Review

Central role of dendritic cells in the regulation and deregulation of immune responses

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Abstract. Dendritic cells (DCs) play a critical role in orchestrating the innate and adaptive components of the immune system so that appropriate, coordinated responses are mounted against infectious agents. Tissue-resident DCs interact with microbes through germline-encoded pattern-recognition receptors (PRRs), which recognize molecular patterns expressed by various microorganisms. Antigens use PRR activation to instruct DCs for the appropriate priming of natural killer (NK) cells, followed by specific T-cell responses. Due to the central role of DCs in regulating the activation and progression of immune responses, minor imbalances in the feedback control of Toll-like receptor (TLR)-activated cells have been associated with autoimmunity in genetically prone individuals. We review here recent findings on the role of DCs in the priming of innate and adaptive immune responses and the possible involvement of DCs in inducing and maintaining autoimmune reactions.

Keywords. Dendritic cells, innate immunity, adaptive immunity, pattern recognition receptors, CD14, natural killer cells, autoimmunity.

Introduction

Dendritic cells (DCs) were initially described as the 'natural adjuvants' inducing adaptive immune responses [1-3]. DCs are special leukocytes capable of alerting the immune system to the presence of infections and responsible for the activation and control of both innate and adaptive immune responses [4, 5]. DCs are particularly frequent in tissues forming an interface with the external environment, such as the skin, gut and lungs [6-8], where they perform a sentinel function – detecting incoming pathogens –

and can recruit and activate cells of the innate immune system [9-11]. DCs take up antigens and efficiently process them for presentation in association with major histocompatibility complex (MHC) molecules. These cells must be sensitive to the amount of antigen present and the persistence of antigens if they are to fulfill their role as sentinels correctly. They use a repertoire of non-clonal receptors to signal downstream to the nucleus, conveying information about what is present in the environment (quality and quantity) and the duration of this signal. This complex activity is revealed by transcriptional responses involving the differential expression of thousands of genes and the integration of a number of signaling pathways. The active transcriptional response leads to

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the acquisition of diverse DC functional phenotypes, orchestrating the appropriate immune response [12, 13].

DCs are highly plastic. The signals determining a particular DC function and, consequently, the type of adaptive immune response therefore depend mostly on the local microenvironment and on the interaction between DCs and microbes. DCs are the critical link between innate and adaptive immune responses, and the deregulation of DC activation via Toll-like receptors (TLRs) has been associated with autoimmunity in susceptible individuals, particularly through the production of type I interferons (IFNs). In this review, we summarize recent findings on the role of DCs in priming innate and adaptive immune responses and the possible involvement of DCs in deregulated autoimmune reactions.

DC heterogeneity

DCs are of hematopietic origin and have been found in many different organs and tissues, including heart, liver, thyroid, pancreas, bladder, kidney, ureter, gut, lungs and skin. Fully developed DCs have also been observed in the circulatory networks of the body, including blood and afferent lymphatic vessels. DCs display a high degree of plasticity within organs and lymphoid tissues, and DC effector functions are often regulated by tissue microenvironment [14].

As superbly described by Shortman [15, 16], DCs can be subdivided into conventional DCs, cells having phenotypic and functional characteristics of DCs, and pre-DCs, cells requiring a further step of development to acquire phenotypic and functional DC features. Conventional DCs can, in turn, be subdivided in migratory and lymphoid tissue-resident DCs. Migratory DCs are the sentinels of nonlympoid tissues and migrate to the draining lymph nodes after the encounter of inflammatory stimuli. Migration to lymph nodes can also occur at low rate in steady-state conditions. Lymphoid tissue-resident DCs do not reach the lymphoid organs through the lymphatics but capture the antigen directely inside the lymphoid organ. Most of thymic, spleen and around half of lymph node DCs are lymphoid tissueresident cells.

Migratory and lymphoid tissue-resident DCs can be further divided into subtypes. For migratory DCs the division is based on the tissue origin, while for lymphoid tissue-resident DCs it is based on the expression of particular markers [17–20]. For instance, six different DC populations have been identified in skin-draining lymph nodes all expressing CD11c: CD8⁺DEC205⁺resident DCs, CD8⁻DEC205⁻ (both CD4⁻ and CD4⁺)-

resident DCs, CD8^{low}CD205^{int} DCs (migratory dermal DCs) and CD8^{low}DEC205^{high} DCs (migratory Langerhans cells, LCs) [20, 21]. In general, in mouse lymph nodes and spleen DCs are characterized by the expression of CD11c and are classified based on the expression of CD4, CD8 and the two uptake receptors DEC205 and DCIR2, recognized by the 33D1 antibody. Thus, CD4⁺CD8⁻, CD4⁻CD8⁺ and CD4⁻CD8⁻ have been identified. Moreover, a subpopulation of CD8⁺ DCs expressing DEC205 and a subpopulation of CD8⁻ DCs expressing DICR2 have also been described [22]. In the spleen, $CD8^{-}$ DCs are mostly found in the marginal zone, whereas CD8⁺ DCs are mostly found in the T-cell area [19]. CD8⁻ DCs migrate to the T-cell areas following stimulation with microbial stimuli [23]. In steady-state conditions, DCs resident in lymphoid and non-lymphoid tissues are phagocytic cells and express low levels of the costimulatory molecules CD80 and CD86, and low levels of MHC class II. Upon activation following microbial stimuli encounter, both migratory and lymphoid tissue-resident DCs downregulate phagocitic activity, increase processing capacity, and upregulate MHC and costimulatory molecules at the cell surface [21]. In addition, migratory DCs acquire the capacity to migrate to lymph nodes. When they reach the lymph nodes, they have a mature phenotype [15].

