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## Cell Signaling Pathways that Regulate Ag Presentation

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### Abstract

Cell signaling pathways regulate much in the life of a cell: from shuttling cargo through intracellular compartments and onto the cell surface, how it should respond to stress, protecting itself from harm (environmental insults or infections), to ultimately, death by apoptosis. These signaling pathways are important for various aspects of the immune response as well. However, not much is known in terms of the participation of cell signaling pathways in Ag presentation—a necessary first step in the activation of innate and adaptive T cells. In this brief review, I will discuss the known signaling molecules (and pathways) that regulate how Ags are presented to T cells and the mechanism(s) if identified. Studies in this area have important implications in vaccine development and new treatment paradigms against infectious diseases, autoimmunity and cancer.

### Introduction of Cell Signaling Pathways

What allows cells to respond to stimuli in specific ways? A priori, one can envisage a stimulus and a cellular response. Unfortunately, in between that stimulus and response is a black box. An external or internal event triggers within a cell a cascade (linear or branched), resulting in the phosphorylation and/or dephosphorylation of specific proteins. As a consequence, these cell signaling pathways have effects upon or within the cell that results in a specific response. For example, the activation of these pathways can stimulate cell migration or arrest. This can be due to the polymerization or depolymerization of cytoskeletal proteins, or the rearrangement of proteins or intracellular compartments. A potential effect can also result in activation-induced cell death.

Studies to dissect the specific paths (i.e., proteins that are phosphorylated or dephosphorylated and consequent effects on “downstream” intracellular proteins) followed by cell signaling pathways, have helped us understand many ways in which cells react to the environment— including infections by pathogens. As this is a Brief Review in *The Journal of Immunology*, I will focus my comments on cell signaling pathways that control the presentation of Ag to conventional and unconventional T cells.

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Why would cell signaling pathways even be important for the immune system? Certainly, APCs need to be able to capture and internalize Ag in various forms--and by various routes (1-5). This could be by phagocytosis, pinocytosis, infection by a pathogen, or even taken from within a cell as an endogenous protein or lipid. Ag-loaded molecules need to be able to be transported intracellularly along the cytoskeletal network, to their ultimate expression on the cell surface for recognition by T cells. That "movement" needs direction--this is provided by cell signaling pathways.

APCs mainly utilize three pathways of Ag presentation; Ags are presented by MHC or MHC-like molecules (1-5). The first pathway involves MHC class I molecules (2, 6-18). In the cytosol, endogenously-synthesized polypeptide chains are threaded into a barrel-like structure called the proteasome, which contains a variety of proteolytic enzyme activities. As the polypeptide is cleaved, a diverse array of peptides consisting of approximately 9 – 15 amino acids is generated. These peptides are then delivered into the endoplasmic reticulum (ER) by the transporter associated with Ag processing (TAP). Upon being loaded onto peptide-receptive MHC class I molecules, ER resident peptidases cleave amino terminal amino acids, resulting in the 8 – 9 amino acid peptides that are usually found associated with MHC class I molecules. The peptide-loaded MHC class I molecules are then transported through the Golgi to the cell surface, where they are recognized by CD8+ T cells. The second Ag presentation pathway involves MHC class II molecules (17, 19-31). Rather than being synthesized intracellularly within an APC, Ags are taken up by phagocytosis (or pinocytosis) and delivered to late endocytic compartments where they are processed into longer (e.g., 15 – 20) peptide-sized fragments than those loaded onto MHC class I molecules. Initially, MHC class II molecules are complexed with the invariant chain (Ii). The CLIP portion of the Ii prevents peptide loading until the MHC class II molecules traffic to late endocytic compartments (e.g., MIIC). It is here that an antigenic peptide replaces the Ii chain's CLIP. The newly-loaded MHC class II molecule is then transported to the cell surface where it is recognized by CD4+ T cells. The third Ag presentation pathway does not involve peptide Ag presentation. CD1 molecules are MHC class I-like molecules that generally present lipid Ags to invariant, relatively oligoclonal or even diverse T cells. These lipids can be of microbial origin or from mammalian cells themselves (5, 32). The CD1 family of Ag presenting molecules consists of two members (based on the human CD1 molecules): Group 1 includes CD1a, CD1b and CD1c molecules, whereas Group 2 consists of CD1d as its sole member (33). Each of these molecules differ somewhat in how they traffic intracellular and thereby how they acquire Ag.

