61]. Moreover, synovial fluid concentrations of

IL-6 were higher in patients with ReA^[41]. Interestingly, we found that mice TNFRp55-deficient macrophages are hyperactivated to secrete common pro-inflammatory mediators such as NO and IL-6 following stimulation with *Yersinia* antigens. The higher concentrations of IL-6 production detected in stimulated TNFRp55^{-/-} macrophages may be associated with our previous *in vivo* results demonstrating the increased susceptibility of TNFRp55^{-/-} mice to *Yersinia*-induced ReA^[14]. Furthermore, higher concentrations of IL-6 were detected in the joints of these mice which showed a severe chronic synovitis^[15]. This data suggests that over-synthesis of IL-6 may be related to the development of ReA.

TNF- α

TNF- α is a cytokine prototype of a large family of over 40, known as TNF superfamily, and TNF receptor (TNFR) proteins. TNF- α is a cytokine with pleiotropic functions produced by a large number of cells, but are monocytic lineage cells (macrophages, astroglia, microglia, Kupffer cells and alveolar macrophages) major sources. Initially, this cytokine is produced as a pro-TNF and is expressed on the cell surface. Subsequently it is cleaved by the action of a metalloproteinase (TACE) and released into the extracellular medium as a soluble protein^[62]. Often, TNF- α is not detected in high concentrations in serum or tissues, but increases intensively on various inflammatory and infectious conditions. Two receptors, TNF-R1 (TNF receptor type 1; CD120a; p55/60) and TNF-R2 (TNF receptor type 2; CD120b; p75/80) bind to membrane-integrated TNF (memTNF) as well as soluble TNF- α (sTNF- α). In the vast majority of cells, TNF-R1 appears to be the key mediator of TNF- α signaling, whereas in the lymphoid system, TNF-R2 seems to play a major role. Low TNF- α secretion by blood mononuclear cells may be related to ReA development since TNF- α deficiency may interfere with eradication of bacterial infection in its early stages^[34,63-66]. However, other studies suggest that TNF- α could have a pathogenic role during the chronic stage of ReA in line with the role of this cytokine in RA. In this regard, some studies have revealed significant increase of TNF- α production in chronic ReA compared with acute ReA^[66]. These data support the possibility that anti-TNF- α treatment in ReA during the chronic phase of the disease could be beneficial. However, considering that TNF- α may be required for the elimination of ReA-associated bacteria, anti-TNF- α biologics might favor bacteria growth. Results obtained in our laboratory showed that TNFRp55 deficiency favors the development of ReA after infection with *Y. enterocolitica*^[14]. These data support the idea that the relative lack of TNF- α may play a protective role in ReA at acute phase of disease. On the other hand, we have demonstrated an *in vivo* regulatory role for TNFRp55 signaling in fine-tuning of Th17 and Th1 programs during bacterial-induced ReA through modulation of the common p40 subunit of IL-23 and IL-12^[15]. This evidence suggests that TNF- α might have a dual role in ReA, playing a protective role first and during the initial

stage. However, during the chronic stage of the disease, TNF- α would act as a pro-inflammatory cytokine.

IFN- γ

IFN- γ is produced mainly by natural killer (NK) cells and a particular subset of T cells, namely Th1 cells^[67]. As previously mentioned, IL-12 is the main stimulator of IFN- γ production^[47,50]. Thus, IL-12 and IFN- γ coordinate the link between pathogen recognition by innate immune cells and the induction of specific immunity by mediating a positive feedback loop to amplify the Th1 response. The functional IFN-receptor (IFN-R) consists of 2 ligand-binding IFNGR1 chains and 2 signal-transducing IFNGR2 chains^[68]. Mice deficient in IFN- γ or its receptor are susceptible to an array of intracellular pathogens^[69-71]. It was thought that Th1 cells cause damage in the joints mainly through IFN- γ driven inflammatory mechanisms. However, similar to TNF- α , conflicting data have been reported about the role of IFN- γ in ReA. As previously mentioned, some authors have reported an aberrant lower production of IFN- γ in patients with ReA^[28-34,52]. In contrast, in patients with *C. trachomatis*-induced ReA, the synovial fluid concentrations of IFN- γ were significantly higher than in OA patients but no significant differences were found between ReA and RA patients^[45]. Similar results were reported by Singh *et al*^[41]. Other studies have shown that the percentages of IFN- γ positive CD3⁺ cells were significantly higher in peripheral blood and synovial fluid of chronic ReA patients^[66]. These data support the idea that, as with TNF- α , IFN- γ may play a significant protective role in ReA in the acute phase of disease. However, in the chronic phase, this cytokine, as in RA, could play a pathogenic role in ReA.

IL-10

IL-10 is an anti-inflammatory cytokine with a major role in preventing inflammatory and autoimmune pathologies^[72]. Based on a large body of evidence, T cells are thought to be the main source of IL-10 *in vivo*. Regulatory T (Treg) subsets are also a key source of IL-10 *in vivo* and play a central role in mediating the inflammation control. However, it is now accepted that IL-10 is expressed by subsets of all CD4⁺ T helper populations, including Th1, Th2 and Th17^[73]. Nevertheless, this cytokine is also expressed by B cells and cells of the innate immune system (DCs, stimulated macrophages, mast cells, NK cells, eosinophils and neutrophils)^[74]. This cytokine binds to IL-10 receptor (IL-10R), which consists of two subunits. They are members of the interferon receptor family and belong to JAK/STAT3 class of receptors^[74]. Extensive studies have demonstrated that IL-10 inhibits the production of pro-inflammatory cytokines and chemokines in activated monocytes/macrophages and inhibits proliferation of CD4⁺ T cells^[75]. However, the role of IL-10 in ReA is less clear. Appel *et al*^[32] reported that the amount of IL-10 and TGF- β secreting cells was higher in ReA than in RA patients. This result was accompanied by a lower level of TNF- α secretion in ReA patients. Interest-

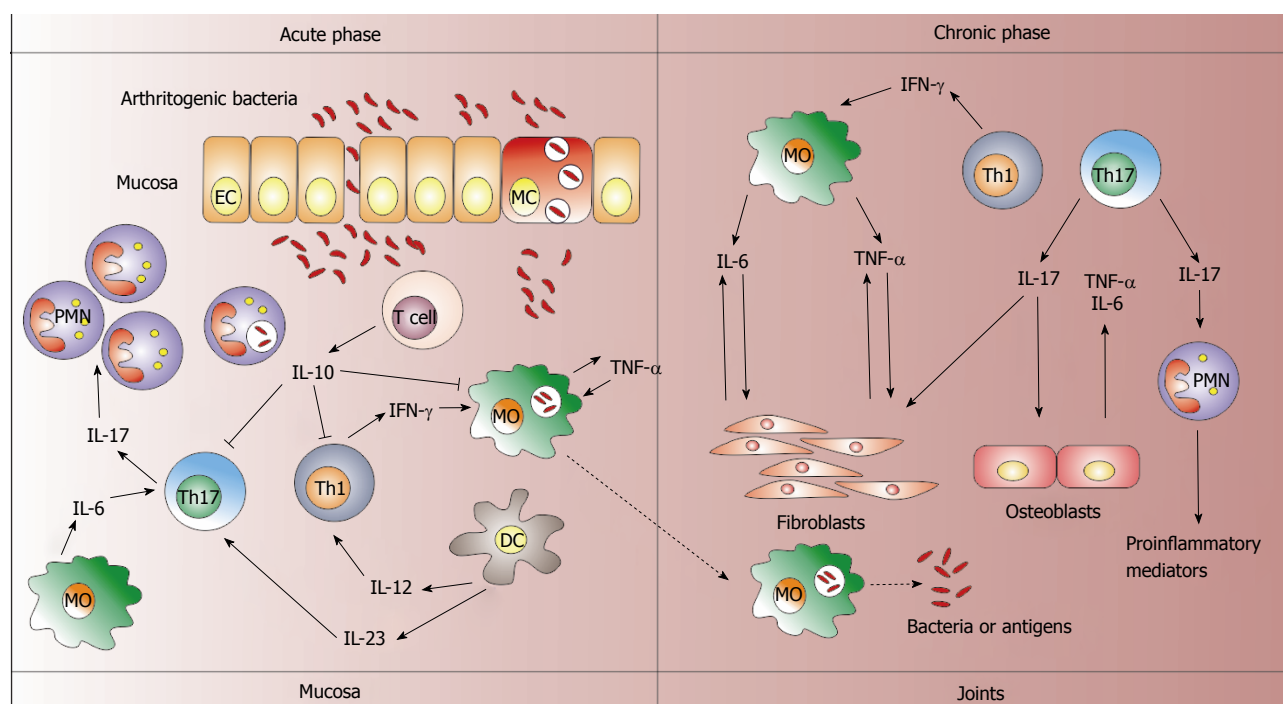


Figure 1 The role of cytokines in reactive arthritis depending on the state of disease. Arthritogenic bacteria enter through the gastrointestinal or genitourinary mucosa using different strategies (M cells; epithelial cells) and induce an inflammatory response. During the acute stage, interleukin (IL)-12 and IL-23 plus IL-6 promote the development of Th1 and Th17 cells, respectively. These cells are a major source of interferon (IFN)- γ and IL-17, favoring the bacterial clearance. The IFN- γ activates macrophages to kill phagocytosed bacteria and secrete tumor necrosis factor (TNF)- α . IL-17 induces the migration of polymorphonuclear cells to the site of infection. However, this effect could be disrupted by the action of regulatory T cells producing IL-10. This regulatory event contributes to the bacterial persistence in the mucosa. Then, the bacteria could reach the joint transported by macrophages. In chronic stages, IL-6, TNF- α , IFN- γ and IL-17 exert pro-inflammatory roles in the joint. These cytokines stimulate articular cells (e.g., fibroblasts, osteoblast) and immune cells to produce more cytokines and pro-inflammatory mediators that contribute to chronic articular inflammation. These effects may be enhanced by the presence of bacteria or bacterial antigens in the joint. EC: Epithelial cell; MC: M cell; MO: Macrophage; PMN: Polymorphonuclear cell; DC: Dendritic cell.

ingly, all ReA patients had a disease course of less than 6 mo. These authors suggest that this cytokine milieu might contribute to the lack of elimination of the triggering agent. Similar results were reported by Yin *et al.*^[28]. These authors found that synovial fluid mononuclear cells secreted low amounts of IFN- γ and TNF- α , but high amounts of IL-10 upon stimulation with specific bacteria, which was responsible for the suppression of IFN- γ and TNF- α ^[28]. There is also evidence indicating association of the IL-10 promoter region with the development of ReA. This raises the possibility that high levels of IL-10 in the joints of patients with ReA may be genetically determined, making these individuals more prone to the persistence of arthritogenic bacteria^[76].

Despite these clinical findings suggesting a pathogenic role of IL-10 in human ReA, IL-10 depletion and IL-10 treatment in other types of arthritis models have demonstrated the anti-inflammatory properties of IL-10 in arthritis^[77-80]. Results obtained in our laboratory showed that the number of Treg cells as well as the *FoxP3* mRNA expression and IL-10 levels were significantly decreased in joint regional lymph nodes of *TNFRp55*^{-/-} mice at the arthritis onset^[81]. These results would indicate that IL-10 plays a protective role during the acute phase of arthritis. However, the clinical evidence suggests that high levels of IL-10 could promote bacterial persistence, favoring

the development of ReA.

TREATMENT BASED ON BIOLOGICAL AGENTS

IL-6 antagonists

Published data on the effects of IL-6 blockade in patients with SpA are very scarce. Thus, in 1996 a report describes a patient with ReA who received a murine anti-IL-6 antibody^[82] and, in 2009, tocilizumab was reported to be successful in another patient with ReA^[83]. Only two injections of tocilizumab led to complete clinical remission from symptoms caused by ReA^[83]. Recently, Kwan *et al.*^[84] reported successful results of tocilizumab in the treatment of a case of ReA precipitated by intravesical bacillus Calmette-Guérin (BCG) which did not respond completely to disease modifying antirheumatic drugs (DMARDs). As previously mentioned, IL-6 is one of the cytokines that favor the differentiation of naïve T cells into Th17 cells^[39]. Therefore, it is possible that the inhibitory action of tocilizumab is exerted indirectly interfering with the differentiation of Th17 cells. These data indicate that IL-6 may play a pivotal role directly or indirectly in the pathogenesis of ReA and tocilizumab treatment can be an option for an alternative treatment.

TNF-antagonists

The pathogenic role during the critical stage of the disease supports the idea that TNF- α blocking agents could be an effective treatment for patients with ReA who develop severe arthritis that does not respond to conventional lines of treatment. Thus, Kaipainen-Seppönen *et al.*^[85] reported two cases of ReA post *Y. enterocolitica* treated early with infliximab (an anti-TNF- α antibody). One patient that received this treatment within 2 mo after the disease onset exhibited an improvement after the third infusion. The second patient that was treated after one month of evolution showed an immediate clinical improvement with almost complete regression after 15 d^[85]. Recently, Thomas-Pohl *et al.*^[86] obtained the same result in one patient with ReA triggered by a gastrointestinal infection. Similar results were reported by Edrees in a patient with a severe case of *C. trachomatis*-related ReA that was successfully treated with etanercept (a fusion protein of TNFRp75)^[87]. Thus, anti-TNF- α therapy has proved efficacious in some cases. However, sufficient data are lacking and theoretical concerns with their use remain. Large controlled trials are needed to evaluate the role of TNF- α blocking agents in ReA.

CONCLUSION

The network of cytokines is complex with feedback regulatory circuits that make it difficult to elucidate the role of a particular cytokine in ReA. In addition, the clinical reports of cytokine levels in patients with ReA have included patients in different stages of the disease or they are not large enough to support the role of different cytokines in ReA development. However, the current evidence in patients with anti-cytokine treatments suggests that IL-6 and TNF- α may play central roles in ReA pathogenesis. Furthermore, the IL-17/23 axis should be considered in the picture of ReA development, although further investigations are necessary for these cytokines. According to the presented evidence in this review, Figure 1 shows the different functions of the cytokines in ReA depending on the disease phases. Moreover, animal models may contribute to provide insight into the immunopathogenic mechanisms mediated by a particular cytokine in ReA and to support anti-cytokine treatments.

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Update on pythiosis immunobiology and immunotherapy

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Abstract

Pythiosis is an invasive, ulcerative, pyogranulomatous disease caused by *Pythium insidiosum*, a fungus-like oomycete that has been reported to affect humans, horses, dogs, and other mammals mainly in tropical and subtropical areas of the world. The disease is characterized by an eosinophilic granulomatous and a Th2 immune response which in turn helps to protect the fungus from the host cells. Pythiosis can present clinically in subcutaneous, gastrointestinal, and vascular tissues or in a systemically disseminated form depending on the species and site of infection. Changes in iron metabolism and anemia are commonly observed. The diagnosis is accomplished through clinical and pathological features, laboratory characteristics of cultures, serological and molecular tests. Treatment includes radical surgery, antimicrobial drugs, immunotherapy or a combination of these treatments. Immunotherapy is a practical and non-invasive alternative for treating pythiosis which is believed to promote a switch from a Th2 to Th1 immune response, resulting in a favorable

clinical response. This therapy has demonstrated cure rates above 70% and 55% in horses and humans but low cure rates in dogs and cats. Despite the curative properties of this type of immunotherapy, the antibodies that are produced do not prevent host reinfection. Thus, development of effective adjuvants and new diagnostic techniques for early disease diagnosis are of utmost importance. The aim of this review was to promote pythiosis awareness and to provide an update about the immunotherapy and immunobiology of this disease.

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Key words: *Pythium insidiosum*; Treatment; Pythiosis; Immunotherapy; Pathogenesis

Core tip: Pythiosis is a life-threatening disease for which there is no gold standard chemotherapy. Immunotherapy derived from killed mycelium from *Pythium insidiosum* is a non-invasive therapy that has demonstrated cure rates above 90% when associated with the surgical removal of the lesions and early disease diagnosis.

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INTRODUCTION

Pythium insidiosum (*P. insidiosum*, an oomycete also known as water mold) is a filamentous microorganism that shares many characteristics with fungi (*i.e.*, it grows by polarized hyphal extension, engages in an absorptive mode of nutrition, and it can form spores for reproduction). However, *P. insidiosum* is classified in a completely different taxonomic group, namely the Stramenopiles, together with diatoms and brown algae^[1]. This classifica-

tion is the first essential information for understanding pythiosis in humans and other mammals; infections have similar clinical and histopathological characteristics as those of certain mycoses. Conversely, treating pythiosis with antifungal drugs is generally inefficient because the oomycetes do not synthesize ergosterol, which is a component of the plasma membrane of true fungi and the primary target of those drugs^[2]. Similarly, the immune response of animals with pythiosis presents similar features to those of fungal infections, and there are peculiarities found only in infections caused by this oomycete^[3]. The challenge of treating pythiosis is characterized by the severity of the disease in mammals and by the absence of a gold standard chemotherapy. Nevertheless, immunotherapy is a practical and non-invasive alternative for treating pythiosis, and there is a favorable clinical response. In this context, the aim of this review was to promote pythiosis awareness and to provide an update about the immunotherapy and immunobiology of this disease.

THE EPIDEMIOLOGY, IMMUNOBIOLOGY AND PATHOGENESIS OF PYTHIOSIS

The proposed life cycle of *P. insidiosum* is characterized by the colonization of aquatic plants and the soil of wetlands or swampy areas, which serve as a substrate for mycelial vegetative growth and the asexual formation of mobile biflagellate zoospores that move through the water, find another host, encyst and form a new mycelium that can then start a new colonization^[4-6].

In view of this biological cycle, pythiosis cases are associated with human or animal contact with areas in which zoospore-containing water accumulates (such as wetlands and lakes) and environmental temperatures range between 30 °C and 40 °C. Most reports of animal pythiosis are described in horses that live in swampy areas or periodically enter ponds or lakes. These cases are distributed primarily between the peak months of the rainy season in each region. A higher human disease frequency has been observed in thalassemic patients in Thailand, where it is common for people to work in flooded rice cultivation areas^[7-9].