Finally, a DC population producing large amounts of type I interferons (IFNs) following microbial infections – IFN-producing plasmacytoid DCs (pDCs) – has been described in mouse blood and lymph nodes [24]. In steady-state conditions, these cells can be classified as preDCs [15]. Upon activation they acquire not only the capacity to produce large amounts of type I IFNs but also some DC antigenprocessing and -presentation properties [25].

Human DC phenotypes have been less well typed. DCs expressing CD11b, CD11c and CD4 have been described in the spleen and tonsils [19]. No CD8-expressing DCs have been identified. Human IFN-producing pDCs are CD45RA⁺CD123⁺ and CD11c⁻ [26].

Migratory and lymphoid tissue-resident DCs can sense the presence of a pathogen through a large innate receptor repertoire. The signal transmitted by these receptors is crucial for DC maturation and possible migration to secondary lymphoid tissues, leading to the initiation of adaptive immune responses.

How do DCs sense pathogens?

DCs interact with microbes through germline-encoded pattern-recognition receptors (PRRs) [27], which recognize molecular patterns expressed by various micro-

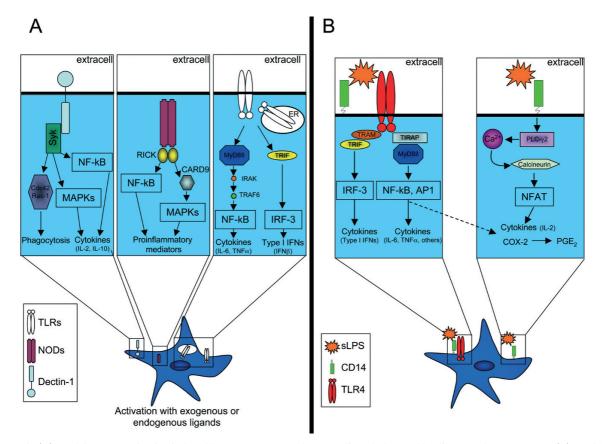


Figure 1. (*A*) Models of DC activation induced by exogenous or endogenous ligands detected by different classes of PRRs. (*B*) Model of CD14 functions. CD14, in addition to enhancing TLR4-dependent cellular responses to low doses of LPS and being required for the LPS-induced recruitment of TRIF and TRAM, is also involved in Ca^{2+} mobilization and TLR4-independent NFAT activation following sLPS engagement. The activation of this pathway, together with that of the NF- κ B pathway, leads to the efficient production of COX-2 and PGE₂ and other cytokines, such as IL-2.

organisms. PRRs comprise a large superfamily, including the C-type lectin family [28], the nucleotide binding and oligomerization domain (NOD)-like receptors (NLRs) [29], the retinoid acid-inducible gene I (RIG)-like receptors (RLRs) [30] and TLRs [31].

Dectin-1 is a C-type lectin that plays an important role in anti-fungal defense [28, 32, 33]. Dectin-1 is a betaglucan-specific receptor that mediates the phagocytosis of yeast and yeast-derived particles, such as zymosan. In mouse DCs, the dectin-1-mediated phagocytosis of zymosan depends at least partly on tyrosine kinase Syk activation, leading to activation of the Rho family GTPases Cdc42 and Rac-1. This, in turn, leads to actin polymerization and pseudopod protrusion around the particle [34, 35]. Dectin-1 engagement in DCs triggers the production of pro-inflammatory and anti-inflammatory cytokines, including interleukin (IL)-2 and IL-10 [35] (Fig. 1A).

NLRs comprise a large family of intracellular PRRs, all bearing a conserved NOD domain [36]. The binding of a ligand to the leucine-rich repeat (LRR) motif within this domain leads to a change in the conformation of the molecule and its activation.

Unlike dectin-1 and TLRs, NLRs are cytosolic receptors. Their location suggests a possible role in the detection of microbes escaping the surveillance of extracellular or endosomal receptors. NOD1 and NOD2 are the best-characterized NLRs. They recognize molecules produced during the synthesis or degradation of peptidoglycan [37-39]. In vitro studies have shown that NOD1 can sense pathogens, such as Shigella flexneri [38], Listeria monocytogenes [39], *Campylobacter jejuni* [40] and enteroinvasive Escherichia coli [41]. NOD2 has also been implicated in the recognition of intracellular pathogens, such as Listeria monocytogenes [42], Mycobacterium tuberculosis [43] and Streptococcus pneumoniae [44]. The interaction of the LRR motif of NOD molecules with a ligand leads to recruitment of the adaptor molecules RICK and CARD9 [45], resulting in activation of the kinase TAK1, which is responsible for activating the IKK complex [46, 47]. This results in degradation of the nuclear factor (NF)-KBa inhibitor and translocation of NF- κ B to the nucleus. NOD1 and NOD2 stimulation activates not only the NF-kB pathway but also MAP kinase p38, ERK and JNK

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[48, 49]. The NF- κ B and MAP kinase pathways cooperate in the induction of proinflammatory molecule expression [29] (Fig. 1A).