For the sake of completeness, I will note there are the very interesting MHC class I-like MR1 molecules, which present microbial vitamin B-derived metabolites to a novel T cell subpopulation called MAIT [(mucosal-associated invariant T cells; ref. (34, 35)] Because so little is known about the cell signaling pathways regulating their function, they will not be discussed here.

The presentation of specific Ags to T cells by cell-to-cell interactions, results in the production of various cytokines that, in turn, stimulate the APCs. For T cells to be stimulated by APCs, cell signaling pathways within the APCs themselves need to be activated; this results in the proper Ags being processed and loaded onto the appropriate Ag

presenting molecule to be expressed on the surface. This is absolutely required for Ag-specific T cells to be activated and perform their effector cell functions.

Which are the most widely studied cell signaling pathways that control classical (i.e., MHC class I and II) and non-classical (e.g., CD1d) Ag presentation and the mechanism/s (if known) by which they do this? One of the best understood cell signaling pathway family is that mediated by the MAPK (Fig. 1; left side). Following a cell stimulus, a MAPKKK is phosphorylated which, in turn, phosphorylates a MAPKK. Finally, the MAPKK activates the MAPK which then is transported into the nucleus to mediate its function. The MAPK family consists of three main members: p38, ERK and JNK [reviewed in (36)]. Upon receiving a cell stimulus, such as infection with a pathogen, exposure to inflammatory cytokines, etc., the resultant activation of the MAPK pathways results in inflammation, cell growth, differentiation or apoptosis. Consequently, the activation of MAPK pathways has the potential to impact the ability of a host's immune cells to appropriately respond to an infection. Of these three pathways, p38 has been studied the most in terms of aspects relating to Ag processing and presentation.

### **Role for p38 on APC maturation and function**

The MAPK p38 can be phosphorylated by two upstream kinases: MKK3 and MKK6 (37). For macrophage (MΦ) maturation (20) and production of IL-12 (38), p38 is required via its stimulation by MKK3 (38). This occurs because MKK3 indirectly activates the IL-12 p40 promoter through its phosphorylation of p38 (39). In MΦ, anisomycin (a p38 activator) enhances LPS-induced IL-12 production; this is blocked by the p38-specific inhibitor, SB203580 (39). Blocking p38 also impairs DC/T cell clustering, which can, of course, reduce effector T cell activation (39). Interestingly, p38 inhibits (whereas ERK promotes) the differentiation of monocytes into DCs (40). As will be mentioned below, p38 and ERK have similar reciprocal control over CD1d-mediated Ag presentation (41-43). Unstimulated DCs have a basal level of p38 that is enhanced following stimulation with anisomycin, a drug that activates both p38 and JNK (44). In both human (44) and mouse (45) DCs, activation of TLR4 results in the phosphorylation of p38. TLRs have a variety of known effects on APCs; these are discussed later in this review. The other MAPKK that can activate p38, MKK6, increases the APC activity of Langerhans cells by stimulating the NF-κB pathway (46).

The MAPK p38 has been shown to be important for Ag presentation by classical MHC class I and II molecules. Ag uptake is increased in DCs treated with cyclophin A, which results in p38 activation (47). p38 (and ERK) activation by osteoprotegerin ligand increases costimulatory molecule expression (48), readying APCs for interaction with Ag-specific T cells. In the context of Ag presentation by MHC class I, p38 can help--or hinder. For example, p38 phosphorylation following CD40L engagement results in the activation of DCs and expansion of HIV-specific memory CD8+ T cells (49). It was presumed that the expansion of these T cells is MHC class I-dependent; however, it has recently been shown that SIV peptides can be presented to CD8+ T cells by MHC class II molecules (50). I indicated above that TLR engagement activates p38 in DCs (44, 45); this also results in enhanced Ag presentation by DCs to antitumor T cells via MHC class I molecules (51). In

contrast, there is increased Ag uptake for cross-presentation by MHC class I molecules in a Japanese Encephalitis Virus model when p38 is inhibited (7); thus, p38 appears to be a negative regulator in this model.

p38 activation in DCs (52) and its induction by fragments of the food product gliadin (53), increases costimulatory and MHC class II molecule expression, which, in turn, enhances Ag presentation to CD4<sup>+</sup> T cells. This is in contrast to one report, in which the role of p38 in MHC class II-mediated Ag presentation by multiple myeloma patient DC was studied. In that system, p38 activation inhibited Ag presentation by MHC class II molecules, concomitant with reduced costimulatory molecules and MHC class II expression on the cell surface (54).