Human and animal pythiosis cases have been described in tropical and subtropical climatic regions. Although these cases are most often diagnosed in Australia, Asia, Latin America and United States, some cases have originated from temperate areas of Japan, South Korea, Oceania and Africa. There are no reports of animal-animal or animal-human transmission^[10,11].

P. insidiosum hyphae do not exert sufficient pressure to penetrate undamaged skin through mechanical means alone^[12], and they must effect a decisive reduction in tissue strength by proteinase secretion or by finding prior skin damage to invade their host. Indeed, *P. insidiosum* possesses a strong tropism for mammalian injured tissue^[10]. Interestingly, *P. insidiosum* has been recovered from a mosquito larva (*Culex quinquefasciatus*)^[13] and hematophagous insects prefer the same anatomical areas for blood feeding in which pythiosis lesions are more prevalent in

horses^[9]. Given this information, future studies should investigate if insect bites could favor the penetration of zoospores into injured skin or if infected mosquitoes could directly transmit the disease.

Once inside the host, pythiosis pathogenesis involves the Splendore-Hoepli phenomenon (reaction), which is characterized by the presence of radiating, star-like asteroid or club-shaped eosinophilic material around the infectious agent^[14]. Thus, *P. insidiosum* triggers an eosinophilic granulomatous reaction similar to other fungi, such as *Basidiobolus* spp. and *Conidiobolus* spp.^[15], with characteristic histopathological features depending on the species and the clinical form^[16].

Mendoza *et al.*^[17] proposed that the antigens released by *P. insidiosum* hyphae modulate the host's immune response and may be responsible by keeping an eosinophilic granulomatous response, locking the immune system into a Th2 immune response through the continuous stimulatory production of more eosinophils and mast cells, which in turn helps to protect the fungus from the host cells and leads to a worsening condition, and if not treated properly, can lead to host death. As a consequence, the *P. insidiosum* hyphae surrounded by degranulated eosinophils would be camouflaged inside the eosinophilic micro-abscesses, preventing their full presentation to the immune system and thereby ensuring their viable presence in infected tissues. These features and the subsequent finding of elevated IgE levels in humans and horses with the disease strongly validated the concept of a Th2 modulation by this pathogen during natural infection^[3,17]. High Th2 interleukin levels [interleukin (IL)-4, IL-5 and IL-10] have also been detected in human patients with pythiosis, confirming a Th2 immune response^[18,19].

The eosinophil degranulation in equids and camels with pythiosis is remarkable, forming around the hyphae cores of necrotic yellow-gray and firm materials called *kunkers*, which are easily shed from lesions^[4,15,20,21]. The *kunkers* range from 2 to 10 mm in diameter, have an irregular shape and sandy aspect, may be branched and invade the granulation tissue within the sinus formed along its trajectory. This pronounced degranulation is also associated with extensive tissue damage and with the tumor-like appearance of lesions that can reach over 50 cm in diameter^[22]. Horses are the mammals that are most affected by pythiosis, with no predisposition according to their age, race or sex. However, although young animals are also susceptible, the disease is rarely observed in animals under one year of age, and the bodily lesions are predominant in dark pigmented areas^[9].

The lesions are subcutaneous and present primarily in the distal extremities, the ventral portion of the thoraco-abdominal wall and face, which represent anatomical structures that remain in contact with contaminated water containing *P. insidiosum* zoospores^[7,23,24]. The *kunkers* are considered to be pathognomonic of pythiosis in equids, and they have also been described in camels with vulvar pythiosis^[21] and in a case of equine conidiobolo-

mycosis^[25]. The disease was also described in cattle^[26-29], cats^[27,30], dogs^[16,17,27,31-39], sheep^[40,41] and occasionally in animals kept in captivity in zoos^[42,43] and birds^[44].

P. insidiosum can cause superficial infections in humans, namely keratitis with corneal involvement^[45-47]; cutaneous and subcutaneous infections^[48]; orbital pythiosis and bone involvement^[49,50]; and systemic infections, namely arteritis of the lower limbs and/or dissemination^[8,19,51]. Although pythiosis can affect apparently healthy individuals^[48,50,51], most cases are reported in patients with thalassemia and other hematological diseases^[8]. The same authors have argued that iron overload, which is a marked characteristic of patients with thalassemia, could increase host susceptibility to pythiosis by promoting the infectivity of the pathogen or by impairing host immunity.

In fact, both iron overload and deficiency can weaken the immune system^[52-54]. Additionally, many microorganisms are known to be avid for iron during infection^[53,55] and changes in iron metabolism may increase host susceptibility to infection by *P. insidiosum*. Krajaeun *et al*^[56] described that *P. insidiosum* expresses a gene encoding a ferrochelatase and Krajaeun *et al*^[57] reported, through the transcriptome analysis of this species, an extensive repertoire of proteins that may be involved as virulence factors during infection. Although the role of iron in pythiosis has not been fully explained, the disease is more frequently found in human patients with thalassemia and with other hemolytic anemias^[18,19,58]. Anemia as a consequence of the disease has already been described in horses^[59-65], dogs^[33,34,37,39,66], cats^[39,67], camels^[21,68] and in a jaguar^[42] and Bengal tiger^[69]. Santos *et al*^[9] also argue that the iron deficiency is common in lactating foals (< 1-year-old and, which are less susceptible to pythiosis) because of the low iron levels in the milk. In contrast, iron deficiency is uncommon in adult horses, and they may have increased levels of circulating iron, especially in the Brazilian Pantanal, which contains high levels of this mineral in the soil, plants and water^[70], and where it is observed a high incidence of pythiosis.

Loreto *et al*^[71] reported an increase in the unsaturated iron binding capacity (UIBC) in rabbits experimentally infected with *P. insidiosum*, suggesting that there was an increase in the transferrin concentration and/or an increase in the number of transferrin iron receptors, which is compatible with a physiological decrease in the iron availability. Similar results were observed by Zanette *et al*^[72], who noted that rabbits experimentally infected with pythiosis presented decreased serum iron levels, increased transferrin levels with low saturations (increased UIBC) and markedly decreased levels of stainable iron in the hepatocytes, which suggests an affinity for iron by *P. insidiosum*.

DIAGNOSIS AND HUMORAL RESPONSE

A classical pythiosis diagnosis is accomplished through clinical and pathological features, in addition to cultural, morphological and reproductive characteristics *in vitro*. A differential diagnosis includes habronemiasis, neoplasms,

exuberant granulation tissue, and fungal or bacterial granulomas^[73,74]. Microscopic evaluations using 10% KOH (direct examination) can reveal *P. insidiosum* hyaline hyphae and eventually septate-morphology, depending on the clinical material evaluated. This material can easily be confused with filamentous fungi, particularly those of the orders Entomofthorales and Mucorales^[11]. A culture from *kunkers* or biopsies can usually be performed on V8 agar, corn meal agar and Sabouraud dextrose agar.

Hyphal growth can be observed after 24 h of incubation at 37 °C when submerged in culture medium, and it exhibits a hyaline or white color^[75]. Because *P. insidiosum* does not produce reproductive structures in traditional culture media, the induction of zoosporogenesis (asexual zoospore formation) can be obtained by cultivating *P. insidiosum* in sterile blades of grass that are then transferred to a mineral solution^[76]. However, the correct identification of this species should be confirmed by molecular methods^[77-81].

The production of anti-*P. insidiosum* antibodies was one of the first immunological features described for pythiosis, and these antibodies were easily detected by immunodiffusion and complement fixation tests with antigens that were extracted from the pathogen^[82,83]. Studies then confirmed that humans and animals suffering from pythiosis exhibited a humoral immune response upon host-pathogen interaction^[3,36,77,84-86], but this response was not sufficient to clear the infection^[19,50,87,88]. However, the serological tests developed for detecting antibodies, such as agar gel immunodiffusion, enzyme-linked immunosorbent assay (ELISA), Western blot, latex agglutination and immunochromatographic tests^[77-80,89-93], are highly useful for the early diagnosis of pythiosis. In equine pythiosis cases in which the animal is far from reference laboratories, sending serum for ELISA and collecting *kunkers* and tissues for microbiological culture and histopathological analysis are among the primary forms of diagnosis. An early pythiosis diagnosis can also be performed through immunohistochemical^[116,94] and molecular methods^[80,95].

TREATMENT

Antimicrobial and surgical treatment

Because primary antifungal drugs act directly or indirectly on ergosterol and *Pythium* spp. are unable to synthesize any sterols, it is understandable that pythiosis cases do not respond satisfactorily to antifungal treatments. However, contradictory results have been reported in the use of antifungal agents to treat pythiosis^[8,10,49,96].

P. insidiosum isolates have varying *in vitro* susceptibility to antifungal compounds^[97,98]. Reviews of antifungal drug associations show that *in vitro* synergism occurs in AmB + terbinafine^[99], terbinafine + azole antifungals and terbinafine + caspofungin associations^[100]. Additionally, some antibacterial drugs that act as protein synthesis inhibitors (macrolides, tetracyclines and glycylcycline) have been shown to inhibit the *in vitro* growth of *P. insidiosum*^[101,102]; nonetheless, experimental *in vivo* tests have not been con-

ducted to demonstrate the clinical effectiveness of these antibiotics.

Successes and failures of pythiosis treatment cases have been reported with combinations of antifungal therapies. The surgical removal of the lesion, the amputation of the affected limb or the enucleation of the affected eye represents the last resort in human pythiosis treatment. However, recurrence rates of 40% have been observed, which illustrates the difficulty of controlling this disease^[11]. The implementation of surgical treatment with antifungal drugs or potassium iodide was described in cases of therapeutic healing^[73].

Surgically removing all affected tissue is the traditional and most commonly used method for equine pythiosis treatment. The surgery yields good results for small and superficial lesions. However, removing the lesion with a safety margin to avoid recurrences is often hampered by the anatomical regions that are typically involved (distal extremities and the ventral portion of the thoraco-abdominal wall)^[73].

Immunotherapy

Although the antigens used in vaccine preparation (usually from the infectious agent itself) are intended to trigger a protective response in the host immune system (antibody production), the aim of immunotherapy (antibodies or antigens from the infectious agent) is the objective modification of the host immune response to mount an effective response against a disease that is already present. Despite the fact that a protective vaccine against pythiosis does not currently exist, the immunotherapy developed from protein extracts of *P. insidiosum* cultures is a non-invasive alternative for treating this disease in humans and animals.

Immunotherapy was discovered by serendipity when investigators were working on a skin test for pythiosis in horses, and they found that almost half the animals were cured upon inoculation with *P. insidiosum* immunogen^[88,103,104]. The first investigator to use a culture-derived antigen for a skin test was Witkamp^[83], but he did not report cure rates in his experiments. Miller^[103] was the first researcher to report the use of *P. insidiosum* antigens (sonicated hyphae) with therapeutic potential when injected into horses ($n = 30$), resulting in 53% healing in the animals with pythiosis (Table 1). During the following year, the same author observed an immunotherapeutic efficiency ratio of 75% when associated with surgical removal^[105]. Subsequent studies showed that lesions presenting with more than two months of progress in cases of chronic pythiosis had cure rates of approximately 20%-40% with immunotherapy, and cure rates of 100% were obtained when the lesions had less than 20 d of evolution^[17,88,104].

In addition to the lesion evolution time, the manner by which the *P. insidiosum* mycelium is broken to obtain the antigens is also associated with immunotherapy efficacy. In this context, modifications to the original technique as described by Miller^[103] have been developed with

the aim of increasing the effectiveness and safety of immunotherapy.

Mendoza *et al.*^[104] tested two immunotherapies by using the cell mass or a concentrated soluble antigen as an antigen, and they observed efficacies of 60% and 70%, respectively, when treating 71 horses. Mendoza *et al.*^[17] reported that immunotherapy derived from the soluble antigen and sonicated hyphae of *P. insidiosum* cured 72% of the horses ($n = 18$) with pythiosis.

Santurio *et al.*^[106] compared the immunotherapy obtained from sonication, maceration (or liquidification) or the combination of these two techniques in experimental pythiosis cases in rabbits and observed that the macerated immunotherapy had a higher efficiency, with a reduction of 71.8% in the lesion sizes and the clinical cure of two rabbits ($n = 5$). This macerated immunotherapy was lyophilized, and it was valid for more than one year without refrigeration^[106]. This treatment exhibited a cure rate of 50% to 83% ($n = 19$)^[107], or 75% ($n = 8$)^[7] and 90% when combined with surgical excision ($n = 11$)^[24] in horses in the Brazilian Pantanal. The best results are typically observed when the disease is in its early stages.

Despite the good immunotherapy performance in equines, immunotherapy in cats and dogs has been disappointing^[17,27,31]. One explanation for this failure might be that most dogs and cats with pythiosis are diagnosed several months after the initial onset of infection, resulting in animals with weakened immune systems that respond poorly to immunotherapy^[3]. However, the healing of a dog was demonstrated by the combination of immunotherapy and antifungal therapy^[108].

The immunotherapy treatment period (no. of doses) is related to the size, location, time of lesion development, and individual patient response. Santos *et al.*^[24] reported that a horse with 90 d of disease evolution required five months of treatment (eight doses) for complete lesion healing, and they noted that the slowness in the immunotherapy response cannot be interpreted as refractory and in turn end in the premature withdrawal of treatment. Conversely, only two to three doses promoted the effective healing of four horses bearing lesions with seven and 45 d of development.

Field tests with macerated immunotherapy have demonstrated that the efficacy of this treatment is directly associated with early diagnosis. The borderline between a clinical cure and an unsatisfactory response or even non-responsive cases seems to be 60 d from the appearance of lesions in horses^[3]. The treatment consists of subcutaneous applications at 14-d intervals until the complete healing of the granulomatous ulcerative tissue. A mild reaction at the injection site is often observed, and in most cases, it subsides in a few weeks. The number of doses is variable, and some animals respond better to weekly applications. In fact, the only disadvantage of this treatment is the production of protective IgG classes, which impairs serodiagnostic tests such as ELISA and immunochromatography. In this context, blood collection for serological diagnosis of pythiosis should be performed

Table 1 Review of animal pythiosis cases reported in the literature when treated with immunotherapy

| Species/ <i>n</i> | Lesions | Adjunctive therapy | Immunotherapy type ³ , doses | Outcome | Ref. |
|-------------------|-----------------------|--------------------|---|------------------------|-------|
| <i>Horses</i> | | | | | |
| 40 | Various ⁴ | No or surgery | UF, 3 ¹ doses at 7-d intervals | C (53%), I (33%) | [103] |
| 5 | Limbs | ATM, surgery | UF, 3 doses at 7-d intervals | C (20%), 60(E), 20 (D) | [60] |
| 5 | Various ⁴ | No | SA, 2 doses at 15-d intervals | C (60%) | [88] |
| 1 | Limb, bones | No | SA, 2 doses at 7-d intervals | E | [109] |
| 71 | Various ⁴ | Nr | FH or SA, 1 or 2 doses at 7-d intervals | C (66%) | [104] |
| 1 | Limb, bones | Surgery, ATM | Nr, 3 doses postsurgical | D | [110] |
| 2 | Abdomen | Surgery, ATM | SH, 3 doses at 7-d intervals | C (50%), E (50%) | [111] |
| 19 | Various ⁴ | No | LMH, 3 to 9 doses at 14-d intervals | C (50%-83%) | [107] |
| 18 | Various ⁴ | Surgery, ATM | SA + SH, 2 ¹ doses at 15-d intervals | C (72%) | [17] |
| 1 | Limbs, sub-maxillary | Surgery | Nr | E | [23] |
| 1 | Limb | ATM | LMH, 7 doses at 14-d intervals | D | [112] |
| 1 | Hind pastern, fetlock | ATB | SA, 3 doses at 1, 7 and 21 d | E | [113] |
| 1 | Face | Surgery, ATM | LMH, 5 doses at 14-d intervals | E | [114] |
| 1 | Face | ATM | LMH, 5 doses at 14-d intervals | C | [64] |
| 1 ² | Limb, abdomen | No | LMH, 4-5 doses at 14-d intervals | C | [115] |
| 11 | Limbs, abdomen | No or surgery | LMH, 2-5 doses at 14-d intervals | C (70%-90%) | [24] |
| 8 | Limbs, abdomen | No or surgery | LMH, Nr | C (75%) | [7] |
| 47 | Various ⁴ | No or surgery | LMH, Nr | C (79%-84%) | [9] |
| <i>Dogs</i> | | | | | |
| 1 | Cutaneous | AMB, surgery | UF, 1 dose | C | [38] |
| 6 | Cutaneous, intestinal | ATM, surgery | SA + SH, 2 ¹ doses at 15-d intervals | C (33%) | [17] |
| 2 | Cutaneous | Itraconazole | SA, 1 or 2 doses at 7-d intervals | E | [31] |
| 1 | Cutaneous | No | SA, 2 doses at 14-d intervals | C | [35] |
| 1 | Gastrointestinal | ATF, surgery | Nr, 3 doses at 1, 7 and 21 d | C | [32] |
| 1 | Gastrointestinal | ATF | SA, 6 doses at 15-d intervals | C | [108] |
| <i>Camels</i> | | | | | |
| 1 | Face, stomach | Surgery, ATM | SA + SH, 2 ¹ doses at 14-d intervals | D | [68] |
| 2 | Vulvar | Surgery, ATM | SA, 3 doses at 1, 10, 17 d | C (50%) | [21] |
| <i>Sheep</i> | | | | | |
| 6 | Oronasal | No | LMH, 1-5 doses at 14-d intervals | C (16.7%) | [41] |

¹At least; ²Same animal, cured twice with immunotherapy with reinfection within an interval of two years; ³Manufacturing process for immunotherapy; ⁴Not reported individually (subcutaneous). Nr: Not reported; AMB: Amphotericin B; UF: Ultrasonication of hyphae; SA: Soluble antigens; SH: Sonicated hyphae; FH: Fragmented hyphae; LMH: Lyophilized macerated hyphae; C: Cured; I: Clinically improved; D: Died; E: Euthanized; ATM: Antimicrobials; ATB: Antibacterials; ATF: Antifungals.