Like NLRs, RLRs are located in the cytoplasm and defend the host against viral infections within the cytoplasm [50]. Following dsRNA binding, RLRs recruit the adaptor molecule CARDIF (CARD adaptor-inducing IFN- β) through a caspase recruitment domain (CARD)-CARD interaction. Mitochondrial bound CARDIF recruits the appropriate molecules for the activation of NF-κB and IRF3 [51]. Although several receptors recognize microbial structures, TLRs are the only PRRs identified to date that directly mediate full DC maturation. Thirteen different TLRs have been identified in mammals [52]. Some of these receptors - TLRs 1-6 and 11 - are expressed at the cell surface and recognize different products of bacterial, fungal or protozoan origin, including lipopeptides, lipopolysaccharides (LPSs) and peptidoglycans. Others, such as TLRs 3, 7, 8 and 9, are located in the endoplasmic reticulum and recognize microbial nucleic acids [52]. TLRs can also bind to a large set of endogenous ligands, including heat shock proteins (HSPs), hyaluronate and heparan sulfate (extracellular matrix breakdown products), fibronectin, high mobility group box 1 protein (HMGB1) and modified low-density lipoproteins [53]. Moreover, myeloidrelated protein-8 (Mrp8) and Mrp14 - two abundant cytoplasmic proteins of phagocytes, released after phagocyte activation [54] - have been also identified as endogenous ligands of TLR4.

By recruiting different combinations of adapter proteins, individual TLRs turn on signal transduction pathways leading to the activation of different transcription factors, such as NF-kB, activation protein (AP)-1 and IFN regulatory factors (IRFs) [55]. TLRs transduce the signal through two major pathways: the MyD88-dependent pathway and the Toll/IL-1R domain-containing adaptor-inducing IFN- β (TRIF)-dependent pathway. The MyD88-dependent pathway leads to the production of proinflammatory cytokines, such as IL-6 and tumor necrosis factor (TNF)- α , via the recruitment of signaling molecules, including IRAK4 (IL-1R-associated kinase 4), IRAK1 and TRAF6 (TNF receptor-associated factor 6). The TRIF-dependent pathway may be activated by the engagement of TLR3 or TLR4, and leads to the production of type I IFNs, including IFN-β in particular [56] (Fig. 1A).

Coreceptors may assist TLRs in their functions. For example, CD14 amplifies the signals transduced by TLR4, TLR2 and TLR3 in the presence of particular ligands. CD14 may therefore serve as a coreceptor for TLRs both at the cell surface and in the endosomal compartment [57, 58]. CD14 may be expressed on the cell membrane as a glycosylphosphatidylinositolanchored receptor (GPI-AR) [59] or secreted as a soluble recirculating serum protein. Cells of both hematopoietic and non-hematopoietic origins can express CD14 [60]. However, the precise role of this particular PRR remains unclear. Most of the information available concerns the role of CD14 as a coreceptor working with TLR4. Two functions have been attributed to CD14 in this context: i) recruitment of TRIF and TRAM for type I IFN production [61]; and ii) LPS presentation to TLR4, facilitating cellular responses to low doses of LPS [57, 62]. An absolute requirement for a full response to the smooth form of LPS (sLPS) has been demonstrated [63]. We recently showed that CD14 may have a third function [unpublished data]. Following LPS stimulation, CD14 activates the Ca²⁺/calcineurin and NFAT pathway in DCs in a TLR4-independent manner. This function of CD14 is necessary to induce IL-2 and cyclooxigenase-2 (COX-2) production, leading to prostaglandin E_2 synthesis (PGE₂) (Fig. 1B).

 PGE_2 is the most versatile prostanoid known, regulating many physiological and pathophysiological responses. In particular, it regulates or mediates various DC functions, including DC migration and the polarization of T-cell responses [64, 65] through autocrine or paracrine effects on different receptors [66]. DC-derived PGE₂ facilitates Th1 differentiation via the EP1 receptor expressed on naive T cells [66], whereas PGE₂-mediated activation of the EP2 and EP4 receptors promotes Th2 differentiation [67, 68]. Given the importance of PGE₂ for the regulation of DC function, this prostanoid is one of the components of the non-microbial stimulus cocktail used to activate DC for in vivo therapies. The definition of this new role for CD14 provides new insight into the molecular signaling occurring during the initial phases of host defense to bacterial infections. These initial events can then influence the development of the inflammatory process.

DCs and innate immunity: DCs as a conductor of NK cell responses

DCs have clearly been demonstrated to play a role in NK cell activation in many different experimental systems [11, 69–76]. For instance, a key role for DCs in this priming process during herpes simplex virus (HSV)-1 as well as *Listeria monocytogenes* infections has recently been shown in experimental models in which DCs can be conditionally ablated [75, 76]. Starting from the pioneering work of Fernandez et al. [11], many groups have investigated the role of DC-derived cytokines and membrane-bound molecules in

the activation of NK cells. These studies have generally reported a major role for DC-derived type I IFN in NK cell cytotoxic activity [72, 77–79], but two main pathways have been identified as accounting for DCmediated NK cell IFN- γ release in both humans and mice: i) DC-mediated NK cell activation is dependent on IL-12 and other DC-derived cytokines/molecules [69, 71, 80–93]; and ii) NK cell functions are strongly boosted by DC-derived IL-2 in association with other cytokines/molecules [72, 74, 94, 95].