We have done extensive analyses on signal transduction pathways that can regulate lipid Ag presentation by CD1d. It is well known that viruses (along with other external stimuli) activate p38 in cells (43). When we analyzed the role for p38 in regulating CD1d-mediated Ag presentation following infection with vaccinia virus or vesicular stomatitis virus, we found it was inhibitory; blocking p38 actually increased Ag presentation to natural killer T (NKT) cells (42, 43). However, this does not only occur in a virus infection. Inducing apoptosis in CD1d<sup>+</sup> APCs stimulates p38 activation; not surprisingly, these cells are poorer stimulators of NKT cells (41). Interestingly, another group has looked at Ag presentation by Group 1 CD1 molecules. As we have observed with CD1d, p38 is inhibitory in that system as well (55). Notably, p38 has an NKT cell-intrinsic negative effect, as treatment of iNKT cells with a p38-specific inhibitor impairs their stimulation by the CD1d-binding (and NKT cell-stimulating) glycolipid,  $\alpha$ -galactosylceramide [ $\alpha$ -GalCer; ref. (56)] or by an anti-CD3-specific mAb (57). Therefore, p38 can affect both the APC and T cell sides of a host's immune response.

### Participation of JNK

As indicated above, JNK has effects on many of the same cellular functions as p38, although there is not total overlap (37). Certainly, analyses of JNK in DCs have reported that, like for p38, anisomycin induces JNK in human monocyte-derived DCs, although at higher concentrations (39). Unlike that for p38, at baseline, there is no detectable JNK in human DCs (39), nor does TLR4 activation stimulate JNK in murine DCs (45). Does JNK have any role in Ag processing and presentation? It has been shown that JNK2-deficient mice generate more CD8<sup>+</sup> T cells in response to IL-2 (58) and more antiviral CD8<sup>+</sup> cells are found in these mice upon infection with lymphocytic choriomeningitis virus (59). This suggests that JNK can have a negative effect on MHC class I-mediated Ag presentation; alternatively (or additionally), this could be T cell-intrinsic. In line with those two reports, we have found that JNK2 is a negative regulator of Ag presentation by CD1d (Liu et al., manuscript in preparation). Studies on the JNK signaling pathway in the control of Ag presentation by classical and/or non-classical MHC molecules are still limited to date.

### Role of ERK

There are a few reports that have asked whether the ERK MAPK pathway is important for M $\Phi$  or DC maturation, or if it can be activated in either cell population. For example, one

report suggested that LPS or GM-CSF induces ERK in macrophages, albeit with different kinetics [the latter induces ERK activation much more quickly—5 min vs. 15 min, respectively; ref. (60)]. LPS activates ERK in M $\Phi$  (44, 61); however, it apparently does not do so in DCs (62). In terms of M $\Phi$  maturation, it is both ERK- and p38-dependent (20). In contrast, ERK promotes, but p38 impairs, the differentiation of human monocytes into DCs (40). We have reported that, in the context of lipid Ag presentation by CD1d, ERK is a positive regulator (43).

As indicated above, a number of cytokines can activate MAPK signaling, with an impact on APC maturation or Ag presentation abilities. In some cases, such as with TGF- $\beta$ , even though that cytokine can activate MAPKs, which negatively regulate CD1d-mediated Ag presentation [(41-43); Liu, et al., in preparation], the ultimate effect on Ag presentation by CD1d in the TGF- $\beta$  model appears to be (at least) p38-independent (21).

### Regulation of Ag presentation by protein kinase C (PKC) isoforms

The protein kinase C (PKC) family members are ser/thr kinases that consist of three main subgroups: 1. Conventional/Classical [(PKC $\alpha$ ,  $\beta$  (I and II)), and  $\gamma$ ]; 2. Atypical (PKC  $\zeta$  and  $\lambda/\iota$ ); and 3. Novel ( $\delta$ ,  $\epsilon$  and  $\theta$ ) [reviewed in (63)]. Within these subgroups are 10 kinases that play distinct roles in the regulation of gene expression and cell proliferation. The activation of PKCs modifies them from a quiescent cytosolic form, to an active, membrane-associated form (64). Beyond their role as cytoplasmic signal transduction molecules, there is also evidence to suggest they can serve as nuclear kinases as well. In terms of the control of Ag presentation, PKC isoforms have been shown to promote Ag presentation by MHC class II molecules. In particular, the use of PKC activators such as bryostatin, which activates PKC- $\alpha$ ,  $\delta$  and  $\iota$ , or PKC activation by phorbol esters and ionomycin, increases the surface expression of MHC class II molecules and thereby increases Ag presentation (27, 65, 66). The use of PKC-specific (i.e., PKC- $\alpha$  and/or - $\delta$ ) inhibitors by our laboratory and others, further supports the positive correlation between PKC- $\delta$  activation and Ag presentation by MHC class II molecules (23, 27, 67). Interestingly, we have found that Ag presentation by CD1d, which is an MHC class I-like molecule that traffics intracellularly more like MHC class II molecules, is promoted by PKC- $\delta$  (67). In contrast to MHC class II and CD1d, Ag presentation by MHC class I molecules is not impacted by PKC- $\delta$  (27, 67).

