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## New Advances in Invasive Aspergillosis Immunobiology Leading the Way Towards Personalized Therapeutic Approaches

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### Abstract

Invasive aspergillosis (IA) remains a devastating disease in immune compromised patients despite significant advances in our understanding of fungal virulence and host defense mechanisms. In this review, we summarize important research advances in the fight against IA with particular focus on early events in the interactions between *Aspergillus fumigatus* and the host that occur in the respiratory tract. Advances in understanding mechanisms of immune effector cell recruitment, antifungal effector mechanisms, and how the dynamic host-fungal interaction alters the local microenvironment to effect outcomes are highlighted. These advances illustrate exciting new therapeutic opportunities, but also emphasize the importance of understanding each unique fungus-host interaction for improving patient outcomes.

### Introduction

Humans breathe 10–15 m<sup>3</sup> of air daily, a volume that typically contains several hundred to several thousand airborne *Aspergillus* conidia (VandenBergh et al, 1999). For the most part, this lifelong encounter results in asymptomatic fungal clearance, facilitated in part by mucociliary clearance mechanisms. However, owing to their small size (i.e. 2–3 μm in diameter), inhaled conidia can reach terminal airways where they activate the respiratory innate immune system via soluble and membrane-bound receptors. Critical immune effector cells, including neutrophils, inflammatory monocytes, and macrophages, must be recruited and activated to thwart fungal invasion.

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Inhalation of *Aspergillus* conidia results in its deposition into a new microenvironment. In immune competent murine models of invasive aspergillosis (IA), germination of *Aspergillus* conidia in the airways is rarely observed, although there appears to be some strain dependency that remains to be fully appreciated (Rizzetto et al, 2013). However, the large inocula typically used to establish a bronchopneumonia in these murine models results in significant inflammation in the lower airways of the lung. While large inocula of fungal conidia are plausible under specific exposure conditions (e.g., during mulching/gardening), it is unclear whether inocula capable of inducing robust airway inflammation in mice are responsible for disease development in susceptible patient populations. Yet, even a low number of inhaled fungal conidia likely induce localized microenvironment changes that can impact subsequent host immune responses in immune compromised patients. How this microenvironment impacts IA outcomes has not been defined and many open questions remain. For example, questions such as how the microenvironment alters fungal pathogen associated molecular pattern exposure (PAMP) and virulence and how the microenvironment alters immune signaling and antifungal activity of phagocytes such as macrophages, monocytes, and neutrophils remain under appreciated.

Neutrophils are one of the key inflammatory cells that mediate resistance against infection with *A. fumigatus*. This is highlighted by the observation that patients who become neutropenic after chemotherapy are at a higher risk for developing IA (Gerson et al, 1984). Animal models clearly demonstrate that timely neutrophil recruitment to the respiratory tract following *A. fumigatus* exposure is critical for resistance to invasive disease and control of fungal growth (Bonnett et al, 2006; Mehrad et al, 1999a). Moreover, appropriate neutrophil activation and antifungal activity are necessary for resistance to invasive *A. fumigatus* infection as both patients with chronic granulomatous disease (CGD) and mice that lack NADPH oxidase subunits are highly susceptible to infection (Morgenstern et al, 1997; Pollock et al, 1995). However, recent epidemiological studies suggest that the incidence of IA is also increasing in non-neutropenic patients (Steinbach et al, 2012). Interestingly, IA in chronic granulomatous disease or following corticosteroid immunosuppression is associated with excessive accumulation of functionally impaired neutrophils that contribute to tissue damage (Balloy et al, 2005; de Luca et al, 2014). Therefore, precise regulation and calibration of pulmonary inflammation and leukocyte recruitment may ameliorate disease in these contexts. Surprisingly, our understanding of neutrophil recruitment and activation in response to *A. fumigatus* challenge has been slow to emerge. The goal of this mini-review is to highlight new advances in the last 3 years regarding our understanding of how the immune system prevents host damage from *A. fumigatus* challenge. We focus on recognition of the fungus as it enters the airway and mechanisms of immune cell recruitment, activation, and antifungal effector activity. Fungal components that effect these interactions with the host are discussed, and we discuss emerging awareness of how changes in the tissue microenvironment, such as oxygen and nutrient levels, can alter the outcome of the host-pathogen interaction.