IL-12 appears to be essential for the induction of IFN- γ by NK cells in different experimental settings [69, 80]. It is required for NK cell activation and is released after DC and NK cells come into contact [81], following the stimulation of DC derived from CD34⁺ precursors with LPS [71], the priming of monocyte-derived DCs with Actinobacillus, E. coli or Bacillus Calmette-Guèrin (BCG) [82, 84], the activation of myeloid DCs with poly-I:C [77] or of PBMCderived DC with LPS [92]. DC-derived IL-12 seems to be presented to NK through the formation of 'stimulatory synapses', ensuring the efficient presentation of low doses of IL-12 to both human and murine NK cells [86]. In some experimental settings, IL-12 has also been shown to be a key regulator of NK cell cytotoxicity [85]. In other studies based on peripheral blood DCs, IL-12 and cell-cell contacts were found to play only a marginal role, suggesting that other factors inducing NK cell cytotoxicity may be present [91]. Other cytokines released by DC, such as type I IFN, IL-15 and IL-18, may also affect NK cell functions such as IFN- γ production [87], migration [89], cytotoxic function [93] and proliferation [83]. In particular, IL-18 seems to play an important role in enabling NK cells to migrate to secondary lymphoid organs, where they can interact with DCs [89]. Human NK cells exposed to IL-18, but not IL-2, display rapid CCR7 induction and an increase in responsiveness to CCL21, with no increase in lytic activity. Once in the lymph nodes, these NK cells produce large amounts of IFN- γ in response to IL-12, TNF- α and IL-2. A membrane-bound form of DC-derived IL-15 seems to be required to trigger activation, or at least proliferation, of NK cells [83, 88]. Indeed, the presence of the IL-15 receptor on the surface of DCs is required to mediate the effects of IL-15. This suggests that DCs may present IL-15 in trans to NK cells. Finally, different human DCs display different patterns of cytokine secretion correlated with their ability to activate NK cells in vitro [90]. Monocyte-derived DCs produce IL-12p70, which induces NK cell activation in terms of NK cell proliferation, cytotoxicity and the upregulation of CD56. CD34⁺ hematopoietic progenitor cell (HPC)-derived LCs do not produce sufficient IL-12p70 and have too few IL-15 receptors to induce NK cell activation. Nonetheless, once activated by recombinant IL-12, LCs provide additional factors (leading candidates include IL-15 and IL-18, which are produced in larger amounts by these cells) that promote NK cell proliferation and survival, sustaining IL-12-induced activation. Finally, CD34⁺ HPC-derived dermal interstitial DCs show intermediate levels of cytokine production and NK cell activation.

IL-2 has always been added to NK cell cultures in vitro to obtain hyperresponsive cells. However, this cytokine was not considered important for NK cellmediated anti-tumor or antimicrobial responses in vivo, as IL-2 was thought to be produced exclusively by T cells during the late, antigen-specific phase of the immune response, after the peak of NK cell activation [96]. Following the first reports of IL-2 production by activated DCs in the first few hours after stimulation [12], we investigated the possible physiological role of this early production of IL-2 in NK cell activation. We found that E. coli-activated DCs were potent activators of NK cells both in vitro and in vivo and that this process was dependent on DC-derived IL-2 (necessary for NK cell IFN- γ production), type I IFN (required for optimal NK cell cytotoxicity) and other unknown factors [72]. It was subsequently shown that TLR-dependent, as opposed to TLR-independent full-maturation stimuli, render DCs able to elicit IFN-γ production by NK cells [74]. In particular, LPS, CpG and BCG have been shown to induce IFN-y production in vitro and in vivo in an IL-2-dependent manner, whereas stimuli that did not induce the release of IL-2 by DCs, such as pertussis toxin (PT), cholera toxin (CT), Leishmania mexicana, and - in the C57/BL6 background but not in the BALB/c background - Pam-3-Cys, did not lead to the induction by DCs of IFN-y production by NK cells. IL-2 was necessary for NK cell activation in all these experimental settings, but was unable to induce such activation if supplied alone as a recombinant molecule, highlighting the need for other soluble or membrane-bound DC-derived factors. These observations were recently called into question by the work of Schartz et al. [97], who suggested that IL-2 derived from LPS-activated DCs was not required for NK cell functions. However, these authors were unable to confirm this hypothesis experimentally, as they assessed only CD69 upregulation as to evaluate NK cell priming. CD69 upregulation, although associated with activation, does not actually indicate the acquisition of any real effector functions [98]. Monocyte/DC-derived IL-2 has also been shown to play a role in NK cell activation in humans. Newman et al. [94] demonstrated that the capacity of human NK cells to produce IFN- γ in response to stimulation with *Plasmodium* falciparum-infected red blood cells was strictly de-

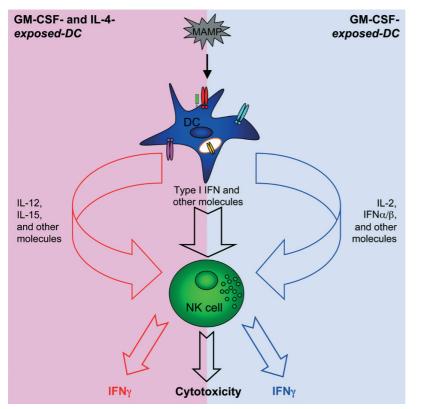


Figure 2. Mediators of NK cell activation produced by activated DCs differentiated in the presence of GM-CSF alone or GM-CSF and IL-4.

pendent upon cell contact-dependent and IL-2/type I IFN-mediated signals derived from monocytes and myeloid DCs. They excluded a major role for IL-12 and IL-15 in the activation of NK cells in their experimental setting, but could not totally exclude the possibility that contaminating cells that could produce IL-2 were present.