### TLRs and Ag processing and presentation

In general, when one thinks about what constitutes the innate immune response, the first thing that often comes to mind is a response via Toll-like receptors [TLRs; reviewed in (68)]. The TLR family of molecules consists of up to 13 structurally similar molecules in mammals, which are homologues of the *Drosophila toll* gene product (69). TLRs are molecules on the cell surface and/or in intracellular (e.g., endocytic) compartments (i.e., TLR3, TLR7/8, TLR9), to which microbial or viral products bind; this results in the activation of various cell signaling pathways, including MAPK as well as other kinases (70). The majority of TLRs (TLR3 is the exception) use the MyD88 adaptor molecule for signaling down the TLR activation cascade (68, 70). These responses can have important effects on Ag presentation by classical MHC molecules (17), as well as by CD1d (71-76). Globally, the binding of a ligand to its specific TLR can regulate immunodominance; this

has been shown in the context of the *Toxoplasma gondii*-encoded protein, profilin, via MHC class II molecules (77). In contrast, TLR7/8 agonists can impair the differentiation of monocytes into DCs (78). Thus, activation via TLRs can promote (or inhibit) APC function.

In terms of MHC class I-mediated Ag presentation, TLR engagement can enhance (or have a minimal effect on) overall surface MHC class I expression (79, 80). However, ligands for TLR2 and other TLRs can impair conventional Ag presentation by MHC class I (80, 81). TLR signals can also have very important regulatory (albeit not direct) roles in triggering the delivery of MHC class I molecules to phagosomes for cross-presentation. These signals result in the I $\kappa$ B-kinase 2-mediated phosphorylation of phagosome-associated SNAP23, which stabilizes SNARE complexes, ultimately facilitating cross-presentation (11). Similar to endogenous Ag presentation by MHC class I, cross-presentation can also be reduced upon TLR engagement (7, 15, 18). Alternatively, cross-presentation can be enhanced via the binding of TLR2- (13, 82), TLR4- (18), TLR7- (8) or TLR9-specific agonists (83). Differences in terms of the activation vs. inhibition of cross-presentation are likely due to the timing of APC exposure to the TLR ligands, as compared to the cross-presented Ags.

Ag presentation by MHC class II molecules is also differentially affected by the engagement of distinct TLRs. Interestingly, in some cases, it seems to be a means of immune evasion by a pathogen. For example, 19 and 24 kDa lipoproteins from *Mycobacterium tuberculosis* can inhibit both MHC class II expression and Ag processing via TLR2 signaling (25, 84, 85). In contrast, a variety of TLR ligands (including those for TLR2), can upregulate MHC class II molecules on microglia (29). Ligands for TLR1/2, 4, 7 and 9 were shown to enhance the ability of APCs to present Ag-85B of Bacillus Calmette-Guerin (BCG) to CD4+ T cells specific for that Ag, via the upregulation of MHC class II molecules (86). Moreover, the stimulation of TLR signaling and delivery of a TLR-specific ligand (in this case, the TLR4 ligand, LPS) into phagosomes, can contribute to the generation of peptide/MHC class II complexes; this is as a means to segregate self vs. non-self peptides in a phagosome-autonomous manner (22). This delivery of TLR4 ligands is due to adaptor protein-3 (AP-3)-dependent transport of TLR4 from endosomes to phagosomes (87). Sometimes, MHC class II-mediated responses--in this case, flagellin-specific CD4+ T cell responses--can be enhanced in a TLR5-dependent (but nonconventional TLR signaling pathway) manner (26). In that report, DCs from MyD88-deficient mice could increase flagellin-specific CD4+ T cells in a TLR5-dependent manner that was comparable to DCs from wildtype mice (26). This response is regulated by CD103-CD11b+ DCs (88). Type I interferons can work with TLR ligand-mediated signals in order to generate type B peptide/MHC class II complexes (pMHC); type B pMHC are complexes formed in early endosomes from exogenous peptides (89). In fact, type I interferons are very important for such peptide generation, as DCs deficient in the receptor for type I interferons are impaired in their ability to generate type B pMHC (89). However, in the context of DC maturation, whereas TLR ligands can inhibit MHC class II synthesis and presence in intracellular compartments, type I interferons can prevent this from occurring (30).