Table 2 Review of human pythiosis cases reported in the literature when treated with immunotherapy

| <i>n</i> | Lesions | Adjunctive therapy | Immunotherapy type ² , doses | Outcome | Ref. |
|----------|-----------------------|--------------------------------|--|---------|-------|
| 1 | Vascular | ATM, surgery | SA, 2 doses at 14-d intervals | C | [19] |
| 8 | Vascular | Surgery/amputation, ATF | SA, 2 ¹ doses at 14-d intervals | C (50%) | [18] |
| 1 | Vascular | Above-knee amputation | SA, Nr | C | [116] |
| 1 | Vascular | ATM, limb amputation | SA, Nr | D | [117] |
| 1 | Ocular | ATM, enucleation | Nr | D | [118] |
| 1 | Vascular | Above-knee amputation | Nr | C | [119] |
| 1 | Vascular | ATM, above-knee amputations | Nr | C | [120] |
| 1 | Vascular | ATM, above-the-knee-amputation | Nr, 4 doses at 7-d intervals | C | [95] |
| 1 | Vascular/disseminated | ATM | SA, 2 doses at 7-d intervals | D | [121] |
| 3 | Ocular | ATM, surgery | Nr, 3 doses | C (66%) | [122] |

¹At least; ²Manufacturing process for immunotherapy. Nr: Not reported; SA: Soluble antigens; C: Cured; D: Died; ATM: Antimicrobials; ATF: Antifungals.

before the application of immunotherapy, thus preventing false-positive results.

Because of the higher incidence of pythiosis in horses, most data on the efficacy of immunotherapy are described in this animal species^[7,9,17,23,24,60,64,88,103,104,107,109-115]. However, there are also descriptions of its use in dogs^[17,31,32,35,38,108], camels^[21,68] and sheep^[41] (Table 1). Human immunotherapy was described for both successful and failed treatments in association with surgical proce-

dures and the use of various antimicrobials^[18,19,95,116-122] (Table 2). These studies suggest that the injection of *P. insidiosum* immunogens in the form of immunotherapy make antigens available to the host immune system that are not produced during active infection, stimulating a healing response and the formation of immune responses with the presence of mononuclear cells and the disappearance of the eosinophilic reaction around the hyphae.

The proposed mechanism for immunotherapy success is based on a change in the type of cellular response. The immune response observed during pythiosis involves eosinophilic inflammation and the expression of T helper lymphocyte type 2 (Th2) with the release of interleukins 4 and 5 and the mobilization of eosinophils and mast cells. However, the expression of T helper lymphocyte type 1 (Th1) occurs after the immunotherapeutic treatment with the release of interleukin 2 and $\text{INF-}\gamma$ and the mobilization of T lymphocytes and macrophages, which destroy the *P. insidiosum* cells^[3]. This approach was observed for the immune response to human pythiosis when interleukin 4 and 5 production was detected in association with high IgE titers; a large amount of inflammatory cells (eosinophils and mast cells) was identified, which indicated a Th2 response during the infection. After immunotherapy, the patients presented high blood levels of interleukin 2 and $\text{INF-}\gamma$ with a mononuclear immune response, which is typical of a Th1 response^[18,19]. Additionally, an increase in the enzyme activity of ecto-adenosine deaminase (E-ADA) was observed in a rabbit model of experimental pythiosis, which is also associated with the switch from a Th2 to a Th1 response^[123].

Despite the curative properties of this type of immunotherapy, the antibodies that are produced do not prevent host reinfection^[2,115]. Santos *et al.*^[115] described a case of reinfection that occurred two years after the end of a successful immunotherapy treatment against pythiosis. Reinfection occurred at a different anatomical site than the initial infection (abdomen versus left pelvic limb), and although the new lesion was larger (60 cm perilesional edema and ulcerated lesions with approximately 20 cm in diameter), a cure was achieved with four immunotherapy doses (versus the five doses needed in the primary treatment). It is important to note that the levels of antibody's anti-*P. insidiosum* are associated with the response to treatment. Antibody titers are stable or increase in cases of unsuccessful treatment or when there is a persistent or recurrent infection. In cases of healing, substantial reductions of antibody's titers are seen during the subsequent months after the resolution of the infection^[35].

Given the above information, we can conclude that effective immunotherapy treatment can be obtained in association with a rapid and accurate diagnosis, and it may or may not be associated with surgical excision.

CONCLUSION

In summary, although the current immunotherapies used for treating pythiosis make use of crude *P. insidiosum* antigens, some studies have described the identification of immunodominant antigens^[124,125], and the best aspects of these immunotherapeutic elements could lead to a new vaccination strategy that is more effective and protective. A recent description of the *P. insidiosum* transcriptome^[57] uncovered many putative virulence proteins, and it provided a set of candidate targets for the development of better pythiosis diagnosis and treatment modalities.

Because the production of IgG by stimulated B cells is known to protect the host for short periods of time^[2,115], the development of effective adjuvants and new diagnostic techniques for early disease diagnosis are of utmost importance, primarily for animal and human use in endemic areas.

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GM3-containing nanoparticles in immunosuppressed hosts: Effect on myeloid-derived suppressor cells

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Abstract

Cancer vaccines to date have not broadly achieved a significant impact on the overall survival of patients. The negative effect on the immune system of the tumor itself and conventional anti-tumor treatments such as chemotherapy is, undoubtedly, a key reason for these disappointing results. Myeloid-derived suppressor cells (MDSCs) are considered a central node of the immunosuppressive network associated with tumors. These cells inhibit the effector function of natural killer and CD8⁺ T cells, expand regulatory T cells and can differentiate into tumor-associated macrophages within the tumor microenvironment. Thus, overcoming the suppressive effects of MDSCs is likely to be critical for cancer immunotherapy to generate effective anti-tumor immune responses. However, the capacity of cancer vaccines and particularly their adjuvants to overcome this inhibitory population has not been well characterized. Very small size proteoliposomes (VSSP) is a nanoparticulated adjuvant specifically designed to be formulated with vaccines used in the treatment of immunocompromised patients. This adjuvant contains immunostimulatory bacterial signals together with GM3

ganglioside. VSSP promotes dendritic cell maturation, antigen cross-presentation to CD8⁺ T cells, Th1 polarization, and enhances CD8⁺ T cell response in tumor-free mice. Currently, four cancer vaccines using VSSP as the adjuvant are in Phase I and II clinical trials. In this review, we summarize our work characterizing the unique ability of VSSP to stimulate antigen-specific CD8⁺ T cell responses in two immunocompromised scenarios; in tumor-bearing mice and during chemotherapy-induced leukopenia. Particular emphasis has been placed on the interaction of these nanoparticles with MDSCs, as well as comparison with other cancer vaccine adjuvants currently in preclinical or clinical studies.

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Key words: Very small size proteoliposomes; Adjuvants; Tumors; Myeloid-derived suppressor cells; Leukopenia; Chemotherapy

Core tip: Very small size proteoliposomes (VSSP) is a nanoparticulated adjuvant being used in the formulation of several cancer vaccines that are currently in clinical trials. In this review we summarize the unique ability of VSSP to stimulate antigen-specific CD8⁺ T cell responses in tumor-bearing mice and in mice with chemotherapy-induced leukopenia, both immunosuppressive scenarios frequently found in cancer patients. As a possible mechanism of this efficacy, we have focused on the modulation of myeloid-derived suppressor cells (MDSCs) by these nanoparticles, in the context of the current knowledge about the interaction of cancer vaccine adjuvants with MDSCs.

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INTRODUCTION

The central importance and complexity of the interactions between tumors and the immune system has only recently been recognized, with rapidly expanding investigations in the last decade. Tumors are not only shaped by the immune system^[1,2] but actively induce impairment of antigen-presenting cells (APCs) as well as effector T lymphocytes^[3,4], contributing significantly to both tumor progression and metastasis. One of the key cellular mediators of tumor-induced immunosuppression are myeloid-derived suppressor cells (MDSCs), which not only are the manifestation of the myeloid differentiation block that causes loss of mature APCs, but also actively and directly inhibit the lytic activity of both CD8⁺ T cells^[5,6] and NK cells^[7].

MDSCs are currently thought of as a heterogeneous population of immature myeloid cells with suppressive activity. In mice these cells are routinely identified by the co-expression of CD11b and Gr1 markers. More recently, two subpopulations of MDSCs have been identified with different phenotypes and mechanisms of suppression: monocytic (Mo-MDSCs) and granulocytic (G-MDSCs)^[8-11]. In tumor-bearing mice, as well as in cancer patients, the G-MDSCs constitute 70%-80% of overall MDSCs, whereas Mo-MDSCs represent only 20%-30%^[11-14]. Mo-MDSCs (CD11b⁺Ly6C^{hi}Ly6G⁻) are highly immunosuppressive and exert their suppression *via* antigen-independent mechanisms^[15-18]. In comparison, G-MDSCs (CD11b⁺Ly6C^{lo}Ly6G⁺) are moderately immunosuppressive, release reactive oxygen species (ROS) and require antigen-specific interaction with T cells to induce tolerance^[9,11,19,20]. Several mechanisms of MDSC-mediated suppression have been described and are extensively detailed in other reviews^[3,21]. Among these, the depletion of L-arginine, production of nitric oxide (NO) and generation of ROS/reactive nitrogen species have been linked to the overexpression of arginase 1 (ARG1), inducible nitric oxide synthase (NOS2) and NADPH oxidase^[3,13,22]. MDSCs are also able to expand regulatory T cells (Tregs) populations^[23,24] and can differentiate into tumor-associated macrophages within the tumor microenvironment^[25,26]—both regulatory populations that play an important role in tumor-induced immunosuppression. Recent findings suggest that MDSCs can also facilitate tumor-progression and metastasis by increasing angiogenesis^[27,28], *via* secretion of matrix metalloproteinases^[29,30] and by aiding in the formation of the metastatic niche^[27,31].

Given the pro-tumor importance of MDSCs, many efforts have been undertaken to find drugs capable of reducing the number of circulating MDSCs, abrogate MDSCs suppressive function or differentiate these cells into mature APCs. For instance, it has been demonstrated that 25-hydroxy vitamin D3 and all-trans retinoic acid reduce the frequency of MDSCs by inducing their differentiation towards HLA-DR⁺ cells and dendritic cells (DCs), respectively, in patients with advance head and neck squamous cell carcinoma and metastatic renal cell

carcinoma (RCC)^[32-34]. Sunitinib, a pan-receptor tyrosine kinase inhibitor, and chemotherapeutic agents (taxanes, gemcitabine and 5-fluorouracil) also decrease circulating MDSCs in patients with RCC, melanoma, pancreatic and esophagogastric cancer^[35,36]. Finally, the phosphodiesterase-5 inhibitor sildenafil diminishes the suppressive function of human MDSCs^[37].

Although the pharmacological modulation of MDSCs represents a potentially important strategy for cancer treatment, none of these drugs detailed above have thus far improved the clinical outcome in cancer patients. These data suggest that inhibiting MDSCs alone (unlike the T cell checkpoint inhibitors) is not sufficient to achieve an effective anti-tumor response, and that combination with strategies to specifically activate immune responses against the cancer are needed. However, most cancer vaccines have not shown significant objective responses in clinical trials. But, the unimpressive clinical impact of active immunotherapy in cancer patients may be in turn tied to the immunosuppressive environment generated by tumors^[3,4,21] as well as the aggressive chemotherapeutic treatments used in patients, which frequently induce leukopenia^[38-40]. Thus, the combination of cancer vaccines with agents interfering with MDSCs number/function may be an effective approach to generate fully functional tumor-specific immune effectors. Even more desirable would be to find agents that are capable of simultaneously activating tumor-specific effector cells, inhibiting the suppressive function of MDSCs, and diminishing leukopenic period after chemotherapy. As detailed below, these are all properties of the VSSP adjuvant.

Adjuvants are critical but largely unappreciated components of vaccine formulations, necessary to potentiate the immune response specific for the nominal antigen. This is particularly important in cancer, where the vaccine antigen is often a self protein for which self-tolerance needs to be broken. In recent years the interaction of adjuvants with regulatory cells, and particularly MDSCs, have begun to be studied^[41-45]. This field is still in its infancy however, and there is only strong evidence for the modulation of tumor-induced MDSCs by synthetic oligodeoxynucleotides containing unmethylated CpG motifs (CpG)^[44], formalin-inactivated Herpes Simplex Virus^[43] and VSSP^[42], while indirect evidence suggests that other adjuvants may expand MDSCs once inoculated in the hosts. Therefore, the selection of suitable adjuvants for cancer vaccines is a very complex matter, and needs to be based in the ability to overcome the immunosuppression generated by tumors and chemotherapy. In this review we summarize the immunomodulatory properties of VSSP, a novel adjuvant for cancer immunotherapy.

GENERAL PROPERTIES OF VSSP

VSSP is a nanoparticulated adjuvant obtained through the hydrophobic incorporation of the GM3 ganglioside into outer membrane vesicles (OMVs) from *Neisseria meningitidis*^[46]. It has been shown that VSSP contains TLR4

Table 1 Modulation caused by very small size proteoliposomes on different immune cell populations

| Immune cell | Effect of VSSP | Ref. |
|--------------------------|---|---------|
| DCs | Increases costimulation and MHCII expression | [47] |
| | Enhances production of IL-12, IL-6, IL-18, IL-1 β and reduces secretion of IL-10 | [47,48] |
| | Induces Th1-polarizing capacity | [47] |
| | Facilitates cross-presentation of protein antigens | [50] |
| MDSCs | Expands poorly suppressive MDSCs | [42] |
| | Reduces the suppressive function of tumor-induced MDSCs | [42] |
| | Impairs migration of tumor-induced MDSCs towards the tumor microenvironment | [42] |
| | Promotes differentiation of tumor-induced MDSCs into mature DCs | [42,59] |
| | Reduces the suppressive function of MDSCs generated during chemotherapy-induced leukopenia | [62] |
| | Induces Th1 polarization | [47] |
| CD4 ⁺ T cells | Potentiates CTL responses in healthy mice. | [50] |
| CTL | Primary expansion independent of CD4 ⁺ T cell help | |
| | Generates similar CTL responses in tumor-free and tumor-bearing mice | [42] |
| | Increases CD8 ⁺ T cell counts, with memory phenotype, and protects CTL response in leukopenic mice | [62] |

VSSP: Very small size proteoliposomes; MDSCs: Myeloid-derived suppressor cells; DCs: Dendritic cells; CTL: Cytotoxic T lymphocytes.

and TLR2 ligands, which play an important role in the immunomodulatory properties of this compound^[47,48]. Immunization of mice, monkeys and humans with VSSP generated IgM and IgG antibodies specific for both GM3 and OMPs^[46,49]. This adjuvant also induced DC maturation, as evidenced by the increased expression of MHCII and CD40, CD80 and CD86 costimulatory molecules (Table 1)^[47]. Additionally, VSSP-treated DCs secreted inflammatory cytokines such as IL-12p40/70 and IL-6^[47]. DCs from healthy donors treated *in vitro* with VSSP produced not only higher levels of IL-6 but also decreased amount of IL-10, in comparison to lipopolysaccharide [LPS, the prototypic TLR4 agonist (Table 1)]^[48]. Experiments with antigen-specific transgenic T cells demonstrated that VSSP-treated DCs induced a Th1 phenotype in stimulated naïve CD4⁺ T cells^[47]. Furthermore, VSSP expanded CD8⁺ T cells specific for the co-injected antigen and promoted an effective *in vivo* cytotoxic T lymphocytes (CTL) response^[50]. In the latter case, CD8⁺ T cell activation was mediated by the cross-presentation of exogenous antigens and did not require help from CD4⁺ T cells (Table 1)^[50].

More recently, we have found that VSSP treatment of naïve mice (without a vaccine antigen) significantly increased the frequency of splenic CD11b⁺Gr1⁺ cells^[42]. However, these CD11b⁺Gr1⁺ cells were poorly suppressive on both antigen-specific and allogeneic CTL assays (Table 1). The residual suppressive capacity of VSSP-derived MDSCs depended on NOS but not ARG, which was associated with a significant increase of NOS3 en-

zyme. Although VSSP contains TLR2 and TLR4 ligands, the interaction of these particles with the immune system appears to be more complex than can be explained by just TLR activation. For example, OMPs containing the same TLR ligands induced a significantly lower expansion of CD11b⁺Gr1⁺ cells than did VSSP, indicating that the presence of the GM3 ganglioside is also relevant for the immunomodulatory properties of this compound.

VSSP-induced expansion of MDSC numbers is not entirely unexpected, as MDSCs have also been reported to accumulate in mice treated with granulocyte and macrophage colony-stimulating factor (GM-CSF)^[51,52], LPS^[41], CpG^[53], complete Freund's adjuvant^[45] and Bacillus Calmette-Guérin from *Mycobacterium bovis*^[54]. Similar MDSCs expansion has been described for other conditions involving major inflammatory responses, such as superantigen vaccination^[55], polymicrobial sepsis^[56], after burn^[57] and traumatic injuries^[58]. These findings are consistent with a physiological role of MDSCs as a counterbalancing mechanism to inflammation, preventing collateral damage to the tissue caused by activated T cells once the "dangerous" antigen has been eliminated.

EFFECT OF VSSP ON TUMOR-BEARING IMMUNOCOMPROMISED HOSTS

The effect of VSSP on the phenotype, suppressive function and differentiation status of tumor-induced MDSCs has been evaluated in mice bearing C26GM, EL4, EG.7 and MCA203 tumors (Table 1)^[42]. Splenic MDSCs derived from VSSP-treated tumor-bearing mice (MDSCs-T+V) contained a higher frequency of CD11b⁺Gr1^{hi} and Ly6C^{lo}Ly6G⁺ G-MDSCs than untreated tumor-bearing counterparts (MDSCs-T). In addition, IL-4R α is down-regulated on MDSCs-T+V, and these cells showed an increase of the homing molecule CD62L. Consistent with our *in vitro* studies, the suppressive function of tumor-induced splenic MDSCs was significantly reduced when VSSP is given *in vivo*. Several different findings support this effect of VSSP. First, MDSCs-T+V were unable to suppress the hemagglutinin (HA) peptide-specific proliferation of CD8⁺ T cells from CL4 TCR transgenic mice, in the same experimental setting where equal number of MDSCs-T were significantly inhibitory. *In vitro* ⁵¹Cr release CTL assays demonstrated that, as expected, MDSCs-T completely suppressed both antigen-specific and alloantigen-specific lytic activity of CD8⁺ T cells. In contrast, MDSCs-T+V isolated from EL4 and C26GM tumor-bearing mice only marginally affected the generation of the CTL.