It is possible that the two different modes of NK cell activation by DCs described in published studies reflect different conditions for DC culture and the heterogeneity of DC populations differentiated in vivo (Fig. 2). Indeed, mouse and human DCs secrete bioactive IL-12 efficiently only if previously exposed to IL-4 [99]. DCs exposed to the semi-maturation stimulus IL-4 acquire the capacity to activate NK cells independent of microbial stimuli and IL-2, although microbial stimuli do enhance this process [82, 100]. IL-4 also inhibits microbe-induced IL-2 production by DCs ([101] and our personal observations). Thus, IL-12 may contribute to DC-mediated NK cell activation if DCs have previously been exposed to IL-4 in vitro or in vivo. Moreover, blockades of IL-2 activity in vivo [72] or *in vitro* with DCs derived *ex vivo* [74] result in strong inhibition of the activities of NK cells, but not in the complete inhibition of NK cell functions, suggesting that the heterogeneity of in vivo differentiated DCs may result in two different pathways of NK cell activation, as previously described.

Many studies have suggested that cell-cell contact, in addition to soluble factors, may play a role in the DCmediated NK cell activation process [71, 72, 86, 102, 103]. On the one hand, cell-cell contact probably reflects a need for the formation of 'activating synapses' between DCs and NK cells, facilitating the local delivery of high concentrations of known or unknown cytokines. On the other hand, surface receptor-ligand interactions may be required for optimal NK cell activation. Xu et al. [95] recently found that DCs constitutively express a membranebound form of TNF that may bind TNFR2 on the surface of NK cells. Indeed, NK cells upregulate this receptor after long or short periods of culture with IL-2. This finding provides strong evidence supporting a role for DC-produced IL-2.

DCs and adaptive immunity

How do DCs internalize, process and present antigens?

Despite several early descriptions of the uptake of particulate material and cells by DCs, it was long thought that DCs had no phagocytic capacity. This view arose partly from the technical difficulties involved in the culture of immature DCs. Early procedures for DC purification and culture *in vitro* tended to result in DC-enriched preparations containing mostly terminally differentiated cells with a mature phenotype and function. Once it became possible to grow and maintain immature mouse DCs in vitro [104, 105], these cells were found to have marked phagocytic activity that decreased with increasing DC differentiation. Indeed, immature DCs express a large array of phagocytic receptors, including lectins, scavenger receptors, Fc receptors and other PRRs. DCs have been shown to internalize latex and zymosan beads [106, 107], apoptotic bodies [108] and a number of microbes, including many bacteria and viruses, in vitro and in vivo [109]. In vivo, Listeria monocytogenes and Salmonella typhimurium have been colocalized with DCs in intestinal Peyer's patches after oral infection [110, 111], and Listeria monocytogenes has also been found in the DCs of the mesenteric lymph nodes 6 to 12 h after infection [111]. Splenic DCs have been found to be associated with Salmonella typhimurium, Mycobacterium bovis or BCG 4 h after intravenous infection [112, 113]. The phagocytic activity of DCs is designed to facilitate antigen processing and presentation. DCs have no bacterial scavenging function and are highly inefficient at bacterial clearance, but they do have unique mechanisms for antigen processing and for the antigen loading of MHC molecules. For instance, DCs produce various lysosomal proteases, but cannot recruit these enzymes efficiently to the phagosome. DC phagosomes therefore have a low protease concentration, accounting, at least partly, for a much lower efficiency of antigen degradation than observed for macrophages [114, 115]. DCs also produce several cystatin protease inhibitors, which inhibit proteolytic activity in lysosomes and phagosomes [116]. Thus, the proteolysis of antigens taken up by DCs is geared to antigen processing rather than to total destruction, whereas macrophages and neutrophils destroy antigens [117].

Stimuli inducing DC activation and maturation increase the efficiency of antigen processing, for both the class I and class II pathways, and the half-life of peptide-MHC complexes at the cell surface that would otherwise be rapidly internalized and recycled [9, 118, 119]. DC activation induces the de novo synthesis of class I molecules and increases the efficiency of preformed class II molecule transport at the cell surface. DCs have large numbers of multivesicular bodies (MVBs) containing a pool of MHC class II molecules. Following the activation of DCs by contact with a microbe, extensive MVB vesicle fusion occurs, resulting in the formation of long tubular compartments, in which MHC class II molecules and DM molecules are closely associated and directed towards the tips of the dendrites. This reorganization of the MVBs facilitates the efficient loading of class II molecules with exogenous peptides generated in the early endosomes and the presentation of complexes at the cell surface [120].