The activation of TLR signaling pathways by TLR-specific ligands has also been investigated in terms of its effect on the CD1d/NKT cell axis. Mimicking APC stimulation of NKT cells (i.e., a panel of murine NKT cell hybridomas) using anti-CD3 and IFN- $\alpha$



upregulates TLRs on the cell surface (75). Moreover, the exposure of NKT cells to a variety of TLR ligands enhances NKT cell production of IFN- $\gamma$ , IL-4 and TNF- $\alpha$  (75). However, another report indicated that although human NKT cells express all TLRs (except TLR8), they are not activated when directly exposed to TLR ligands; yet, they are stimulated when TLR ligands are added to total PBMCs (73). The differences could simply be due to the fact that these studies analyzed mouse NKT cell hybridomas (75), as opposed to normal human NKT cells from PBMCs (73). Culture of murine mononuclear cells (MNCs) with the CD1d-binding glycolipid,  $\alpha$ -GalCer, and poly I:C (a TLR3 ligand), resulted in NKT cell activation in a model of airway inflammation (76). Certainly, the effects observed in that report could be NKT cell- and/or APC-specific. Murine bone marrow-derived DCs (BMDCs) exposed to LPS or infected with *Salmonella typhimurium* were able to stimulate NKT cells at a high level. This suggests that APC TLR4 signaling enhanced Ag presentation by CD1d molecules (71). Additionally, TLR4 has been shown to work with Nod1 and Nod2, two members of the Nod-like receptor family that are cytosolic pattern recognition receptors. Here, LPS treatment of BMDCs resulted in IFN- $\gamma$  production by NKT cells (74). An *in vivo* infection with *S. typhimurium* (which contains LPS) can activate iNKT cells (71, 72), but does so without the need for a CD1d-presented lipid Ag (72).

### JAK/STAT pathway effects on MHC and CD1d

The JAK/STAT signaling pathway is activated by most cytokines involved in the development and regulation of the host's immune response (90). There are four receptor-associated JAKs that, upon phosphorylation of the receptor they are bound to, recruit one of seven STATs to the receptor to be phosphorylated by that JAK. This process then results in the dimerization of the phosphorylated STATs which are translocated into the nucleus, where they regulate the expression of a variety of genes (91).

JAK/STAT signaling upon activation by IFN- $\gamma$  is critical for MHC gene expression and, ultimately, expression of MHC class I and class II molecules on the cell surface (90, 91). Of importance, it has been shown that phosphorylated STAT1 facilitates human MHC locus chromatin remodeling, as a first step for the subsequent expression of HLA genes (92). Impairing the ability of IFN- $\gamma$  to stimulate JAK/STAT signaling and thereby preventing MHC gene expression, is one mechanism by which viruses can evade recognition by the host's immune response (16). For example, MHC class I and/or class II molecules can be targeted by herpesviruses (19, 28, 93) or influenza virus (31). In each of these cases, it is likely that a virus-encoded protein(s) prevented IFN- $\gamma$ -induced activation of the JAK/STAT pathway. Similarly, immune evasion by solid tumors can be due to an impairment of JAK/STAT signaling that prevents the upregulation of MHC class I molecules (12, 14) or TAP1 expression (9).

In contrast to the immune evasion examples presented above, activation of JAK/STAT signaling can have beneficial effects. For example, IL-10, which activates a JAK1/STAT3 complex, inhibits DC maturation by mesenchymal stem cells (94). A case where this could be important is in the prevention of NKT cell-mediated colitis. Here, crosslinking CD1d on colonic epithelial cells results in STAT3 activation; the transcription of the *il-10* gene (by STAT3) and consequent IL-10 production controls inflammation in those cells (95).

Recently, we showed that STAT3 is essential for CD1d-mediated Ag presentation, due to its ability to regulate the transcription of UDP glucose ceramide glycosyltransferase, an enzyme involved in the first step of glycosphingolipid biosynthesis—from which the natural ligands of CD1d are derived (96). The critical nature of STAT3 in the CD1d/NKT cell axis is evident in patients with loss-of-function mutations in STAT3. Those patients have a significantly reduced number of NKT cells (97).