The effect of VSSP on MDSCs *in vivo* was further examined in adoptive transfer experiments. In the first approach, MDSCs-T and MDSC-T+V were adoptively transferred into CD45.1⁺ B6 congenic mice, which previously received the transference of ovalbumin (OVA)-specific CD8⁺ T cells from OTI transgenic mice, and vaccinated with the immunodominant OVA₂₅₇₋₂₆₄ (SIINFEKL) peptide emulsified in incomplete Freund's adju-

vant (IFA). Similar frequencies of IFN- γ ⁺ antigen-specific CD8⁺ T cells were found in recipient mice transferred with MDSCs-T+V compared to control mice receiving no MDSCs, whereas transfer of MDSCs-T significantly impaired the activation of OTI lymphocytes. Additional experiments were performed to compare VSSP with other adjuvants or well-established vaccination systems. On this regard, we found that VSSP-based vaccines are more efficient than vaccination with DCs or vaccines employing the adjuvant polyinosinic:polycytidylic acid (polyI:C) in activating antigen-specific CTL responses in the presence of MDSCs-T. In fact, vaccination of BALB/c mice, which had been adoptively transferred with both congenic antigen-specific CD8⁺ T cells and MDSCs-T, with HA peptide in VSSP adjuvant prevented the MDSCs-T-mediated suppression of CD8⁺ T cell responses that was observed in mice vaccinated with HA-pulsed DCs. Also congenic OTI CD8⁺ T cells transferred to EG.7 tumor-bearing mice produce IFN- γ in response to VSSP admixed with SIINFEKL peptide- but not to a vaccine consisting of SIINKEKL-pulsed DCs. Importantly, the OVA-specific *in vivo* CTL response generated in mice with EL4 tumors by the administration of OVA/VSSP was comparable to that observed in tumor-free mice, whereas vaccination with OVA/polyI:C was unable to overcome the tumor-induced impairment of the CTL response.

In addition to TCR transgenic T cell responses to a model antigen, we have found that VSSP blunts MDSC-mediated suppression of endogenous T cell responses to native tumor antigen, by measuring the inhibition of tumor-specific CD8⁺ T cells by MDSCs in an ELISPOT assay. CD8⁺ T cells isolated from MCA203 tumor-bearing mice did not release IFN- γ when stimulated with MCA203 tumor cells, irrespective of the presence of MDSCs. In contrast, a significant frequency of CD8⁺ T cells derived from VSSP-treated tumor-bearing mice were activated by tumor cells and produced IFN- γ , even when MDSCs-T+V were added to the culture. Importantly, MDSCs-T maintained their ability to suppress tumor-specific CTL in this experiment.

Within the tumor microenvironment itself, VSSP treatment did not change the phenotype and functional capacity of CD11b⁺ sorted MDSCs. However, adoptively transferred congenic MDSCs-T had a reduced ability to infiltrate tumors in EL4 tumor-bearing mice treated with VSSP. More importantly, in these VSSP-treated mice, tumor-infiltrating transferred MDSCs-T were more differentiated into CD11c⁺MHCII⁺CD11b⁻ phenotype characteristic of DCs, and did not differentiate towards MHCII⁺F4/80⁺ macrophages. A similar differentiation pattern was observed *in vivo* in the spleen and lymph nodes from VSSP-inoculated tumor-bearing mice. In a more recent work, it was demonstrated that *in vitro* treatment with VSSP of tumor-induced MDSCs was sufficient to differentiate this immature population towards phenotypically mature DCs and, more importantly, causes the loss of their suppressive function^[59]. Since VSSP contains a TLR4 ligand, a comparison with

LPS was done in the same experimental setting. Interestingly, incubation with LPS fails to differentiate tumor-induced MDSCs into DCs and, consequently, these cells retain their inhibitory activity^[59]. In agreement with these results, Greifenberg *et al.*^[60] have shown that incubation of bone marrow (BM)-derived MDSCs with the combination of LPS and IFN- γ increases NO secretion, enhancing the suppressive activity of these MDSCs and impairing their maturation into DCs. These findings further suggest that VSSP's effect on MDSCs is not a shared characteristic of all TLR4 agonists, but is a unique property of VSSP. Other authors have reported that TLR4 signaling is involved in the promotion of tumor growth associated with the recruitment of G-MDSCs, through the interaction with S100A9 protein^[61]. VSSP also expands G-MDSCs subpopulation in tumor-bearing mice, however it also potentiates CTL responses and anti-tumor activity on those mice^[42]. Therefore, the complexity of signals in the structure of VSSP (TLR2 agonist, GM3 ganglioside, *etc.*) likely makes these particles distinct from single TLR4 agonists. In fact, VSSP can induce activation of BM-derived DCs obtained from LPS hyporesponsive mice (C3H/HeJ)^[47].

It has been shown in the literature that other adjuvants can also reduce the suppressive function of tumor-recruited MDSCs. For instance, intratumoral injection of CpG reduces the suppressive function of Mo-MDSCs and induces their differentiation towards macrophages with tumoricidal capability^[44]. However, CpG does not modify G-MDSCs, and intratumoral injections in patients may be difficult to impossible. Formalin-inactivated Herpes Simplex Virus also decreases the suppressive function of MDSCs-T, but whether this adjuvant is able to differentiate MDSCs has not been addressed^[43].

INFLUENCE OF VSSP ON CHEMOTHERAPY-ASSOCIATED IMMUNOSUPPRESSED HOSTS

The ability of VSSP to rescue the number and functionality of relevant immune populations on mice undergoing chemotherapy-induced leukopenia has been also tested (Table 1)^[62]. The widely used chemotherapy agent cyclophosphamide (CY) was used to induce the leukopenic setting for these studies. In this model, VSSP accelerated the recovery of specific leukocytes population when administered in the early stages of leukopenia. Splenic CD4⁺ and CD8⁺ T cells (with a memory CD4⁺CD44^{hi} and CD8⁺CD44^{hi} phenotype) and CD11c⁺CD11b⁺ DCs were some of the populations most enhanced by VSSP in leukopenic mice. Interestingly, MDSCs were also significantly expanded. However, similar to what was seen in the tumor-mediated immunosuppression setting, MDSCs from leukopenic mice treated with VSSP showed a reduced capacity to suppress T cell responses, compared to CY-induced MDSCs (Table 1). Importantly, in the same experimental setting, we found that polyI:C treat-

ment induced none of the effects observed with VSSP inoculation.

The ability of VSSP to activate antigen-specific CD8⁺ T cells was also tested in leukopenic mice. In this immunocompromised scenario, vaccination with a single dose of OVA/VSSP, at the time point corresponding to the lowest CD8 counts, induced significant antigen-specific CTL responses. In comparison, vaccination with three doses of OVA/polyI:C was not capable of inducing antigen-specific effector CD8⁺ T cell activation. Furthermore, VSSP treatment of OVA/polyI:C vaccinated animals restored the dampened CTL responses in polyI:C-treated leukopenic mice, indicating that VSSP can function as an immunomodulator as well. This effect could be associated to the capacity of VSSP, different from polyI:C, to accelerate the recovery of effector CD8⁺ memory T cells and to induce the expansion of DCs and less suppressive MDSCs.

Granulocyte colony-stimulating factor (G-CSF) is the standard growth factor used in the clinic to revert chemotherapy-induced leukopenia, but also has been reported to be a tumor-derived factor that induces MDSCs generation and recruitment^[63]. Therefore we assessed whether treatment with recombinant G-CSF could restore the *in vivo* CTL response barely induced by OVA/polyI:C vaccine in CY-treated mice^[62]. Administration of G-CSF has no impact in the impaired antigen-specific CTL response, possibly due to the expansion of MDSCs but also *via* G-CSF-induced Th2 responses^[64] and the resulting differentiation of Tregs that may impair effector T lymphocyte proliferation^[65]. However, when VSSP was given with G-CSF, the ability of VSSP to restore CD8⁺ T cell function was not affected, which opens the possibility for their concomitant use in the clinic. Moreover, the functionality of MDSCs recruited in these experiments was additionally evaluated. As expected from previous reports, our data also demonstrated that, in leukopenic mice treated with G-CSF, the induced MDSCs were highly suppressive. Importantly, the concomitant treatment with VSSP dampened the inhibitory function of MDSCs expanded after G-CSF injection. To our knowledge, no other adjuvant has been tested in this immunosuppressive leukopenic scenario induced by chemotherapy.

ANTI-TUMOR ACTIVITY OF VSSP

Several pre-clinical studies support the anti-tumor efficacy of VSSP, whether used alone or in combination with other tumor-associated antigens different from the GM3 ganglioside. The combination of surgery and VSSP alone prevented tumor recurrence and improved survival in melanoma B16F10 tumor-bearing mice^[66]. In a different tumor model, treatment of mice bearing MCA203 tumors with three doses of VSSP was sufficient to significantly delay tumor growth^[42]. Of interest, GM3 ganglioside, an important component of VSSP, is highly expressed on both melanoma B16F10 and MCA203 sar-

coma. Particularly in MCA203 tumor-bearing mice, treatment with VSSP alone caused a significant increase in the frequency of classical IFN- γ -producing CD8⁺ T cells specific for MCA203 antigens, suggesting an antigen-spreading likely induced by the initial response against the GM3 ganglioside^[42]. Moreover, VSSP-adjuvanted vaccines (both peptides and whole proteins) have shown anti-tumor activity. For instance, a vaccine containing the extracellular domain of murine epidermal growth factor receptor (EGFR) and VSSP has a potent anti-metastatic effect in the Lewis lung carcinoma model^[67]. In a mouse model of cervical cancer induced by Human Papilloma Virus (HPV), the immunization with an E7-derived CTL peptide from HPV 16 mixed with VSSP induced regression of established tumors^[68]. Therapeutic vaccination of EG.7 tumor-bearing mice with OVA or SIINFEKL peptide adjuvanted in VSSP, but not SIINFEKL emulsified in IFA, caused a significant reduction of tumor growth^[42]. However, VSSP administration alone to EL4 and C26GM tumor-bearing mice, with the same schedule associated with the inhibition of MDSCs suppressive function, does not delay tumor growth. One possible explanation for the absence of an anti-tumor effect of VSSP alone in these models is the lack of a tumor-associated antigen during treatment, and consequently, the absence of antigen-specific CD8⁺ T cell activation. In fact, EL4 tumors express low levels of GM3 whereas an inappropriate exposure of this ganglioside on the surface of C26GM tumor cells has been observed^[42]. Altogether, these data strongly suggest that the best induction of anti-tumor responses requires combining the abrogation of tumor-induced MDSCs with a specific stimulation of T lymphocytes, which can be successfully done by mixing a proper tumor-associated antigen with VSSP.

Finally, four therapeutic cancer vaccines employing VSSP as adjuvant are in clinical trials. An EGFR-based vaccine^[67] is currently in Phase I clinical trials. A Phase I clinical trial in patients with advanced solid tumors using a formulation of a mutated vascular endothelial growth factor^[69] and VSSP has been recently completed. In this trial, the most common adverse events were Grade 1 pain and erythema at injection site and Grade 1 fever^[70]. Additionally, a gonadotropin releasing hormone-based vaccine^[71] and a HPV-derived peptidic vaccine^[72] are currently in Phase II trials in prostate cancer patients and women with high-grade cervical intraepithelial neoplasia, respectively. Both vaccines have previously shown to be safe and immunogenic. The most frequent adverse event in patients receiving the HPV vaccine was local pain at the vaccination site, whereas fever, tremors and cramps were seen in few cases, but none exceeded Grade 1^[72]. Another Phase I trial using VSSP alone in metastatic melanoma patients demonstrated the safety of this preparation even in the presence of Montanide ISA 51, with toxicity consisting of local reaction at the site of injection and mild fever and chills^[49]. In this trial both humoral and cellular responses were induced by the VSSP treatment. Additionally, an ongoing physician-lead trial is evaluat-

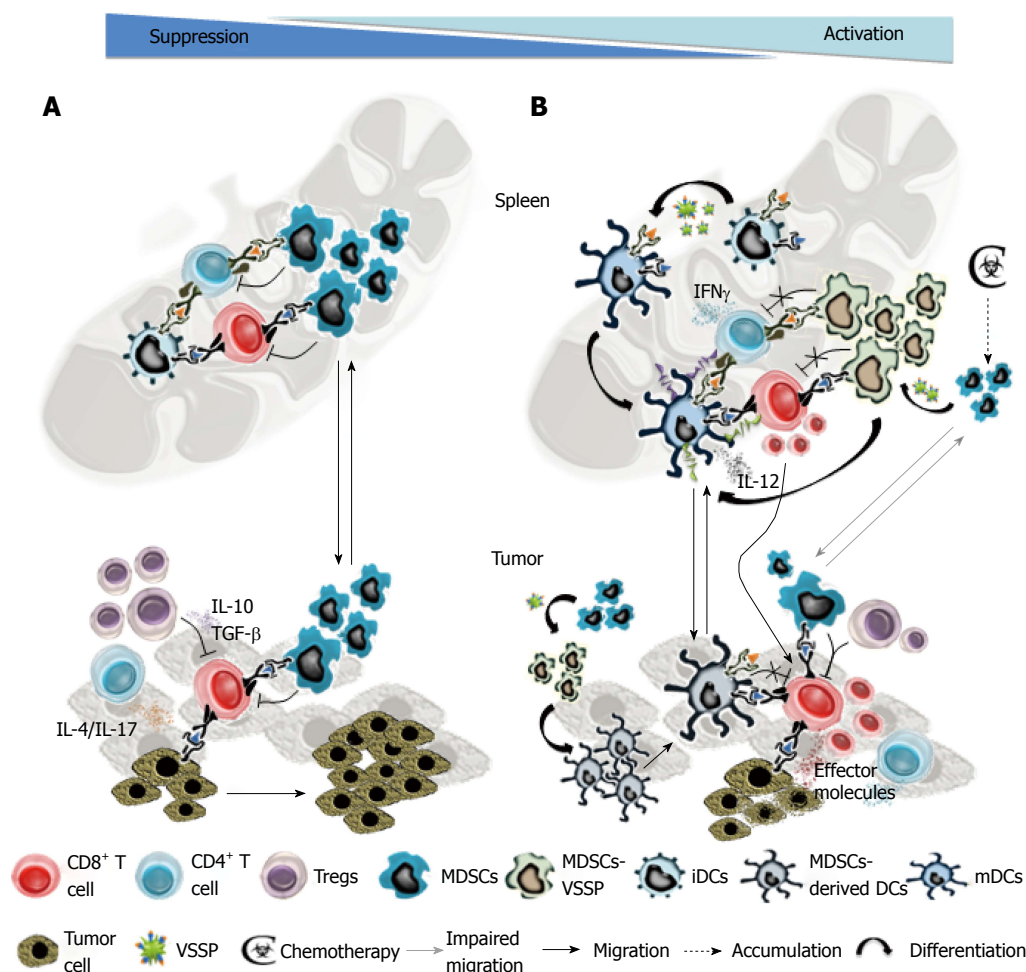


Figure 1 Schematic of potential immunomodulatory effects of very small size proteoliposomes in tumor-bearing hosts. A: Tumor-associated immunosuppressive networks prevent the elimination of neoplastic cells by specific T cells, thus contributing to tumor growth and metastasis; B: VSSP administration reduces the suppressive function of tumor-induced MDSCs, impairs their migration to the tumor microenvironment and promotes their differentiation towards DCs, both at the tumor and secondary lymphoid organs. VSSP also stimulates the activation and effector function of tumor-specific CTL, and combined with the concomitant reduction in the frequency of suppressive MDSCs and Tregs at the tumor site, further enhances elimination of neoplastic cells. An accelerated recovery from chemotherapy-induced leukopenia with VSSP treatment also contributes to a better anti-tumor response. VSSP: Very small size proteoliposomes; MDSCs: Myeloid-derived suppressor cells; DCs: Dendritic cells; CTL: Cytotoxic T lymphocytes; IL: Interleukin; TGF: Transforming growth factor.

ing the modulation of tumor-induced MDSCs by VSSP treatment alone in RCC patients.

CONCLUSION

The immunomodulatory and anti-tumor properties of VSSP are summarized in Figure 1. In tumor-bearing mice, activation and effector function of tumor-specific CD8⁺ and CD4⁺ T cells are impaired, among other factors, due to ineffective antigenic presentation by immature DCs and through multiple suppressive mechanisms exerted by MDSCs. Experimental evidence suggest that VSSP-based vaccines could promote cross-presentation of the formulated antigen by DCs, drive the full maturation of the DCs and, simultaneously, inhibit tumor-induced MDSCs immunosuppression. In addition, VSSP could induce Th1 polarization on tumor-specific CD4⁺ T cells. All these effects may significantly enhance the proliferation and activation of tumor-specific CD8⁺ T cells, thus eliciting robust anti-tumor immunity. VSSP

also diminishes the migration of MDSCs towards the tumor site and promotes their differentiation into DCs. Tumor-infiltrating MDSCs have been related with the recruitment and expansion of Tregs^[23,24,73], in addition to an impaired migration of effector T cells^[74]. Thus, within the tumor microenvironment, VSSP treatment may tip the balance between functional T cells vs suppressive MDSCs/Tregs to favor the immune effectors that ultimately lead to an anti-tumor response. The higher frequency of DCs could additionally contribute to activate T cells specific for other tumor antigens by capturing, processing and presenting the proteins released by dying tumor cells. In chemotherapy-treated individuals, VSSP also accelerates the homeostatic recovery of CD8⁺ T cells and DCs, whereas the suppressive function of chemotherapy-induced MDSCs is abrogated. Altogether, these elements support the use of VSSP as a novel adjuvant or immunomodulator for active immunotherapy and, particularly, for the combination with chemotherapy in the clinical setting.