Another interesting feature of the specific processing machinery of DCs is the ability of these cells to delay the processing of internalized antigens by antigen retention in a mildly acidic storage compartment [121]. Antigens internalized in these vesicles are not immediately degraded, and fusion with the lysosomes is delayed. This mechanism seems to be coordinated with the generation of newly synthesized MHC class II molecules, 12–18 h after DC activation [9].

DCs also present exogenous antigens on MHC class I molecules, in a process known as cross-presentation [122]. It remains unclear how degraded antigens from the exogenous pathway are loaded onto MHC class I molecules, although it has been suggested that this loading may involve endoplasmic reticulum (ER)phagosome fusion [123]. The recruitment of ERresident proteins to the phagosome would allow the retrotranslocation of proteins from the phagosome to the cytosol, via the sec61 protein [124]. This molecule is known to mediate both the translocation of newly synthesized proteins into the ER and the retrotranslocation of misfolded proteins from the ER to the cytosol for proteasomal degradation [124]. The low efficiency of particle degradation in the phagosome of DCs would make this process optimal in these cells [124].

DCs as conductors of adaptive T-cell responses

The requirement of DCs for T-cell activation in lymph nodes was initially demonstrated in vivo for CD8⁺ T lymphocytes. Mice temporarily deprived of CD11c⁺ DCs cannot mount efficient specific CD8⁺ T-cell responses to infections with the intracellular bacterium Listeria monocytogenes, the parasite Plasmodium yoelii, LCMV or antigen immunization [125, 126]. It was subsequently shown that CD11c^{high} conventional DCs are required for the priming of both CD8⁺ and CD4⁺ T cells in the spleen, whereas these cells are dispensable for CD4⁺ T-cell priming in lymph nodes. Indeed, within lymph nodes, pDCs can replace conventional DCs for this function [127]. In the absence of conventional DCs, pDC-mediated CD4⁺ T-cell priming occurs but is not associated with CD8⁺ T-cell activation, indicating that pDCs prime CD4⁺ T celldominated immune responses only [127].

There is indirect evidence to suggest that DCs are necessary for the activation of protective T-cell responses in humans. In particular, a lack of circulating DCs during dengue virus infections or bacterial sepsis is always associated with a poor prognosis [128, 129]. DCs can enter the lymph node via the blood or lymph [130]. If they arrive through the blood, they are initially found clustered together, close to high endothelial venules (HEVs). However, their distribution subsequently changes, such that, one day after reaching the lymph node, DCs are distributed throughout the T-cell area [131]. The process by which DCs reach the lymph node through the lymph and undergo redistribution has been well characterized in the skin compartment. Following skin inflammation, dermal DCs are the first cells to migrate to the draining cutaneous lymph node, where they are first detected after 24 h, their levels peaking after 2 days. LCs migrate to the lymph nodes slightly later, their numbers peaking in the draining lymph nodes 4 days after administration of the stimulus [132]. LCs and dermal-derived DCs localize to different areas of the lymph node. Within the T-cell area, dermal DCs localize to the outer paracortex just beneath the B-cell area, whereas LCs localize to the inner paracortex, suggesting that these two different DC populations may have different functions and encounter different T-cell subsets [132]. During cutaneous viral infections, such as herpes virus infections, the antigen is transported to the draining lymph node mostly by dermalderived DCs, which transfer the antigen to resident CD8⁺ DCs in the cortex, leading to the activation of CD8⁺ T-cell responses through cross-presentation [133]. A continuous slow rate of LC migration to the draining lymph nodes is thought to occur in the absence of inflammation, in steady-state conditions. A few motile immature LCs loaded with tissue-specific antigens should continually reach the draining lymph node, conserving their immature or semi-mature state, probably maintaining T cell-mediated self-antigen tolerance [134-136].

The different DC subtypes present in the lymph nodes display considerable diversity in terms of specialization for antigen presentation. For instance, CD8⁻33D1⁺ DCs preferentially present antigens in association with the MHC class II molecules and, following activation, they increase the efficiency of the class II processing machinery. These cells are, therefore, specialized in CD4⁺ T-cell activation [137]. By contrast, CD8⁺DEC205⁺ cells efficiently present antigens, leading to the clonal expansion and acquisition of effector functions by both CD4⁺ and CD8⁺ T cells [137]. These cells are the only cells able to prime CD8⁺ T-cell responses in the lymph node [125].

There is at least one other important difference between the two DC subtypes. $CD8^+DEC205^+$ DCs primarily trigger Th1 responses, whereas $CD8^-33D1^+$ DCs induce the production of either IL-4 alone or both IFN- γ and IL-4 by T cells [138, 139]. IL-12 has been shown to be an essential cofactor for skewing toward Th1 responses in various experimental systems [140]. CD8⁺DEC205⁺ DCs produce much larger amounts of IL-12 than CD8⁻33D1⁺ cells [141]. However, these cells are thought to induce Th1 skewing by the membrane-bound cofactor CD70, a member of the tumor necrosis family [22], in the presence of TLR4 and TLR3 agonists, rather than through IL-12. This would explain why individuals with inherited IL-12 or IL-12 receptor deficiency respond to many different intracellular pathogens, displaying particularly strong susceptibility only to a limited range of microorganisms, including BCG and *Salmonella* [142].