### **Rho kinase and the actin cytoskeleton in CD1d-mediated Ag presentation**

Rho GTPases are well known for mediating intracellular protein traffic [reviewed in (98)]. This is due to their control over the generation of F-actin. Thus, Rho GTPases activate the Rho kinase (ROCK) which then phosphorylates the LIM kinase (LIMK), which then activates cofilin. Normally, cofilin, in its nonphosphorylated form, prevents the polymerization of actin. The phosphorylation of cofilin by LIMK permits F-actin formation (99, 100). We found that F-actin actually impairs Ag presentation by CD1d (101). When we disrupted the actin cytoskeleton with cytochalasin D, Ag presentation was enhanced. Thus, ROCK is a negative regulator of CD1d-mediated Ag presentation. Interestingly, we found that ROCK actually promoted Ag presentation by MHC class II molecules (101). This was another example in which we have found specific cell signaling pathways that differentially regulate Ag presentation by MHC class II vs. CD1d (21, 96, 101).

Knowing that ROCK impairs Ag presentation by CD1d via the polymerization of actin is only part of the mechanism by which this occurs. How does actin actually do it? Recently, it has been reported that actin segregates CD1d nanoclusters on the cell surface via direct interaction between actin and the CD1d cytoplasmic tail (102). This interaction keeps them at a certain density on the surface. Allowing the formation of larger nanoclusters (by blocking the ability of CD1d's cytoplasmic tail to bind to actin) results in enhanced NKT cell activation—exactly the same observation we made when the actin cytoskeleton was disrupted in our system by cytochalasin D (101).

### **Cell signaling pathways and disease: can these be used as targets in terms of immunotherapy?**

For the most part, cell signaling pathways appear to be important in inflammatory diseases (including cancer), which have a clear--or likely--immune component, where Ag processing and presentation would come into play. Of the MAPK, upstream ERK pathway components (i.e., Ras-Raf-ERK) are more involved. Either Ras or Raf contribute to malignant transformation and are thereby targeted with Ras- or Raf-specific inhibitors (103-106). Moreover, blocking ERK in esophageal and gastric cancers, or in melanoma (in the context of immunotherapy), results in an increase in MHC class I molecules (107-109).

For the p38 MAPK, inflammation has been shown to increase tumor-induced (and immunosuppressive) myeloid-derived suppressor cells (MDSC); the activation of p38 is believed to be important for MDSC survival (110). For the treatment of rheumatoid arthritis, p38 inhibitors have been considered (111). Moreover, p38 is also believed to be a culprit in the development of acquired immune deficiency syndrome and HIV-associated



neurocognitive disorders in HIV patients, which could have an Ag presentation component (112).

An important aspect of p38 signaling needs to be taken into account when considering using inhibitors against that MAPK: there is reciprocal cross-talk between p38 and STAT3 [reviewed in (113)]. In the context of the CD1d/NKT cell axis, this could be critical in the disease that one is attempting to mitigate, as p38 is a negative (whereas STAT3 is a positive) regulator of lipid Ag presentation by CD1d (41-43, 96, 97, 101).

The JAK/STAT pathway (in particular, STAT3), is also important in cancer and inflammation. In a recent study of patients with non-refractory Hodgkin's lymphoma being treated using a PD-1 blockade immunotherapy paradigm, phosphorylated STAT3 was detected in the nucleus of Reed-Sternberg cells (the presence of which is necessary for the diagnosis of Hodgkin's lymphoma) (114). In Behcet's disease, an inflammatory disorder resulting in vasculitis, STAT3 is activated (115). In contrast, there appears to be attenuated IFN- $\alpha$ -induced STAT3 signaling in DCs from patients with Crohn's disease and IL-10 induces enhanced STAT3 activation, which could impact the DC's ability to present Ag (116). Relating Crohn's disease effects to the various cell signaling pathways in this brief review, there appears to be an association with an ICOSL loss-of-function mutation resulting in reduced cell signaling in these patients (117); this likely impacts immune homeostasis.

Lastly, signaling via TLRs have been predominantly associated with infectious diseases (118-124); however, a variety of single-nucleotide polymorphisms in human TLRs have not only been associated with infectious and inflammatory (including autoimmune) diseases, but also with cancer (121, 123-126). As such, TLRs have been looked at as potential targets for immune-based therapy against infectious diseases (118, 119), as well as sepsis-associated pathology (118). Moreover, another approach that is being considered is the specific targeting of TLR-associated adaptors that are negative regulators of TLR signaling (127). This is reminiscent of the CTLA-4 and inhibitory receptor programmed cell death-1 (PD-1) targeting of antitumor T cells that has recently shown promise in clinical trials with cancer patients (128, 129). This approach effectively removes inhibitory signals coming from the APCs to the effector T cells.