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Role of host immune responses in sequence variability of HIV-1 Vpu

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Abstract

Viral protein U (Vpu) is an accessory protein associated with two main functions important in human immunodeficiency virus type 1 (HIV-1) replication and dissemination; these are down-regulation of CD4 receptor through mediating its proteasomal degradation and enhancement of virion release by antagonizing tetherin/BST2. It is also well established that Vpu is one of the most highly variable proteins in the HIV-1 proteome. However it is still unclear what drives Vpu sequence variability, whether Vpu acquires polymorphisms as a means of immune escape, functional advantage, or otherwise. It is assumed that the host-pathogen interaction is a cause of polymorphic phenotype of Vpu and that the resulting functional heterogeneity of Vpu may have critical significance *in vivo*. In order to comprehensively understand Vpu variability, it is important to integrate at the population level the genetic association

approaches to identify specific amino acid residues and the immune escape kinetics which may impose Vpu functional constraints *in vivo*. This review will focus on HIV-1 accessory protein Vpu in the context of its sequence variability at population level and also bring forward evidence on the role of the host immune responses in driving Vpu sequence variability; we will also highlight the recent findings that illustrate Vpu functional implication in HIV-1 pathogenesis.

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Key words: Human immunodeficiency virus type 1; Vpu; Sequence variability; Immune responses; Human leukocyte antigen class I

Core tip: Viral protein U (Vpu) is a highly polymorphic human immunodeficiency virus type 1 (HIV-1) accessory protein; however factors that are attributable to Vpu sequence variability are not well defined. In this review we have focused on the immune responses both innate (natural killer cells) and adaptive (cellular and humoral) immunity that are directed towards HIV-1 Vpu and we also show the interaction between Vpu and host cellular factors. We also highlight evidence that suggests interaction between the host immune responses and Vpu may contribute to Vpu sequence variability. Finally we have summarized the current knowledge on HIV-1 Vpu functions including Vpu evasion activities from the host immune surveillance.

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INTRODUCTION

Human immunodeficiency virus type 1 (HIV-1) demonstrates a significant genetic diversity due to its high

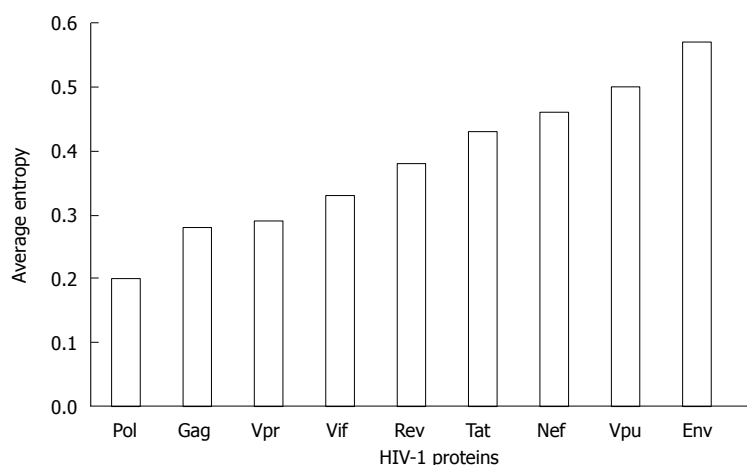


Figure 1 Sequence variability of human immunodeficiency virus type 1 proteins. The sequence variability of nine proteins of human immunodeficiency virus type 1 (HIV-1) shown in the graph was determined by using Shannon entropy approach^[24,90]. The full genome clade B sequences of the individual patients were retrieved from Los Alamos database ($n = 544$). Vpu: Viral protein U.

mutation rate; so far this extraordinary diversity has been a major setback in development of vaccine and antiretroviral drugs. Low fidelity of reverse transcriptase that give rise to error prone replication process, high progeny production, turnover rates and recombination of circulating HIV-1 strains are some of the viral factors that contributes to HIV-1 diversity^[1-3]. The adaptive potential of HIV-1 is shaped by both virus and the host immune factors, in other words both the diversifying and purifying selection factors influence HIV-1 diversity. In fact, strong evidence has also indicated that the host immune responses influence HIV-1 diversity by selection of escape mutations^[4-6]. Thus a comprehensive analysis of the dynamics of polymorphisms in HIV-1 proteins is a powerful tool to reveal actual interactions between HIV-1 and the host immune system^[7-9].

HIV-1 viral protein U (Vpu) is a 16-kDa accessory protein^[10] responsible for various functions such as CD4 down-regulation^[11-13] and enhancement of virion release by antagonizing tetherin/BST2^[14-17]. Interestingly, functionally competent Vpu (with respect to BST-2 antagonistic activity) were only found in the pandemic group M subtypes, suggesting that Vpu functional adaptation may confer pandemic spread of this HIV-1 subtype^[18]. In general, the host genetic factor is one of the main driving force of sequence polymorphism in HIV-1^[18], as evidenced in HIV-1 Nef^[7,19-21] and Env^[22,23] proteins whose highly polymorphic phenotype is mostly attributed by the host immune responses such as HLA class I-restricted CD8+ T lymphocytes and neutralizing antibodies, respectively. However, it is still unclear to what extent the host immune responses influence Vpu sequence variation. This review focuses on the role of host immune responses in Vpu sequence variability. Briefly, we also discuss the current understanding of Vpu functions including evasion of the immune system and their implication in viral pathogenesis.

SEQUENCE VARIABILITY OF VPU

Vpu exhibit a stable reading frame *in vivo* despite being a highly variable protein, suggesting functional importance of Vpu in HIV-1 replication and persistence. Further-

more, it has evidently been shown that only HIV-1 strains of the pandemic M group evolved a fully functional Vpu that efficiently antagonizes human tetherin/BST-2; this suggests that Vpu evolutionary adaptation may be associated with the pandemic spread of HIV-1^[18]. Several studies have demonstrated the extent of Vpu sequence variability both at inter- and intra-patient level. By using the 101 aligned amino acid sequences of entire HIV-1 genome, one study showed that Vpu had the highest average entropy score in comparison to other proteins in HIV-1 genome^[24]. Another study analyzing the intra-patient diversity and adaptation of non-structural genes in primary HIV-1 subtype C infection reported that *vpu* compared to *vif*, *vpr*, *tat exon 1* and *rev exon 1* genes has the highest mean of intra-patient diversity that increased gradually^[25]. We retrieved full lengths clade B sequences ($n = 544$) of HIV-1 proteins (Gag, Pol, Env, Nef, Vif, Vpu, Vpr, Tat and Rev) from Los Alamos database and the average entropy score of each protein was determined. Vpu was observed to be one of the proteins with the highest average entropy score (Figure 1), confirming the highly variable nature of Vpu at population level. However, interestingly, a recent study has shown that despite extensive Vpu sequence variation in HIV-1 infected individuals, Vpu functions (CD4 cell surface downregulation and tetherin counteraction activity) were maintained^[26].

IMMUNE RESPONSES TOWARDS VPU

Humoral immunity

Several studies have reported Vpu-specific humoral immune responses during HIV-1 infection^[27-31]. However there has been some controversy on correlation between the presence of anti-Vpu Ab responses in HIV-infected patients' sera and clinical outcome. Some studies have indicated that anti-Vpu Ab responses may influence the clinical outcomes in HIV-1 infected individuals^[27,28,30,31], while on the other hand other studies have showed no correlation^[29]. These findings indicate that Vpu is indeed a target of antibodies although no evidence yet support that such antibody responses influence the Vpu variability. The epitopic regions for such antibodies reported include 37-50^[30] and 68-81^[28] of Vpu; nonetheless there

is no specific Vpu activity mapped to these regions so far. However, considering that Vpu is a small protein (81 amino acids); it is intriguing to test whether such Vpu-specific antibodies can inhibit Vpu functions and subvert viral replication.

Cellular immunity

A growing number of clinical evidence has suggested that HLA-restricted, HIV-specific CD8⁺ cytotoxic T lymphocytes (CTL) is mainly involved in controlling HIV-1 replication^[32-34]. CTL responses have been well appreciated in SIV-infected macaque's model^[32,33] and in HIV-1 infected patients of both acute^[35,36] and chronic^[37] phases as well as in elite controllers who spontaneously suppress viral replication below detection limit^[38,39]. HLA-restricted CTL responses are thought to be the main driving force of HIV-1 control and viral evolution^[40-43]. The viral polymorphism in response to immune selective pressures follows predictable patterns and kinetics at the population and these immune "footprints/landscape" could be predictable based on the autologous viral sequences and the host immune genetics^[9,42,44]. However, Vpu has been reported to be a poor target for CD8⁺ T cells as revealed by interferon (IFN)- γ Elispot assay^[45], because only some few epitopes were identified and less than 3% of patients showed detectable Vpu-specific CD8⁺ T cell responses. Although several HLA-restricted CTL epitopes of Vpu are reported^[45-49], this protein is less targeted by CTLs at least compared to the Nef protein. Consistently, our previous study showed only three HLA-associated polymorphisms in Vpu at Glu-5 with HLA-C*03 and Arg-37, Lys-37 with HLA-A*3303 in a chronic HIV-infected patient cohort in Japan ($n = 216$), indicating that the HLA class I has minor contribution (2% of the total codons) towards Vpu variability^[50]. The increased numbers of subjects to 516 showed similar results (DK, ZH, and TU: unpublished observation). Furthermore, an international large IHAC cohort (International HIV Adaptation Collaborative, $n = 1888$) identified that only 26.3% of the highly variable Vpu codons exhibited statistically significant HLA class I associations^[20]. Although the HLA class I-associated viral polymorphisms observed in the two cohorts suggested to be influenced by several factors such as the host genetic profiles, mixture of multiethnic populations, studied sample size, geographical location and circulating HIV-strains, these results suggest that HLA-associated polymorphisms are only partly attributable to the Vpu variability (Figure 2). However, it is of note that the low CTL responses observed in the previous studies^[45,51] and subtle numbers of HLA-associated polymorphisms^[20,50] may be an underestimation due to the current technical limitation toward a highly variable protein, even though a number of studies reported a plenty of CTL targeting^[52,53] and HLA-associated polymorphisms in Nef^[19,20,42], which showed comparable variability with Vpu at a population level (Figure 1).

Natural killer cells

A number of evidence suggests that natural killer (NK)

cells have an important role in control of HIV-1 infection^[54-56]. Assuming that NK cells may act as a selective force, as similar to CTLs, HIV-1 may leave footprints as viral polymorphisms in association with polymorphic NK cell ligand such as killer-cell immunoglobulin-like receptors (KIR). In fact, one study identified 22 amino-acid polymorphisms within the HIV-1 clade B sequence that are significantly associated with the expression of specific KIR genes in chronically HIV-1 infected, treatment naïve patients ($n = 91$)^[44]. Three (13.6%) of these KIR associated polymorphisms were located in Vpu at positions Ser-3 and Vpu-Env overlapping region (Met-71 and His-74) (Figure 2)^[44]. In addition, the HIV-1-specific antibody-dependent NK cell cytotoxicity is identified towards a 13-mer Vpu peptide (⁶⁹EMGHHAPWDVDL⁸¹)^[57]. Such responses are also observed toward Env^[58] and Nef^[59] in HIV-1 infected patients as well. However, there is no evidence at the moment that show antibody-dependent NK cell cytotoxicity associates with viral polymorphisms.

VPU FUNCTIONALITY INCLUDING IMMUNE EVASION ACTIVITY

In order to conquer the hostile host environment, viruses need to evolve and develop critical interactions with the host cellular factors. Vpu does not only play important role in HIV-1 pathogenesis through CD4 receptor degradation^[11] and enhancement of virion release from infected cells by antagonizing tetherin/BST-2^[60-62]; but Vpu has also evolved to interact with and modulate other host surface receptors and factors (Figure 3).

Vpu induces CD4 receptor degradation

Vpu induces the rapid degradation of newly synthesized CD4 receptor molecules that are retained together with Env precursor protein (gp160) in the endoplasmic reticulum^[13]. The cytoplasmic domain of Vpu and the DSGxxS motif are critical in interaction with and degradation of CD4, respectively^[12,63] (Figure 2). The degradation process is achieved by Vpu recruiting β -TrCP and then interacts with CD4 cytoplasmic domain and subsequently subject CD4 to degradation by the ubiquitin-proteasome pathway^[11,64]. In doing so Vpu contributes to the suppression of HIV-1 primary receptor at the surface of the infected cell.

Vpu enhances virion release

Enhancement of virion release by Vpu has been shown to be achieved through antagonizing tetherin/BST-2, an IFN regulated host restriction factor. BST-2 directly binds to virions and hence retains them on the surface of infected cells^[61,62]. Vpu through AxxxAxxx motif in transmembrane domain directly interacts with BST-2 transmembrane domain, the Vpu DSGxxS and [D/E]XXXL[L/I/V] motifs in the cytoplasmic domain also play crucial role in ensuring BST-2 downmodulation^[15,65,66] (Figure 2). Previous studies indicated BST-2

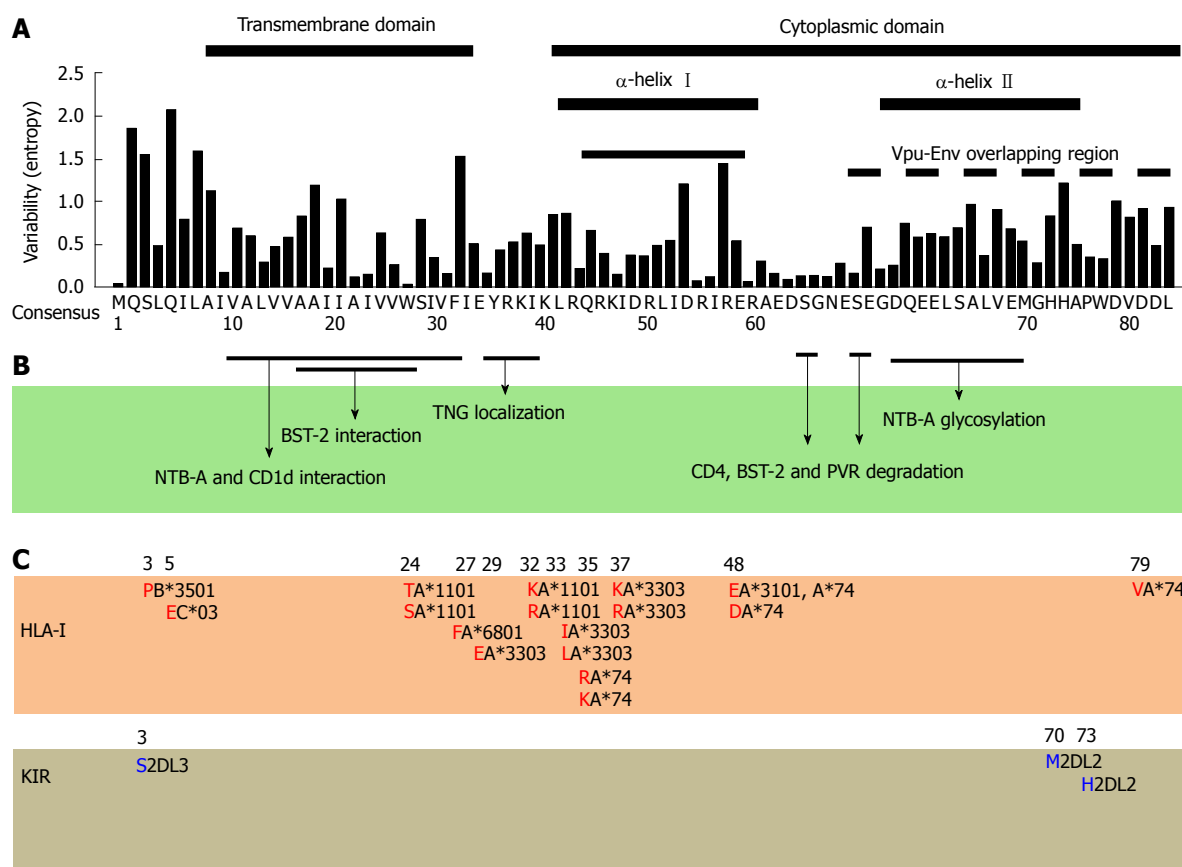


Figure 2 Correlation among amino-acid codon variability, functional regions, and host-mediated immune escape map of human immunodeficiency virus type 1 viral protein U. **A:** Amino acid codon variability is assigned to each position of Vpu using Shannon entropy approach^[24,90]. Sequences were retrieved from Los Alamos database ($n = 1139$), the consensus subtype B sequence is indicated as a reference; **B:** Interacting positions and domains responsible for the indicated functions of human immunodeficiency virus type 1 (HIV-1) Vpu are shown^[14,62,91]; **C:** Immune escape map shows amino acid codons and residues (red and blue) associated with HLA-I alleles^[20,45,50] and killer-cell immunoglobulin-like receptors (KIR)^[44], respectively. The specific alleles are indicated in black adjacent to the amino acid.

downmodulation is through β -TrCP-dependent proteasomal degradation pathway^[67] while others suggested the β -TrCP-dependent endo-lysosomal pathway^[63,68]. In contrast, recent studies showed that BST-2 antagonistic activity by Vpu takes place in the trans-Golgi networks (TGN)^[14]. Vpu interferes with anterograde transport of BST-2 to the cell surface subsequently leading to BST-2 trapping in the TGN^[15-17,69].

Vpu modulation of other cell surface receptors and host factors

Recent studies have indicated that Vpu is emerging as a viral factor with a range of activities devoted to counteracting host innate and adaptive immunity including the modulation of NK cell co-activation ligand NK-T and B cell antigen (NTB-A)^[70], PVR activating ligand of NK cells^[71], and CD1d^[72,73] (Figure 3).