DCs and autoimmunity

DCs play a central role in regulating the activation and progression of immune responses. To limit self-tissue damages while maintaining the ability to respond to pathogens, the immune system has developed mechanisms for maintaining peripheral tissue tolerance. There is increasing evidence that DC and regulatory T cell (Tregs) cross-talk plays a crucial role in the equilibrium between tolerance and immunity [143]. Interaction between organ-specific Tregs and DCs presenting organ-derived antigens is fundamental in preventing autoimmune tissue destruction [144, 145]. Given the fundamental role of DC in controlling tolerance and immunity, a delicate imbalance in the feedback control of TLR-activated cells has been associated with autoimmunity in genetically prone individuals. An increasing number of reports have provided evidence that, in a susceptible genetic background, DC activation through TLRs can induce autoimmune tissue destruction, through the production of type I IFNs in particular.

The DC maturation process leads to DCs releasing various cytokines and chemokines [9] – including type I IFNs, key cytokines directing innate immune responses and favoring the subsequent development of adaptive responses to viruses and bacteria – within a few hours of microbial infection. Type I IFNs are encoded by 13 IFN- α genes and 1 IFN- β gene, clustered on chromosome 9, all with an unusual, intron-less structure. The products of all these genes signal via the IFN- $\alpha/\beta R$ pathway. Type I IFNs are produced by many cells in response to viral challenge. However, DCs, and pDCs in particular, produce large amounts of these cytokines [146, 147], which may also have an autocrine effect on DCs, promoting their activation [148].

TLRs 7 and 9 can induce type I IFN production and are expressed at high levels in both human and mouse pDCs, like TLRs 3, 4 and 9 in myeloid DCs [55]. TLR

stimulation may lead to the activation of two different signaling cascades leading to IFN production: the MyD88/IRAK-1 pathway downstream from TLR7, TLR8 and TLR9, and the Trif/IKK ϵ pathway downstream from TLR3 and TLR4 [63, 149–151]. Activation of the Trif/IKK ϵ pathway leads to the phosphorylation, dimerization and nuclear translocation of IRF-3, which is essential for IFN- β induction, and the activation of NF- κ B and AP-1, which is also required to trigger the production of inflammatory cytokines. The pathways downstream from TLR7–9 are MyD88/ IRF-7-dependent [55].

TLR-mediated tolerance breakdown and autoimmunity have been observed in various experimental disease models. For instance, autoimmune heart failure can be induced by injections of TLR-stimulated DCs loaded with a heart-specific self-peptide [152]. TLR activation and the stimulation of autoreactive CD4⁺ T cells seem to be essential for this process. The pathogenesis of dilated cardiomyopathy depends on genetic susceptibility and microbial infections. The results obtained therefore suggest that the induction of autoimmunity does not necessarily require antigen mimicry, but does require tissue injury and the activation of innate immune cells through innate receptors in susceptible individuals [152].

TLR signaling also seems to be involved in the induction of experimental autoimmune encephalomylelitis (EAE) [153]. B10.S EAE-resistant mice expressing a transgenic TCR specific for the encephalitogenic myelin proteolipid protein do not develop EAE, despite having large numbers of self-reactive T cells. EAE resistance seems to depend on APC activation state. APC stimulation via TLR4 and TLR9 results in tolerance breakdown and the development of autoimmunity [153], suggesting an important role of the innate immune system in maintaining the equilibrium between tolerance and autoimmunity [153].

TLR activation is also required for the induction of autoimmunity in Alb-1 mice - a mouse model of hepatitis. These mice produce the LCMV (lymphocytic choriomeningitis virus) glycoprotein exclusively in the liver, under the control of the albumin promoter [154]. LCMV glycoprotein peptide₃₃₋₄₁ (gp-33) is processed and presented to CD8⁺ T cells by the H-2D^d molecule. The gp-33 peptide is not presented in the thymus, so gp33-specific T cells reach peripheral lymphoid organs. Nevertheless, they do not cause autoimmunity in steady-state conditions. However, the infection of these animals with LCMV induces the expansion and activation of self-reactive (anti-gp33) T cells and the development of hepatitis. Viral infection is essential for disease development, as the immunization of Alb-1 mice with the gp-33 peptide induced expansion of the autoreactive T-cell population but did not cause tissue damage [154]. TLR activation seems to be the key element of viral infection for this process. As a matter of fact LCMV infection induces autoimmunity via TLR3 engagement on macrophages and various DC subsets, leading to the consequent production of type I IFNs and TNF α , which, in turn, activate other DCs and bone marrow-derived cells. Moreover, type I IFNs and TNF α may also elicit the secretion of chemokines, such as CXCL9, from hepatocytes, attracting self-reactive T cells to the liver, leading to tissue destruction. CXCL9 has also been implicated in other autoimmune diseases. It is present in high concentration in the synovial fluids of patients with rheumatoid arthritis [155]. Studies in the Alb-1 mouse model have demonstrated a clear role for the TLR-mediated activation of DCs and other bone marrow-derived cells in tolerance breakdown and autoimmune precipitation in susceptible individuals. Loss of tolerance and autoimmunity has also been observed in an analogous mouse model in which the LCMV glycoprotein was produced exclusively in the pancreas β -cells, under control of the rat insulin promoter [156]. Autoimmune β -cell destruction may be induced by viral infection or the administration of viral proteins together with TLR3 or TLR7 agonists. As in the hepatitis model, disease development was strictly dependent on IFN- α production [156]. Various hypotheses have been put forward to explain the role of IFN- α in destructive insulitis. These hypotheses include the IFN- α -mediated overexpression of MHC class I on β cells, leading to an increase in β -cell susceptibility to CD8⁺ T cell lysis [156], an IFN- α mediated increase in the lytic functions of CD8⁺ T cells and an IFN- α -mediated increase in the efficiency of LCMV glycoprotein cross-presentation by DCs [157].