A last point of emphasis is that emerging studies strongly suggest, perhaps not surprisingly, that the immune response to a given strain of *A. fumigatus* is not stereotypical. Thus, understanding this strain-specific variation represents a major gap in knowledge that is particularly relevant to design immune-enhancing or immune-modulating strategies (a goal

of personalized medicine) for patients afflicted by this menacing mold. Consequently, a dynamic infection microenvironment, strain heterogeneity, patient genetic variability, diverse underlying disease conditions, and a limited antifungal arsenal all contribute to the complex and significant challenge inherent in improving IA outcomes.

## ***Aspergillus* recognition and Innate Immune Activation**

### **Pentraxin-3**

Pentraxin-3 (Ptx3), a soluble collectin and acute phase reactant, binds to conidia and this interaction can be inhibited by soluble galactomannan *in vitro* (Garlanda et al, 2002). Pentraxin-3 regulates complement interactions with fungal conidia and promotes neutrophil conidial uptake by a complement-, CD18/CD11b (a.k.a complement receptor 3/Mac-1)-, and Fc $\gamma$ RII-dependent mechanisms (Moalli et al, 2010). Pentraxin-3 binds the Toll-like receptor (TLR) 4 accessory protein myeloid differentiation protein 2 (MD-2) can modulate lung inflammation via the TLR4/MD-2/CD14 signal transducer TIR domain-containing adapter inducing interferon- $\beta$  (TRIF) to promote fungal clearance (Bozza et al, 2014). Consistent with this model, Ptx3<sup>-/-</sup> and MD-2<sup>-/-</sup> mice are susceptible to conidial challenge compared to control mice (Bozza et al, 2014; Garlanda et al, 2002). In humans, receipt of a donor graft with a specific pentraxin-3 gene variant increases the likelihood of developing IA during hematopoietic cell transplantation (Cunha et al, 2014).

### **Fungal interactions with lung-resident leukocytes through CLRs**

Alveolar macrophages can rapidly phagocytose conidia within airways and this engulfment process can be blocked *in vitro* by antibodies directed against dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin (DC-SIGN/CD209) (Serrano-Gomez et al, 2004). Resting conidia express FleA, a protein that binds to fucosylated molecules found in mucinous secretions (Kerr et al, 2016). Conidial phagocytosis by macrophages can be disrupted by soluble fucose moieties and *fleA* conidia are not engulfed at a rate comparable to wild-type conidia. These data support the notion that FleA mediates conidial interactions with phagocytic cells, though the macrophage receptor(s) responsible for these interactions have not been functionally characterized. Interestingly, the *fleA* strain is hypervirulent compared to its parental strain, which correlates with significantly greater germination and growth in the airways. Collectively, these data suggest that host recognition of *A. fumigatus* FleA contributes to fungal clearance and control *in vivo* (Kerr et al, 2016).

Although resident alveolar macrophages and other phagocytes rapidly phagocytose resting conidia, engulfed conidia do not trigger robust inflammatory responses prior to conidial swelling, the first step in germination. The conidial surface consists of a layer of hydrophobins that are encoded by the *rodA* and *rodB* genes in *A. fumigatus* and that conceal an underlying layer of fungal  $\beta$ -(1,3) glucan (Aimanianda et al, 2009). Conidial swelling coincides with the obligate exposure of particulate  $\beta$ -(1,3) glucan (Hohl et al, 2005) and other cell wall polysaccharides. These polysaccharides are actively recognized by the host to initiate the antifungal immune response.

The C-type lectin receptor Dectin-1 (Clec7a) binds to  $\beta$ -glucans on germinating conidia (Gersuk et al, 2006; Hohl et al, 2005; Steele et al, 2005). Dectin-1 binding to  $\beta$ -glucan extrudes the regulatory phosphatases CD45 and CD148 from the vicinity of receptor-particulate  $\beta$ -glucan complexes (Goodridge et al, 2011) (Figure 1). These events induce Src-dependent phosphorylation of the ITAM-like motif found in the intracellular domain of Dectin-1 and facilitate the recruitment of the SHP-2 phosphatase (Deng et al, 2015). Spleen tyrosine kinase (Syk) docks to this scaffold and transduces signals via protein kinase C (PKC)- $\delta$  (Strasser et al, 2012) to CARD9, which complexes with B cell CLL/lymphoma 10 (BCL10) and Mucosaassociated lymphoid tissue lymphoma translocation protein 1 (MALT1) (Gross et al, 2006) in order to activate NF- $\kappa$ B-dependent cytokine production (i.e., IL-6, IL-12, IL-23, TNF, CXCL1/KC, and CXCL2/MIP-2) (Brown, 2011; Rogers et al, 2005). In macrophages and dendritic cells (DCs), the CARD9-Bcl10-Malt1 complex directs *Il1b* transcription and caspase-1- and -8-dependent IL-1 $\beta$  release (Gringhuis et al, 2012; Gross et al, 2009) (Figure 1). Dectin-1/Syk/CARD9-dependent cytokines are critical for T helper cell differentiation into IL-17A producing cells, which are critical for antifungal immunity (Deng et al, 2015; LeibundGut-Landmann et al, 2007; Rivera et al, 2011).