NTB-A triggering is necessary for induction of efficient lysis of target cells upon engagement of the activating receptor NKG2D^[74]. The Ser-52 and Ser-56 residues important for CD4 and BST-2 degradation did not affect NTB-A expression, indicating that the down modulation of NTB-A by Vpu is mediated by different domains^[70]. A recent study has shown that downmodulation of NTB-A is achieved by Vpu interfering with the anterograde trans-

port of NTB-A by retaining it within the Golgi compartment and hence affects its glycosylation pattern that subsequently reduces surface expression of NTB-A^[75].

PVR (CD155, Necl-5) is a ligand for the activating receptor DNAM-1 (CD226) expressed by NK cells^[76,77]. PVR downmodulation by Nef and Vpu is another strategy evolved by HIV-1 to avoid NK cell-mediated lysis of infected cells^[71]. PVR downregulation alters multiple important PVR-mediated innate cellular immune processes such as adhesion and migration, and therefore may influence HIV-1 pathogenesis.

CD1d molecules are important in dendritic cells for lipid antigen presentation to CD1d-restricted NKT cells^[78,79]. CD1d and CD1d-restricted NKT cells are present at pathogen entry sites thus play a crucial role in early immune responses^[80]. Vpu has been shown to be the major viral factor that inhibit recycling of CD1d from the endosomal compartment back to cell surface through retaining CD1d in early endosomes^[72].

Vpu has also been implicated in inhibition of ubiquitination and degradation of p53 (a substrate of SCF^{β-TrCP} ligase complex). The successful interaction of SCF^{β-TrCP} complex with β -TrCP binding motif (DS₅₂GNE₅₆) present in Vpu has been shown to be essential^[81]. It was observed that Vpu mutants with alanine substitutions

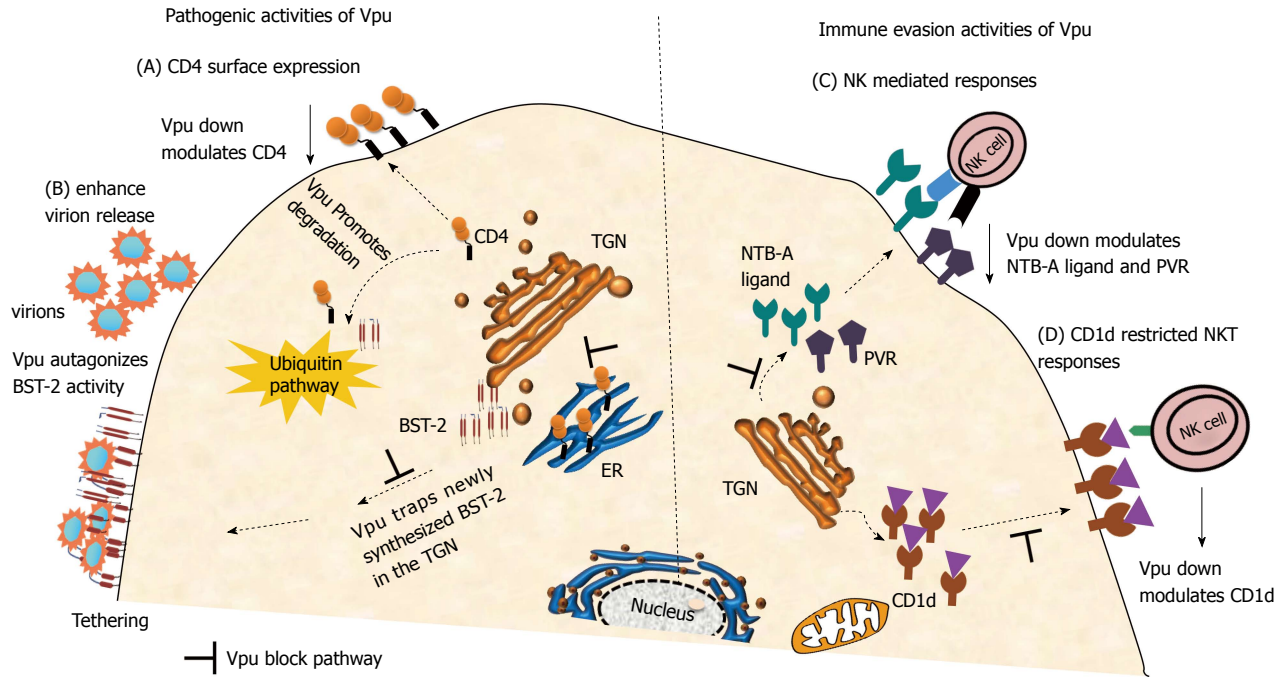


Figure 3 Viral protein U functionality including immune evasion activity. The schematic representation of the cell illustrates some key functions of viral protein U (Vpu) including immune evasion activities. (A): Panel A illustrates CD4 down regulation by Vpu through degradation in a β -TrCP dependent ubiquitination pathway^[11,12,64], (B): Panel B demonstrates enhancement of virion release by Vpu through antagonizing BST-2, which is achieved through direct interaction with BST-2 which subsequently leads to trapping of BST-2 in the trans-Golgi networks^[14-16] and also indicates β -TrCP dependent ubiquitination of BST-2^[62,65,66]; (C): Panel C demonstrates Vpu evasion of NK cell recognition through down modulation of NTB-A ligand^[70] and PVR^[71]; D: Panel D shows down modulation of CD1d from cell surface hence avoid CD1d-restricted NKT cell responses^[72,73]. NK: Natural killer; NKT: Natural killer T.

(DA₅₂GNEA₅₆) failed to stabilize p53 and did not prevent its ubiquitination. This suggested that Vpu is able to achieve modulation of p53 through competing efficiently with p53 protein for the β -TrCP subunit of the SCF complex and hence inhibits subsequent ubiquitination of p53 protein. The modulation of p53 positively correlated with apoptosis during the late stages of HIV-1 infection^[81].

Finally, although Vpu showed multiple functions *in vitro* and *ex vivo*, it is yet clear how and what functions of Vpu are important in viral pathogenesis *in vivo*.

CONCLUSION

The current knowledge on factors that are attributed to Vpu polymorphism has not been quite sufficient; therefore this prompt for further analysis to reveal the unresolved questions of why Vpu is so variable and what factors drive Vpu polymorphism. In order to define the complex dynamics of HIV-1 Vpu evolution, immune escape patterns, and functional adaptation during the course of infection, further insight is needed on the role of host genetics and other immune selection pressures towards shaping HIV-1 Vpu diversity. The emergence of advanced DNA sequencing technologies such as ultra-deep sequence which is superior and more sensitive than Sanger sequence methods has made it possible to accurately detect and analyze minor variants of HIV-1 within a host^[82-85]. Furthermore, the establishment of different contemporaneous cohorts of HIV-1-infected individuals worldwide enables us to examine to what extent the host

immune components play a role on viral adaptation and/or evolution at both intra- and inter-patients' level.

So far the current studies have indicated that the host immune responses directed towards Vpu is not entirely attributable to HIV-1 Vpu variation (Figure 2), it is therefore crucial to apprehend other factors that may explain Vpu variation. Of note previous studies have identified immune responses directed towards Vpu, using peptides of HIV-1 consensus sequences^[45,57]. However, ironically due to Vpu polymorphic nature itself, these results may mask the exact extent to which immune responses contribute to Vpu sequence variation. Alternatively, HIV-1 like other RNA viruses has evolved to shorten its genome length through overlapping its genes^[86]. The overlapping region of Vpu and Env is one of promising aspect to consider when we focus on Vpu variation. Because host immune responses (neutralizing antibodies) contribute to Env polymorphic nature^[87,88], it is enticing to assume that immune responses directed towards Env may influence Vpu polymorphisms through Vpu-Env overlapping region. KIR associated polymorphisms within Vpu-Env overlapping region have been reported previously^[44]. Although it is still unknown whether NK cells recognize Vpu or Env protein, nonetheless these findings indicate the importance of this region for Vpu variability. Furthermore, it is reported that X4- and R5-tropic HIV-1 showed differential amino acid polymorphisms in Vpu^[89], suggesting that cellular compartment influences Vpu variability.

The current increase in number of new findings of

Vpu from pandemic HIV-1 group M strain and other HIV-1 strains, enlighten us the precise role or mechanisms of how Vpu degrade the viral receptor CD4, antagonize tetherin/BST-2, enhance p53 stability and modulate NK-cell activities through modulation of PVR, NTB-A and CD1d receptors (Figure 3). Understanding the mode of action of Vpu and association of the immune factors certainly open plenty of new windows to deciphering the intricate mechanisms associated with HIV-1 immune pathogenesis *in vivo*. Also, understanding pathways of Vpu intra- and inter-patients sequence variability and adaptation may provide us with an alternative approach for prospects of viral persistence and Vpu contributions *in vivo*.

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Targeting TLR4/MAPKs signaling pathway: A better option for therapeutic inhibition of atherosclerosis

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Abstract

Cardiovascular diseases, especially atherosclerosis, found to be the dreadful diseases worldwide. There are diverse pathways associated with the progression of atherosclerosis. One of the important signaling pathways to target atherosclerotic plaque rupture is toll-like receptor 4 (TLR4) Pathway. Several studies are available for illustrating the role of TLR4 in health and diseases. Different types of immune cell are activated in atherosclerosis but primary cells that are activated by the TLR4 signaling are macrophages and endothelial cells. Mechanisms by which macrophages uptake lipids are diverse and it is very important to target signaling pathway responsible for controlling foam cell formation. The process of macrophages transformed foam cell formation is the critical event in progression of atherosclerotic lesion and TLR4 found to have actively participate in the event through mitogen activated protein kinases (MAPKs) activation. The activation of MAPKs signaling pathway leads to the accumulation of cholesterol in the macrophages and also contribute to the dissociation of I κ B and the nuclear translocation of nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) p65 subunit, thereby activating key inflammatory cascade

activation by MAPKs/NF- κ B signaling pathway to induce toxicity by activating different inflammatory parameters. Hence, the review focussed on exploring the role of TLR4/MAPKs signaling pathway for the therapeutic inhibition of atherosclerosis.

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Key words: Atherosclerosis; Toll-like receptor 4; Mitogen activated protein kinase; Foam cells; Inflammatory markers

Core tip: The inhibition of atherosclerosis is one of primary target for the therapeutics of cardiovascular diseases, which is the eminent health problem worldwide. The important function of toll-like receptor 4 (TLR4) in the activation and progression of atherosclerosis is justified here. The TLR4 in turn activates the mitogen activated protein kinases (MAPKs) and nuclear factor kappa-light-chain-enhancer of activated B cells which are responsible for most of the inflammatory events. Hence, therapeutic inhibition of TLR4/MAPKs signaling pathway is one of the best method of inhibiting atherosclerosis.

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INTRODUCTION

Cardiovascular disease, especially atherosclerosis is a main health problem worldwide and it is a disease characterised by the deposition of lipid in the blood vessels. There are several studies undertaken to know the proximal role of

immune system in atherosclerosis^[1]. Macrophages are the primary cells which are present in atherosclerotic lesions and they uptake lipids and get transformed to foam cells. These foam cells are risky and contribute to the development of atherosclerotic plaque rupture.

It was known that inflammatory process and its further cascade by activating immune system may contribute to the development of inflammation related atherosclerosis^[2]. Usually the luminal side of the blood vessel walls are prone to atherosclerotic injury^[3]. The presence of human histocompatibility leukocyte antigen is widely upregulated as the result of inflammatory processes^[4]. There are studies reporting the role of variety of Infectious organisms and HSP60 as trigger of atherosclerosis^[5].

It is very important to know the mechanism by which macrophages uptakes lipid and transformed get into foam cells. Targeting of macrophages transformed to foam cells are very important therapeutic strategies^[6]. The studies on mechanism by which macrophages accumulate OxLDL and its further activation cascades are very important. It usually activates further cascades by activating components like polyoxygenated cholesteryl ester hydroperoxides and in turn activates toll-like receptor 4 (TLR4)^[6].

It was suggested that TLR4 act as a link between inflammation and atherosclerosis^[7]. TLR4 found to have an active participation in the progression of atherosclerotic diseases. It can also interferes with the cholesterol metabolic machinery in macrophages^[8]. The research in TLR4 shown that, silencing of TLR4 gene seems to have reduced the size of atherosclerotic lesion, lipid content and macrophage polarisation in mice fed a high cholesterol diet for continuous six months^[9].

TLR4 found to have act as an important receptor for arterial remodelling^[10]. The activation of TLR4 receptor leads to the further activation of MYD88 protein and through protein cascade further activates mitogen activated protein kinases (MAPKs). The activation of MAPKs are essential for the secretion of chemoattract protein to direct monocytes to the atherosclerotic site^[11]. The study on inhibition of tyrosine phosphatases like MAPKs found to have demolished the atherosclerotic lesion size in mice^[11].

The phosphorylation of MAPKs triggers the activation of several downstream proteins and further activates the nuclear factor translocation (NF- κ B) which ultimately leading to the progression and rupture of atherosclerotic plaque^[12]. Hence, the review focussed on exploring the role of TLR4/MAPKs signaling pathway in therapeutic inhibition of atherosclerosis.

ATHEROSCLEROSIS AND ITS ACTIVATION BY IMMUNE SYSTEM

The immune system is considered to be the guardian of host and its activation as a result to solve the denudation of endothelium. If the immune system unable to control this activation, then it will result in the chronic immune

reaction and can result in the development of atherosclerotic plaque formation^[13]. The regions of atherosclerotic lesions are usually crowded with macrophages and T cells which usually plays an adequate role in innate and acquired immune reactions. It was known in atherosclerotic disease condition there is an clonal expansion of differentiated T cells, which are common in all adaptive immune reactions^[14].

TOLL-LIKE RECEPTOR-4

Toll-like receptor-4 (TLR4) pattern-recognition receptors are found to have an important role in the immune function. TLRs resides in the family of type I transmembrane receptor which consists of intracellular domain and an extracellular leucine repeat domain^[15-17]. It was known that human TLR4 was the first characterised form of mammalian toll^[15]. TLR4 is expressed in different types of cells, among them most abundant cell type is macrophages and dendric cells^[15]. Usually, it is an membrane receptor which act as a signal transducing agent in different inflammatory insult condition like LPS induced^[18-21].

The extensive research in the field of TLRs resulted in knowing mechanism of immune response induced by TLR4, it is by recognition the pathogen associated molecular pattern. The recent studies using mouse knock out genes demonstrated the active role of TLR4 in triggering and development of atherosclerotic plaque^[15].

TLR4 IN HEALTH AND DISEASES

Among the toll like receptors, the best characterised form is the TLR4, which has found to have prominent role in the atherosclerosis^[22]. The tissue slice from aorta of atherosclerotic plaque area showed an prominent expression of TLR4 by immunohistochemical analysis^[23].

The research studies on cardiovascular diseases shown that infection associated with C pneumonia found to have role in the progression of atherosclerotic diseases^[24]. It usually triggers the diseases by activating TLR4 receptor to induce the migration and proliferation of smooth muscle cells^[25]. The patient with up regulated expression of human TLR4 results in the elevation of IL-12 expression on the downstream activation of TLR4^[22].

Lipopolysaccharide are released upon microbial infection and might triggers the plaque cells to promote the production of different cytokines which initiates the progression of plaque and its rupture which results in severe complications^[26]. The up regulated expression of hTLR4 in patients results in the enhanced expression of MYD88 protein level^[27]. Extensive genetic study on TLR4 gene showed that any polymorphism in TLR4 gene found to have slow down the progress of atherosclerosis. It is due to the mutation on TLR4 (Asp 299 Gly and Thr 399ile) residues. The analysis on TLR4 polymorphism in different patient showed that the patient with acute coronary syndrome showed less polymorphism were as healthy old people showed least polymorphism^[28].

ACTIVATION OF IMMUNE CELLS BY TLR4 SIGNALING

Macrophages and the endothelial cells are the main two types of cells which primary respond to the microbial infection. TLR4 expression in macrophages triggers the local differentiation of these cells to antigen presenting one^[29,30]. Finally it act as the bridge between innate and adaptive immune response to local antigen such as heat shock proteins and OxLDL^[31].

TLR4 AND ITS ROLE IN CHOLESTEROL METABOLISM

TLR4 has active role in cholesterol metabolism in macrophages^[8], which elucidates the process by which TLR4 affect the disease pathology. It has been found that deficiency in TLR4 gene was associated with reduction in the atherosclerotic lesion in cholesterol fed mice for six months^[9]. The gene polymorphism in TLR4 results in the 25% reduction in plaque of double mutant mice. The levels of plasma cholesterol didn't affect significantly on TLR4 deficiency. Over all the genetic polymorphism in TLR4 results in the reduction in levels of cholesterol, conforming the active role of TLR4 in atherosclerosis.

TLR4 SIGNALING IN ATHEROSCLEROSIS

The innate immune system can be activated by variety of pathogen by TLR4 signaling pathways^[16,18]. Lipopolysaccharide can specifically activates TLR4 ligand^[31], which is the major component of gram negative bacteria. Cholesterol induced toxicity causes tissue injury and which releases cellular fibronectin and HSP60 which triggers the activation of TLR4 receptor and results in the atherosclerotic progression^[32,33].

The activation of TLR4 leads to the accumulation of different cells in the atherosclerotic walls like endothelial cells^[20,30], macrophages^[7,20,30], adventitial fibroblast^[20,34] and dendritic cells^[20,35,36]. TLRs have two important domains like extracellular leucine rich (LRR) domain and intracellular domain (TIR). When the TLR4 receptor stimulates, the TIR domain bind to TIR domain adaptor protein MYD88, then to adaptor protein (AD) to form TIRAP complex which is known as MYD88-MAIL and TIR domain consist of adaptor inducing IFN- β (TRIF), the TRIF-related adaptor molecule (TRAM) resulting in two distinct signaling mechanism. MyD88-dependent and the MyD88-independent/TRIF-dependent pathways^[37].