Several lines of evidence suggest that type I IFNs may be involved in the pathogenesis of other autoimmune diseases, such as systemic lupus erythematosus (SLE). Patients with SLE have high levels of IFN- α in serum and affected tissues [158]. Moreover, a direct association has been observed between repeated administration of IFN- α in patients suffering from various cancers or chronic viral infections and the development of symptoms associated with SLE [159, 160]. Global gene expression studies on blood lymphoid cells and kidneys from SLE patients have shown that IFN-regulated genes (IFN-signature) are selectively upregulated in these patients [158, 161]. Some typical lupus symptoms have been described in individuals with trisomy of the type I IFN gene cluster [162] and with single nucleotide polymorphisms in the IRF5 and tyrosine kinase 2 (TYK2) genes, the products of which are involved in regulating type I IFN production [163, 164]. Type I IFN has been shown to play a role in lupus in NZB lupus-prone mice, in which deletion of the common subunit of type I IFN receptors reduced the severity of disease and repeated injections of IFN- α accelerated lupus symptom manifestations [165].

Immune complexes isolated from the sera of SLE patients can efficiently induce the production of IFN- α by pDCs [166], and IgG (immunoglobulin) purified from lupus patients and mixed with apoptotic or necrotic cells constitutes a pDC activation stimulus sensitive to DNase and RNase [166]. Immune complexes from individuals with SLE do not stimulate pDCs previously treated with anti-FcyRIIa antibody. pDCs constitutively express TLR7 and TLR9 [167], which were originally identified as receptors for viral single-stranded RNAs and hypomethylated CpG motifs in bacterial DNAs, respectively. Based on these observations, a number of in vitro experiments have been carried out, and the results obtained suggest that the internalization of nucleic acid-containing immune complexes by pDCs, via FcyRs, delivers nucleic acid antigens to intracellular TLR7 or TLR9, triggering these receptors and resulting in cell activation and type I IFN production (reviewed in [168]. Autoreactive antibodies may be produced as a result of defects in B cell-mediated tolerance, such as defects in receptor editing in the bone marrow and spleen and other genetic factors in susceptible individuals [169, 170].

Two different models of disease development have been proposed [168, 171]. In both models, DC-derived type I IFNs are the central factors. However, in the first model, viral infections are considered to be the starting point, whereas, in the second model, the initiation phase is triggered by endogenous TLR ligands (apoptotic material) in the absence of infection. In the first model, viral infections induce pDCs to produce IFN- α , promoting cell death, the release of RNA-based autoantigens, TLR7 upregulation by B cells and the activation of pDCs, which subsequently respond more strongly to immune complexes. Autoreactive B cells can internalize RNA autoantigens through the B-cell receptor and deliver them to TLR7. This process induces B-cell activation, proliferation and differentiation. Differentiated B cells produce autoantibodies, which form immune complexes that are, in turn, internalized, via FcyRs, by pDCs and delivered to TLR7. This results in the production of more IFN- α by pDCs, perpetuating the feedback loop [168].

In the second model – the two-phase model – the initiation phase is induced by apoptotic cell material, which is taken up by a specialized subclass of lymphoid DCs, through TLRs. These DCs produce large amounts of type I IFNs, which induce the maturation

of lymphoid and myeloid DCs. Mature myeloid DCs are potent APCs that activate autoreactive T helper cells that are otherwise quiescent. Primed T helper cells contribute to the activation of autoreactive B cells. Alternatively, mature DCs may activate autoreactive B cells that have interacted with the antigen via the B-cell receptor directly, by producing B lymphocyte stimulator protein (BlyS) and proliferation-inducing ligand (APRIL) [172]. Activated, autoreactive B cells proliferate and differentiate into autoantigen-producing plasma cells. Immune complexes are thus formed that, during the amplification phase, induce further type I IFN production by pDCs (with internalization via $Fc\gamma Rs$) and enhance B-cell proliferation and autoantibody production [171].

Concluding remarks

DCs are key regulators of immune responses. They react to infectious agents with a complex innate receptor repertoire, which, by transducing the appropriate intracellular signal, indicates the type of functional reprogramming DCs should undergo. Thus, DCs show a functional plasticity in their maturation process that depends on the nature of the perturbation and makes it possible to develop a particular, efficient immune response to each pathogen. The various functions of DCs are segregated in time and space, allowing these cells to control immune responses. As DCs play a key role in priming innate and adaptive immune responses, the establishment of a self-renewing inflammatory environment leading to DC activation may lead to the generation of autoimmune reactions and autoimmune symptoms in genetically susceptible individuals. Understanding the biology of DCs should help us make progress toward the successful manipulation of immune responses, enhancing or attenuating these responses depending on pathophysiological conditions.

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