## Conclusions

Although cell signaling pathways have been studied for quite a number of years, very little has been focused on Ag processing and presentation, and how they affect APCs and/or the T cells that recognize them. Nonetheless, Figure 2 summarizes what I have described in this Brief Review in terms of how these cell signaling pathways affect MHC class I, MHC class II and/or CD1d. To help the readers, I have also included a table (Table 1), indicating the reports cited here, that have studied these specific cell signaling pathways and Ag presentation. As is clear from the work done so far, the cell signaling pathways described above have at least some impact on various components of a host's immune response; these could potentially be exploited for adding new weapons to the arsenal against infectious and autoimmune diseases, as well as cancer. We have just begun to scratch the surface.

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## Abbreviations used in this article

<b><math>\alpha</math>-GalCer</b>	$\alpha$ -galactosylceramide
<b>BCG</b>	Bacillus Calmette-Guerin
<b>BMDC</b>	bone marrow-derived dendritic cells
<b>LIMK</b>	Lim kinase
<b>M<math>\Phi</math></b>	macrophage
<b>MAIT cells</b>	mucosal-associated invariant T cells
<b>MDSC</b>	myeloid-derived suppressor cells
<b>MNCs</b>	mononuclear cells
<b>NKT</b>	natural killer T
<b>PD-1</b>	programmed cell death-1
<b>PKC</b>	protein kinase C

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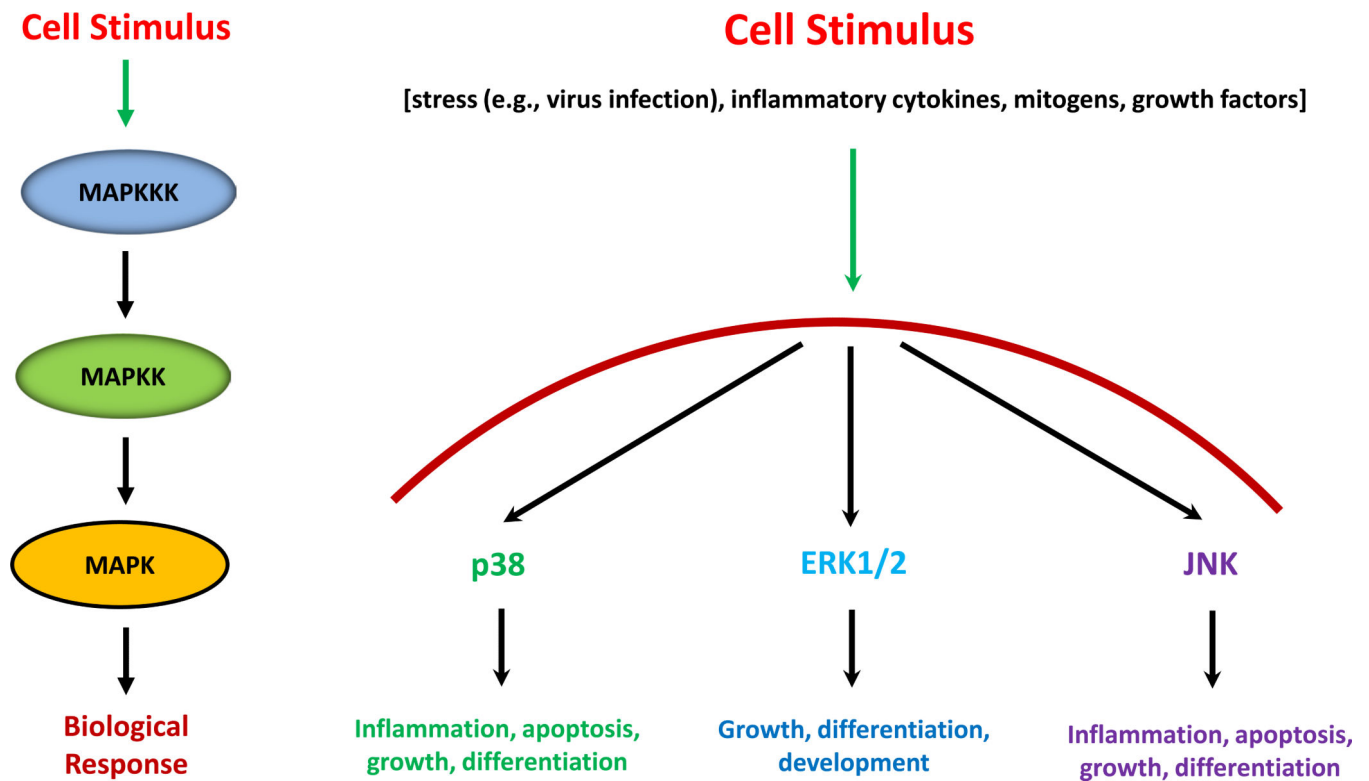
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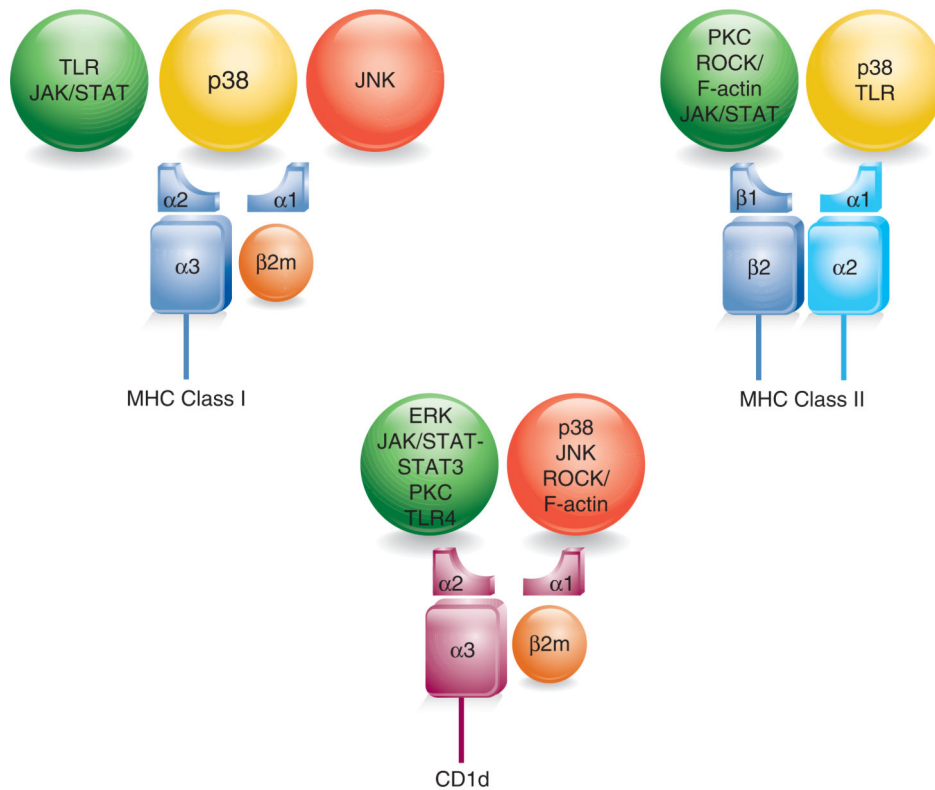
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**FIGURE 1.**