MAPKS ACTIVATION BY TLR4 SIGNALING

TLR4 is widely expressed in atherosclerotic plaques and results in the activation of macrophages and endothelial cells. There comes a link between TLR4/MAPKs/NF- κ B pathway in inducing inflammatory stress and ultimately

resulting in atherosclerotic plaque rupture^[30]. Upon activation TLR4 receptor leads to the activation of IRAK associated protein TRAF6 which induces activation of TAK1 and MKK6 *via* JNK/p38 to activates NF- κ B and resulting in the activation of downstream signaling to promote the progression of the disease^[38,39].

TLR4/MAPKS SIGNALING PATHWAY AS A THERAPEUTIC TARGET

TLR4 found to have an eminent role in the innate immune system. When it comes in with microbial product TLR4 activates intracellular signaling pathway. The execution of the mechanism is through NF- κ B signaling pathway. It is known that TLR4 induced NF- κ B activation is an critical component in ancient host defence system, which is phylogenetically conserved in most of insects and mammals^[40].

The alterations in the mechanisms regulating the activation of MAPKs and NF- κ B are responsible for the most of inflammatory events^[12]. In normal cells the NF- κ B resides in the cytoplasm and usually associated with I κ B, a family of inhibitory proteins, which usually binds to NF- κ B and inhibits the nuclear translocation^[41]. NF- κ B usually regulates the cell survival and inflammatory stress on the active κ B binding sites called the promoter gene^[12]. Active NF- κ B complexes are dimers of combinations of Rel family polypeptides (p50, p52 and p65) that respond to a wide variety of stimuli. The NF- κ B subunit determines the biological effect by nuclear translocation and further binding to κ B-regulatory elements^[42,43].

Research study on MAPKs pathway suggests the active participation of MAPKs in the translocation of NF- κ B subunits. Upon inflammatory stress the cells elicits inflammatory responses *via* MAPKs signaling pathway. It regulates various cellular activities like gene expression, mitosis, programmed cell death, *etc.* The phosphorylation of MAPKs act as switch for tuning the activation of target protein on/off^[44,45].

Natural products have long been recognized as an important source of therapeutically effective medicines. It is recognized that natural-product structures have great chemical diversity, biochemical specificity and other molecular properties that make them favourable lead structures^[46]. There are several plant compounds which can be used to target this pathway. We have recently published our research paper on Robinin a bioflavonoid from *Vigna unguiculata* leaf^[47,48] which selectively modulates TLR/NF- κ B signaling pathway in oxidized LDL induced human peripheral blood mononuclear cells^[49]. Targeting of TLR4/MAPKs signaling pathway (Figure 1) is very essential for the therapeutic inhibition of atherosclerosis. The activation of TLR4 in turn activates cascades of proteins and IKK dependent phosphorylation of I κ B. There is also an activation of MAPKs which contribute to the dissociation of I κ B and the nuclear translocation of NF- κ B p65 subunit (Figure 1) resulting in the activation of key

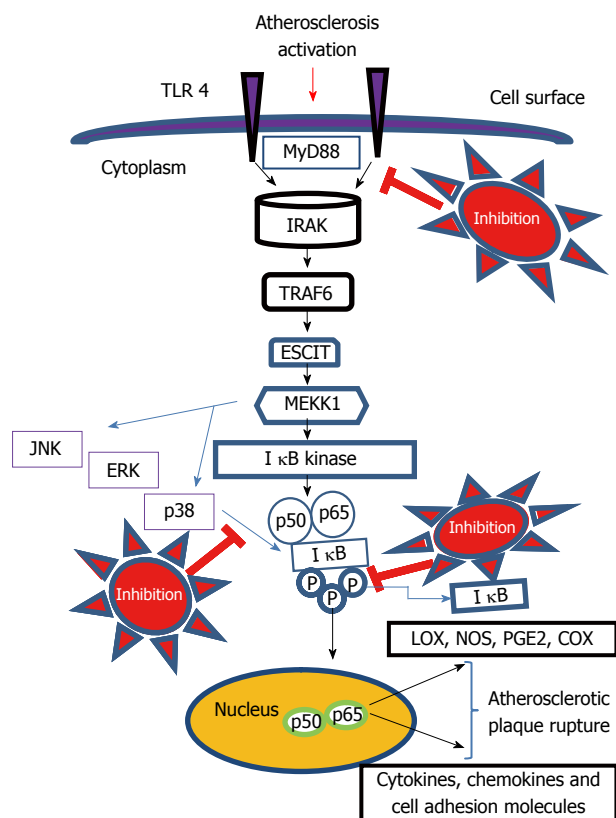


Figure 1 Proposed mechanism of toll-like receptor 4/mitogen activated protein kinases signaling pathway and its suitable targets for therapeutic inhibition of atherosclerosis. The activation of toll-like receptor 4 (TLR4) receptor by various external stimulus leads to the transmittance of signal from cell surface to interior. The TLR4 in turn activates cascades of proteins and finally activates the IKK dependent phosphorylation of I κ B and also there is an activation of mitogen activated protein kinase (MAPKs) which also contribute to the dissociation of I κ B and the nuclear translocation of nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) p65 subunit, thereby activating key inflammatory cascade activation by MAPKs/NF- κ B signaling pathway to induce toxicity by activating different inflammatory parameters. Hence we can target the TLR4/MAPKs signaling pathway at different places in the signaling pathway which indicated in the diagram. IKK: I κ B kinase; JNK- c-Jun N-terminal kinases; ERK: Extracellular signal regulated kinases; MEKK1: Mitogen-activated protein kinase kinase kinase 1.

inflammatory cascade through MAPKs/NF- κ B signaling pathway. Hence we can target the TLR4/MAPKs signaling pathway at different places in the signaling pathway as indicated in the proposed mechanism in Figure 1. Hence, Identification of naturally occurring phytocompounds that can suppress or downregulate TLR4/MAPKs signaling pathway would be an efficient strategy for inhibition of atherosclerosis

CONCLUSION

The inhibition of atherosclerosis is one of primary target for the therapeutics of atherosclerosis, the leading cause of death worldwide. The important role of TLR4 in the activation and progression of atherosclerosis is justified here. The TLR4 in turn activates the MAPKs and NF- κ B which are responsible for most of inflammatory events. Hence, therapeutic inhibition of TLR4/MAPKs signal-

ing pathway is one of the best method for inhibiting atherosclerosis.

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Biologic response modifiers in retinal vasculitis

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Core tip: Corticosteroids play a pivotal role in the treatment of intraocular inflammation. Lately, therapy by immunosuppression has taken the center stage for patients with severe intraocular inflammation. However, biologic response modifiers specifically targeting suppression of the immune effector responses have revolutionized the treatment of intraocular inflammation.

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Abstract

Intraocular inflammation is an important cause of blindness both in the developing and developed world. Corticosteroids play a pivotal role in the treatment of intraocular inflammation. Lately, therapy by immunosuppression has taken the center stage for patients with severe intraocular inflammation. However, the side effects of immunosuppressive drugs are oncogenic, infectious, and hematological. Recently, biologic response modifiers specifically targeting suppression of the immune effector responses have revolutionized the treatment of intraocular inflammation. Anti-tumour necrosis factor agents are etanercept, infliximab, and adalimumab. Newer drugs include certolizumab and golimumab. Infliximab has been found to be superior to corticosteroids in treating retinal vasculitis. Anti-interleukin therapies include rituximab, daclizumab, anakinra, tocilizumab and secukinumab. Rituximab has been proven to be quite effective. Other biologics used are interferons and abatacept. However, there are several limitations and side effects associated with their use.

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Key words: Uveitis; Immunotherapy; Biologic response modifiers; Retinal vasculitis; Non-infectious uveitis

INTRODUCTION

Intraocular inflammation accounts for 5% to 20% of blindness in the developed world and 25% in the developing world^[1]. Though the prevalence of retinal vasculitis is less, still the complexity and heterogeneity of the disease makes it unique. The etiology of most of them is unknown. Uveitogenic proteins that can incite intraocular inflammation include rhodopsin, retinal arrestin, recoverin, phosducin, retinal pigment epithelium derived (RPE-65) and inter-photoreceptor retinoid binding protein. These uveitogenic retinal antigens incite innate immunity by antigen mimicry and have been found to be associated in patients with intraocular inflammatory disease by numerous studies. Involved immunogenic pathway is similar for all types of intraocular inflammation^[2,3]. Over the last two decades, laboratory diagnostic tools have entered into an era of molecular diagnostic tests. With the advent of experimental and cellular biology, several biomarkers are being identified. Many uveitic diseases are known to be strongly associated with particular human leucocyte antigen (HLA) haplotypes. It has largely been supported by continued development of experimental models of autoimmune uveitis along with improved molecular biologic techniques. Novel sophisticated technolo-

gies such as multiplex bead assays have revolutionized the management of complex refractory uveitis. Despite the varied immune etiology, intraocular inflammation poses a significant therapeutic challenge given the heterogeneity of the retinal vasculitis spectrum along with the pressing need and increasing expectations for personalised care. This review attempts to present the current concepts of immunotherapy in retinal vasculitis.

PHYSIOLOGICAL AND PATHOLOGICAL MECHANISM

Immune privilege guards the eye by mechanical sequestration behind an efficient blood-retinal barrier, local inhibition of activation and functioning of adaptive and innate immune cells, and systemic regulation by induction of T regulatory cells^[2]. On the other hand, it leaves the eye vulnerable to an autoimmune attack by lymphocytes primed elsewhere in the body by chance encounter with a self or with mimic antigens.

Immunohistologically, retinal vasculitis is characterized by an infiltration of mainly cluster differentiation 4 (CD4⁺) T cells. Posterior uveitis in humans is considered to be a T cell-mediated autoimmune disease. Importance of T cells is highlighted by the fact that cyclosporin A can be effective in arresting the disease progression in many cases^[4]. In an experimental model, the ability to adaptively transfer disease using activated retinal antigen-specific CD4⁺ T cells is further evidence of CD4⁺ T cell-mediated processes inducing the irreversible destruction of the photoreceptor cells of the retina^[5]. The CD4 interacts directly with major histocompatibility complex (MHC) class II molecules on the surface of the antigen-presenting cell. Recognition of the MHC peptide complex by CD4⁺ T cells leads to secretion of cytokines. T Helper cells (Th) were divided into two subsets: Th1 and Th2. Th1 subset secretes Interferon- γ (IFN- γ) and Interleukin-2 (IL-2) responsible for cellular anti-viral immunity, and a Th2 subset secretes IL-4 required for blood borne parasitic responses. CD4⁺ Th1 cells and IFN- γ are considered to be the major effectors in the pathogenesis of experimental autoimmune uveitis^[6]. Another subset of regulatory CD4⁺ T cells that secrete IL-10 and transforming growth factor- β (TGF- β) was added^[7]. However, the presence of inflammatory diseases in IFN- γ -deficient mice indicated existence of other Th cell subsets and led to the discovery of the Th17 subset secreting IL-17 and IL-23^[8]. Recently, other Th cell subsets have been assigned on the basis of the secretion of IL-9 (Th9) or IL-21 (T follicular helper)^[9].

CYTOKINE PROFILE IN RETINAL VASCULITIS

Ooi *et al.*^[10] conducted a systematic review on inflammatory cytokines in uveitis of various etiologies. Few studies were conducted by us to ascertain the cytokine profile in Eales' disease. Following is a description of the

cytokines involved in some of the important causes of retinal vasculitis.

Eales' disease (retinal periphlebitis)

Eales' disease is an idiopathic obliterative vasculopathy that primarily affects the peripheral retina of young adults. Role of tumor necrosis factor-alpha (TNF- α) in Eales' disease was evaluated by us in several studies. In one such study, quantification of the TNF- α levels was carried out in young adults with Eales' disease and healthy controls of similar age. TNF- α level was found to be significantly raised in cases as compared with controls. It was also observed that higher levels of TNF- α were associated with increased severity of Eales' disease which was graded according to a new grading system based on severity of inflammation^[11]. In another study, we evaluated the levels of TNF in the serum of 52 patients with proliferative stage of Eales' disease and in 32 healthy controls to study its relation with the area of retinal capillary non-perfusion (ischemic retina). TNF levels were significantly increased in the proliferative stage of the disease as compared to controls and higher levels were associated with an increased area of retinal capillary non-perfusion on fluorescein angiography. It was concluded that increased TNF level in proliferative Eales' disease is related to retinal cell death signaling^[12]. We conducted another study in which we for the first time evaluated IL-1 β , IL-6, IL-10, and TNF- α in the serum of 45 consecutive patients with Eales' disease and in 28 healthy controls. It was found that levels of IL-1 β , IL-6, IL-10, and TNF- α were significantly increased in the inflammatory stage of Eales' disease as compared to controls. Also it was observed that IL-1 β levels decreased significantly and TNF- α levels increased significantly during the proliferative stage of the disease as compared to the inflammatory stage. It was concluded that for controlling inflammatory activity and/or the associated long-term sequelae related to angiogenesis in Eales' disease, IL-1 system and TNF- α represent novel target for immunotherapy^[13].

Behcet's disease

It is a systemic vasculitis with recurrent ocular involvement as uveitis and retinal vasculitis. HLA-B51 phenotype association has been found. Raised intraocular levels of the following immune factors have been found: IL-2, IL-6, IFN- γ and TNF- α . Recurrent episodes of Behcet's disease-related uveitis has been found to be positively correlated with serum TNF- α levels^[14].

Sarcoidosis

An acute or chronic granulomatous uveitis of unknown etiology involving the anterior, intermediate or posterior uveal layers. The aqueous immune profile of patients with sarcoidosis revealed elevated levels of IL-1 α , IL-6 and IL-8^[10,15].

Vogt-koyanagi-harada disease

A multisystem chronic granulomatous disorder associated

with HLA-DR1 and HLA-DR4 phenotype with ocular manifestation as a chronic, bilateral panuveitis. Raised intraocular levels of the following immune factors have been identified: IL-6, IL-8 and IFN- γ ^[16].

Fuchs' heterochromic iridocyclitis

A chronic typically unilateral anterior uveitis syndrome with or without associated glaucoma. One study found IFN- γ to be raised in aqueous samples of patients with FHC when compared to patients with idiopathic uveitis. Higher levels of IL-10 was found in larger number of FHC samples than of idiopathic uveitis (not statistically significant)^[17].

Idiopathic uveitis

The commonest form of uveitis and has been found to be associated with increased intraocular levels of IL-1 β , IL-2, TNF- α , IFN- γ , IL-6, IL-8 and MCP-1^[16,18].

Ankylosing spondylitis

A chronic inflammatory disorder of the axial skeleton with a strong association with HLA-B27 phenotype which manifests in the eye as severe acute anterior uveitis. Reports have revealed elevated intraocular levels of IL-2, IFN- γ , IL-6 and TNF- α ^[15].

IMMUNOTHERAPY

Corticosteroids and immunosuppressants

Corticosteroids played a pivotal role in the treatment of intraocular inflammation in the early 1950s, later on therapy by immunosuppression took the center stage for patients with severe intraocular inflammation. Now with the proteomic labeling, we can target specific cytokine pathway and deliver targeted therapy for patients with intraocular inflammation. We have now probably embarked on much specialised stratified care^[4,5,18-23]. The treatment of noninfectious posterior uveitis can lead to severe vision loss, and the first-line conventional treatment includes systemic steroids. When the prednisone doses necessary to control intraocular inflammation are above 0.3 mg/d, a therapeutic association is proposed in order to lower the daily prednisone dose. The combined drugs are immunosuppressive or immunomodulative. The side effects of immunosuppressive drugs are oncogenic, infectious, hematological and can involve reproductive troubles, associated with specific toxic effects depending on the drug used. We undertook a tertiary care center-based prospective interventional study to evaluate the response time and safety profile of low-dose oral methotrexate pulsed therapy in Eales' disease. Twenty one consecutive patients with idiopathic retinal periphlebitis were administered 12.5 mg methotrexate as a single oral dose, once per week for 12 wk. Drug safety was monitored by various laboratory tests that included twice-weekly white blood cells and differential counts, twice-weekly platelet counts, and monthly liver function tests for a mean follow-up period of 6 mo. It was found that all patients

showed improvement in visual acuity. All the side effects of methotrexate were mild to moderate in severity and rapidly reversible on dose reduction or discontinuation. We concluded that low dose oral methotrexate pulse therapy (at a dose of 12.5 mg/wk) is clinically effective within 4 wk and is associated with an acceptable safety profile^[24]. Conventional therapy with corticosteroids and immunosuppressive agents (such as methotrexate, azathioprine, mycophenolate mofetil and cyclosporine) may not be sufficient to control ocular inflammation or prevent non-ophthalmic complications in refractory patients. In a study conducted by us, efficacy of combined oral corticosteroid and low-dose oral methotrexate pulsed therapy in Eales' disease was evaluated prospectively based on weighted visual morbidity scale for disease activity and visual acuity grading in 36 consecutive cases. Oral corticosteroids in a weekly tapering dose for 4 wk and 12.5 mg methotrexate as a single oral dose, once per week for 12 wk were administered simultaneously. We concluded that this combined oral therapy is clinically effective with an acceptable safety profile^[25].

Biologic response modifiers

Biologics specifically target inflammatory cytokines and cause suppression of the immune effector responses that are responsible for damaging tissues. They were first used for ocular inflammation in 1990s. Commonly used biologics are anti-TNF agents and anti-interleukins. Now we have entered into an era of recombinant cytokines.

Anti TNF- α agents

TNF- α is a pleiotropic inflammatory cytokine. It plays a pivotal role in down-regulating both inflammatory and the immune response. Thus, blockade with anti-TNF agents has turned into the most important tool in the management of retinal vasculitis. The three most commonly used TNF inhibitors in the US are infliximab, etanercept and adalimumab. Newer drugs include certolizumab and golimumab.

Infliximab: Infliximab is a chimeric immunoglobulin G1 (IgG1) monoclonal antibody with the antigen-binding region derived from a mouse antibody and the constant region from a human antibody^[26]. It binds to TNF- α with high affinity thereby blocking the binding of TNF- α to its receptor. One of the considerations in giving infliximab is that it can potentially induce antinuclear antibody and anti-double stranded DNA on long term therapy^[27,28]. Early monitoring and optimizing dose regimens can be useful in patients on long term infliximab therapy. Side effects are autoimmune diseases which improve on stopping the drug, blood dyscrasias, allergies secondary to infusion, fever, fatigue, upper respiratory chest infection, headache, gastrointestinal upset, headache.