Activation of the MAPK family of cell signaling molecules. There are three main families of MAPK: p38, ERK and JNK. Each has important roles in the response of a cell to a stimulus. On the left indicates the normal process of events: A cell stimulus results in the activation of a MAP3K (MAPKKK), which in turn phosphorylates a MAP2K (MAPKK). The MAPKK activates the MAPK via phosphorylation which leads to a biological response. The specific biological responses mediated by the individual MAPKs are indicated on the right.

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Width: 29p3  
Height: 24p5

**FIGURE 2.**

Summary of the known effects of cell signaling pathways on Ag presentation by MHC class I, MHC class II and CD1d molecules. The effects are indicated as a traffic light analogy: green is a positive (or upregulating) effect, red is a negative (or downregulating) effect; those pathways in the yellow light suggest some ambiguity for the effects of those pathways (e.g., some are positive; some are negative—it depends on the context).

**Table 1**

Reports addressing Ag presentation via cell signaling pathways \*

Cell Signaling Pathway	Effects on Ag presentation by:		
	MHC I	MHC II	CD1d
p38	7; 47-49; 51	52-54	21; 42,43
ERK	47, 48	47, 48	43
JNK	58, 59		Liu, et al. **
PKC		23, 27, 65-67	67
ROCK		101	101
TLR	7, 8, 13, 15, 17, 18, 51, 79-83	17, 22, 25, 26, 30, 77, 84-86, 88, 89	71-76
JAK/STAT	9, 12, 14, 16, 19, 28, 31, 90-93	16, 19, 28, 31, 90-93	96, 97

\* The table indicates the reference numbers cited in this review that describe a role for the various cell signaling pathways in Ag presentation

\*\* Liu, et al. (manuscript in preparation)

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