Adalimumab: Adalimumab is a fully humanized recombinant IgG1 monoclonal antibody with high binding to

human TNF- α . Side effects are gastrointestinal disturbances including haemorrhage, hyperlipidaemia, hypertension, chest pain, tachycardia, cough, dyspnea, mood changes, paraesthesia, haematuria, renal impairment, electrolyte disturbances, hyperuricaemia, musculoskeletal pain, eye disorders (visual impairment, conjunctivitis, blepharitis, eye swelling), rash, dermatitis.

Etanercept: Etanercept is a soluble fusion protein and prevents both TNF- α and TNF- β from interacting with receptors. It consists of 2 dimers of higher affinity type 2 TNF receptors. Side effects include headache, infection like upper respiratory tract infections, urinary tract infections, butterfly rash on cheeks, dizziness, fatigue, swelling of the arms/legs, unusual bruising/bleeding, severe headache, mental/mood changes, seizures, unexplained muscle weakness, numbness/tingling of the hands/feet, unsteadiness, vision changes, severe stomach/abdominal pain.

Golimumab: Golimumab is a novel fully humanized anti-TNF α monoclonal antibody. Side effects include body aches or pain, chills, cough, difficulty with breathing, ear congestion, fever, headache, loss of voice, muscle aches, sneezing, sore throat, stuffy or runny nose, unusual tiredness or weakness. Blurred vision, burning, crawling, itching, numbness, prickling, “pins and needles”, or tingling feelings, congestion cough with mucus diarrhea, dizziness, general feeling of discomfort or illness, hoarseness, joint pain, loss of appetite, muscle aches and pains, nausea, nervousness, pain or tenderness around the eyes and cheek bones, painful cold sores or blisters on the lips, pounding in the ears, shivering, shortness of breath or troubled breathing, slow or fast heartbeat, sweating, tender/swollen glands in the neck.

Anti-TNF- α agents have improved the treatment armamentarium for refractory immune-mediated uveitis particularly in Behçet disease-associated uveitis. A prospective observational study of patients with panuveitis was undertaken in which 19 eyes received an infliximab infusion, 8 eyes received high-dose methylprednisolone intravenously and 8 eyes received intravitreal triamcinolone acetonide at attack's onset. Unchanged baseline maintenance therapy was continued for 30 d. Visual acuity, anterior chamber cells, vitreous cells and inflammation of the posterior eye segment were assessed at baseline and at days 1, 7, 14 and 29 post-treatment. Infliximab was superior to corticosteroids in treating retinal vasculitis as well as in resolution of retinitis and cystoid macular oedema^[29]. A study was conducted in which anti-TNF α therapy was administered in 15 patients of chronic non-infectious uveitis when no response had been obtained with classical immunosuppressive therapies or in the presence of severe rheumatoid disease. Mean duration of ocular disease was 8 years. Treatment was initiated with infliximab, etanercept, and adalimumab. It was concluded that anti-TNF- α therapy is effective and safe^[30]. Importance of TNF- α in the pathophysiology of

multi-systemic sarcoidosis and refractory retinal vasculitis was emphasized in a case report in which 2 patients experienced an excellent response to infliximab^[31]. A retrospective noncomparative case series was conducted on 6 pediatric patients with uveitis refractory to methotrexate, cyclosporine, mycophenolate mofetil, etanercept, daclizumab and topical steroids. These patients initially received infliximab at doses between 5 and 10 mg/kg at 2 to 4 wk interval and then were maintained at 4 to 8 wk interval at doses of 5 to 18 mg/kg. Reduction in intraocular inflammation after infliximab therapy initiation was seen in all the patients. The only adverse reactions seen were vitreous hemorrhage in 1 patient and a case of transient upper respiratory infusion reaction. It was concluded that for the treatment of refractory pediatric uveitis, infliximab seems to be an effective agent without apparent serious toxicity^[32]. To evaluate the clinical response after switching from infliximab to adalimumab, a prospective, longitudinal and observational study was conducted in 69 patients with Behçet's disease. Seventeen patients were switched to adalimumab for lack or loss of efficacy or infusion reactions to infliximab. Of the 17 treated patients, 9 showed sustained remission of the disease and 3 showed good response. No side effects were observed in any patient. They concluded that adalimumab can be used to treat patients with Behçet's disease showing a scarce response or adverse events to infliximab^[33]. A study was conducted to alert physician for timely recognition and to evaluate current treatment of recurrent hypopyon iridocyclitis or panuveitis in Behçet's disease. It was found that for the control of acute panuveitis, a single infliximab infusion should be considered, whereas in reducing the number of episodes in refractory uveoretinitis with faster regression and for complete remission of cystoid macular edema, repeated long-term infliximab infusions proved to be more effective^[34]. Rifkin *et al*^[35] studied current status of three of the five commercially available TNF inhibitors-etanercept, infliximab, and adalimumab for their efficacy in treatment of ocular inflammation. They found etanercept to be inadequate in controlling ocular inflammation. Infliximab and adalimumab, however, showed encouraging results in multiple trials^[35]. There are only two reports in the literature about the use of golimumab in uveitis, describing four patients with juvenile idiopathic arthritis-associated uveitis and a case of idiopathic retinal vasculitis. Mesquida *et al*^[36] first reported about the use of golimumab in Behçet's disease. William *et al*^[37] reported good outcomes using golimumab in three patients with juvenile idiopathic arthritis.

Anti-interleukin therapies

Rituximab: Rituximab (first used in the treatment of Non Hodgkin's B cell lymphoma) is a recombinant chimeric monoclonal antibody with binding efficacy to CD20. It works by blocking CD20-bearing B cells. Side effects are severe stomach pain with constipation, bloody or tarry stools, coughing up blood or vomit that looks like coffee grounds, painful blistering skin rash with

burning, itching, or tingly feeling, or upper stomach pain, vomiting, loss of appetite, dark urine, clay-colored stools, jaundice (yellowing of the skin or eyes), runny or stuffy nose, sinus pain, sore throat, headache, dizziness, itching, or mild stomach cramps.

Daclizumab: Daclizumab is a recombinant monoclonal antibody of the human IgG1 isotype composed of 90% human and 10% mouse antibody sequences that bind to CD25 with high affinity and inhibit IL-2-mediated responses of activated T cells. It was withdrawn in 2009 based on a report by Wroblewski *et al*^[38] according to which four of 39 patients developed solid malignant tumor while on daclizumab over a follow up period of 11 years. Side effects include poor wound healing, unusual growths/lumps, swollen glands (*e.g.*, on the neck, in the armpits), unexplained weight loss, night sweats, easy bruising/bleeding, abdominal pain/swelling, unusual tiredness. A very serious allergic reaction to this drug is rare.

Anakinra: Anakinra is a recombinant non-glycosylated homologue of HuIL1Ra, a natural immunomodulating molecule, which competitively inhibits binding of IL1 α and IL1 β to the IL1 receptor type 1. Side effects are infections, nausea or diarrhea, headache, sinus infection, or redness, bruising, pain, or swelling at the injection site.

Tocilizumab: Tocilizumab is a recombinant humanized monoclonal antibody and inhibits IL-6 mediated responses by binding to both membrane-bound and soluble IL-6 receptors with high affinity.

Secukinumab: Secukinumab is a fully humanized IgG1k monoclonal antibody neutralizing IL-17A.

Sadreddini *et al*^[39] reported treating a patient with visual loss due to retinal vasculitis resistant to prednisolone and azathioprine with rituximab successfully with a sustained remission of 24 mo of follow-up. Severe retinal vasculitis is a potentially blinding complication of patients with systemic lupus erythematosus (SLE). Hickman *et al*^[40] first reported that rituximab can be used to treat severe bilateral SLE-associated retinal vasculitis. This case suggested that rituximab-induced B-cell depletion may provide an important new therapeutic option in such refractory cases. A study was conducted to evaluate the efficacy of rituximab in patients with retinal vasculitis and edema, resistant to cytotoxic drugs. Twenty patients were randomized to a rituximab group or cytotoxic combination therapy group. Rituximab was given in two 1000-mg courses (15-d interval). Subjects received methotrexate (15 mg/weekly) with prednisolone (0.5 mg/kg per day). The cytotoxic combination therapy group received pulse cyclophosphamide (1000 mg/monthly), azathioprine (2-3 mg/kg per day) and prednisolone (0.5 mg/kg per day). It was concluded that rituximab was efficient in severe ocular manifestations of Behcet's disease as significant improvement after 6 mo was seen with rituximab, but

not with cytotoxic drugs^[41]. A pilot study aimed to evaluate the safety, pharmacokinetics and clinical activity of gevokizumab in Behcet's disease patients with uveitis was conducted. Patients with acute posterior or panuveitis and/or retinal vasculitis, receiving 10 mg/d or less of prednisolone and resistant to azathioprine and/or cyclosporin were enrolled into the study. Patients received a single infusion of gevokizumab (0.3 mg/kg) and immunosuppressive agents were discontinued at baseline. On evaluation of the safety and uveitis status and pharmacokinetics of gevokizumab, it was found that no treatment-related adverse event was observed and rapid and durable clinical response was seen in all patients. Complete resolution of intraocular inflammation was achieved in 4-21 d, with a median duration of response of 49 d. Moreover, despite discontinuation of immunosuppressive agents and without the need to increase corticosteroid dosages, the effect was observed^[42]. In addition, a clinical trial is underway for the use of anakinra in Behcet's disease (clinical trial reference number NCT01441076). Muselier *et al*^[43] showed tocilizumab to be effective in treatment of refractory uveitis. Secukinumab has proved to be quite effective in the treatment of patients with anterior and posterior uveitis with no serious adverse effects^[44].

Interferons

(1) IFN α ; (2) Recombinant IFN α -2a (Roferon-A); (3) Recombinant IFN α -2b (Intron A); and (4) Pegylated interferons.

Interferon- α : Interferon α -2A and Interferon α -2B are human recombinant interferons manufactured using recombinant DNA technology with *E. coli* to produce human proteins. It is a type I interferon and has been used in the treatment of uveitis due to its anti-proliferative, anti-angiogenic, apoptotic effects and the ability to activate dendritic, cytolytic T and natural killer cells. A prospective, open clinical trial was conducted to study long term effects of interferon α -2A on panuveitis in seven patients with Behcet's disease. IFN α -2A was given for a mean duration of 23.6 mo in seven patients. Initial dose of IFN α -2A was 6×10^6 IU/d, followed by 3×10^6 IU/d after 1 mo and 3×10^6 IU every other day after 3 mo. Additionally in the beginning of the therapy, two patients received low dose prednisolone (between 0.2 and 0.4 mg/kg per body weight). In three patients complete cessation of IFN α -2A was possible (observation period was 22, 6, and 4 mo). Six patients who had ocular manifestations of Behcet's disease for the first time or with minor damage during their course of chronic relapsing panuveitis showed marked improvement. New relapses were prevented in one patient with advanced ocular Behcet's disease. Resolution of retinal infiltrates occurred within 2 wk and retinal vasculitis within 4 wk. It was found that complete remission of retinal vasculitis occurred in all patients treated with IFN α -2A alone or in combination with low dose steroids. It was concluded that retinal or optic nerve damage due to vascular occlu-

sion can be prevented by treatment with IFN α -2A. No severe side effects were found^[45]. Evaluation of the efficacy of interferon needs to be done in other etiologies of retinal vasculitis through randomized studies^[46,47]. Another study was conducted to evaluate the long-term development of visual acuity in patients with severe ocular Behcet's disease who were treated with IFN α -2A. Fifteen eyes of 9 patients with an active panuveitis and/or retinal vasculitis due to Behcet's disease refractory to immunosuppressive treatment were included. Visual acuity before initiation of IFN was compared to visual acuity at the end of the follow-up. Increase in visual acuity of two lines or more was seen in 10 eyes during the follow-up. In 5 eyes visual acuity remained stable. No decrease of visual acuity in any eye was seen. In the presence of macular edema, quick response to IFN α -2A was seen. It was concluded that IFN α -2A seems to be much more effective to prevent a loss or decrease of visual acuity over a long period of time in patients with severe ocular Behcet's disease compared to conventional immunosuppressants^[48].

Fusion protein of cytotoxic T-lymphocyte antigen 4

Abatacept: It is a fusion protein that prevents activation of T cells by barring antigen presenting cells from delivering the co-stimulatory signals. There are case reports and case control studies reporting on the effectiveness of abatacept in the treatment of refractory uveitis in patients with juvenile idiopathic arthritis^[49].

IMPORTANT CONSIDERATION

These drugs are contraindicated in patients with tuberculosis or any active infection and in patients with pregnancy or breast feeding. Patients should be instructed to avoid pregnancy till 5 mo after stopping last dose of biologics. Before prescribing them, malignant conditions should be ruled out. Baseline blood counts, liver function tests and Glucose should be measured and subsequently at every 4 wk for three months followed by every 6 wk. If patient develops fever, sore throat or bleeding then examination by a physician needs to be done. Demyelinating diseases should be ruled out before starting these drugs as TNF- α agents can aggravate multiple sclerosis. Caution should be taken as reduced immunity can lead to increased risk of infection including flare up of latent tuberculosis. Also, worsening of heart failure can occur if already present.

LIMITATIONS

There is no proven causal relationship as yet with any of these novel biomarkers, though there is association of these biomarkers with some specific uveitis entities. Whether it is the disease leading to release of a specific biomarker or is it the inflammatory cytokine causing the disease is yet to be determined in future research. In addition, biologic response modifiers are expensive and with

life threatening risks. Hence, a specialist experienced with immunology and the pathophysiology of inflammatory diseases has to supervise. Strict monitoring with awareness of the adverse effects is needed in rendering this specific therapy in refractory uveitis patients.

CONCLUSION

With the advent of experimental and cellular biology, cytokines are increasingly being recognized as biological markers in intraocular inflammatory diseases. Several experimental models and improved molecular biologic techniques have supported it. Biologics provide customized ocular therapy. As shown by various studies and randomized controlled trials, they have been found to be effective in several systemic diseases. Many biologic agents have been found to be efficacious in refractory anterior and posterior uveitis, particularly Behcet's disease. With the advent of novel and advanced sophisticated techniques, newer cytokines are being found. The efficacy of biologic therapies and their comparison with each other are being studied in various randomized controlled trials. In future, evidence based medicine will pave way for tailored treatment by specific biologic regime.

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Acknowledgments

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- 2 **Lin GZ**, Wang XZ, Wang P, Lin J, Yang FD. Immunologic effect of Jianpi Yishen decoction in treatment of Pixu-diarhoea. *Shijie Huaren Xiaobua Zazhi* 1999; **7**: 285-287

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- 3 **Tian D**, Araki H, Stahl E, Bergelson J, Kreitman M. Signature of balancing selection in Arabidopsis. *Proc Natl Acad Sci USA* 2006; In press

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- 4 **Diabetes Prevention Program Research Group**. Hypertension, insulin, and proinsulin in participants with impaired glucose tolerance. *Hypertension* 2002; **40**: 679-686 [PMID: 12411462 PMID:2516377 DOI:10.1161/01.HYP.0000035706.28494.09]

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- 5 **Vallancien G**, Emberton M, Harving N, van Moorselaar RJ; Alf-One Study Group. Sexual dysfunction in 1, 274 European men suffering from lower urinary tract symptoms. *J Urol* 2003; **169**: 2257-2261 [PMID: 12771764 DOI:10.1097/01.ju.0000067940.76090.73]

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- 6 21st century heart solution may have a sting in the tail. *BMJ* 2002; **325**: 184 [PMID: 12142303 DOI:10.1136/bmj.325.7357.184]

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- 7 **Geraud G**, Spierings EL, Keywood C. Tolerability and safety of frovatriptan with short- and long-term use for treatment of migraine and in comparison with sumatriptan. *Headache* 2002; **42** Suppl 2: S93-99 [PMID: 12028325 DOI:10.1046/j.1526-4610.42.s2.7.x]

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- 8 **Banit DM**, Kaufer H, Hartford JM. Intraoperative frozen section analysis in revision total joint arthroplasty. *Clin Orthop Relat Res* 2002; **(401)**: 230-238 [PMID: 12151900 DOI:10.1097/00003086-200208000-00026]

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- 9 Outreach: Bringing HIV-positive individuals into care. *HRS-A Careaction* 2002; 1-6 [PMID: 12154804]

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- 10 **Sherlock S**, Dooley J. Diseases of the liver and biliary system. 9th ed. Oxford: Blackwell Sci Pub, 1993: 258-296

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- 11 **Lam SK**. Academic investigator's perspectives of medical treatment for peptic ulcer. In: Swabb EA, Azabo S. Ulcer disease: investigation and basis for therapy. New York: Marcel Dekker, 1991: 431-450

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- 12 **Breedlove GK**, Schorfeide AM. Adolescent pregnancy. 2nd ed. Wiczorek RR, editor. White Plains (NY): March of Dimes Education Services, 2001: 20-34

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- 14 **Christensen S**, Oppacher F. An analysis of Koza's computational effort statistic for genetic programming. In: Foster JA, Lutton E, Miller J, Ryan C, Tettamanzi AG, editors. Genetic programming. EuroGP 2002: Proceedings of the 5th European Conference on Genetic Programming; 2002 Apr 3-5; Kinsdale, Ireland. Berlin: Springer, 2002: 182-191

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- 15 Morse SS. Factors in the emergence of infectious diseases. Emerg Infect Dis serial online, 1995-01-03, cited 1996-06-05; 1(1): 24 screens. Available from: URL: <http://www.cdc.gov/ncidod/eid/index.htm>

Patent (list all authors)

- 16 **Pagedas AC**, inventor; Ancel Surgical R&D Inc., assignee. Flexible endoscopic grasping and cutting device and positioning tool

assembly. United States patent US 20020103498. 2002 Aug 1

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Write as mean \pm SD or mean \pm SE.

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