In humans, mendelian defects in the *card9* gene promote the spontaneous development of IA, notably at extrapulmonary sites (M. Lionakis and colleagues, personal communication; manuscript under review at the *Journal of Allergy and Clinical Immunology*). Similarly, immune competent CARD9<sup>-/-</sup> mice develop lethal invasive pulmonary aspergillosis after intratracheal challenge with resting *A. fumigatus* conidia (Jhingran et al, 2012). Consistent with a role in CARD9 activation, PKC- $\delta$ <sup>-/-</sup> mice display defective lung fungal clearance (Li et al, 2016). In contrast to the *card9* gene, mendelian defects in the *clec7a* gene have not been associated with the spontaneous development of IA in humans. However, a Dectin-1/Clec7a (Y238X) polymorphism is associated with increased susceptibility to IA during allogeneic hematopoietic cell transplantation (Cunha et al, 2010), in the context of immune damage associated with conditioning chemotherapy, hematopoietic cell engraftment, or graft versus host disease. In murine models, Dectin-1<sup>-/-</sup> mice show variable susceptibility to respiratory *A. fumigatus* challenge (Jhingran et al, 2012; Werner et al, 2009). This finding may reflect differences in mouse strain backgrounds or in fungal strains that were tested in these studies. Additional CARD9-coupled receptors may provide molecular redundancy with respect to *A. fumigatus* recognition and may promote host defense as described below.

Dectin-2 (*Clec4n*) forms complexes with Dectin-3 (*Clec4d*) to bind *Candida*  $\alpha$ -mannans (Zhu et al, 2013) or with Mincle (*Clec4e*) to bind *Malassezia* glycolipids (Ishikawa et al, 2013; Yamasaki et al, 2009). Both complexes signal via the ITAM-coupled adaptor FcR $\gamma$  (Sato et al, 2006) and can activate Syk- and CARD9-dependent signal transduction (Figure 1). *A. fumigatus* germination exposes Dectin-2 ligands on germings and hyphae, activating cytokine responses in cultured murine bone marrow DCs (Jhingran et al, 2012) and in human plasmacytoid DCs in vitro (Loures et al, 2015). In a murine *A. fumigatus* corneal challenge model with mutant conidia that lack the hydrophobin layer, both Dectin-1- and Dectin-2-dependent signals are required for optimal neutrophil recruitment to the corneal stroma and for fungal killing (Carrion Sde et al, 2013). Notably, fungal killing of wild-type conidia in this model did not depend on Dectin-1 or Dectin-2 signaling function (Carrion

Sde et al, 2013). A recent study illustrated that Dectin-2 can regulate autocrine IL-17A-IL-17RC signaling that increases neutrophil fungal killing capacity upon secondary ocular challenge with wild-type *A. fumigatus* conidia (Taylor et al, 2014). The relative contribution of dectin-1 and FcR $\gamma$ -dependent C-type lectin receptors to CARD9-dependent host defense in the lung remains to be elucidated. Since CARD9 integrates signals from multiple pattern recognition receptors, such as RIG-I/MAVS (Poeck et al, 2010), Toll-like receptors (TLR) (Hara et al, 2007), or Nod2 (Hsu et al, 2007), it is possible that CLR-independent mechanisms may contribute to CARD9 activation following *A. fumigatus* challenge as well.

### Fungal interactions with lung-resident leukocytes through TLR9

Recent work has found that transplant patients on calcineurin inhibitors are at elevated risk of invasive fungal infections, including *Aspergillus* spp. (Herbst et al, 2013). However, until recently, the mechanism was not well understood. Elegant work by Armstrong-James and colleagues demonstrated that calcineurin signaling is central in regulating early neutrophil airway influx to prevent IA (Herbst et al, 2015). Moreover, mice that are treated with cyclosporine A or that lack the calcineurin B subunit (CnB) in the myeloid compartment are highly susceptible to systemic *Candida albicans* challenge (Greenblatt et al, 2010). Tissue-resident macrophages phagocytose *A. fumigatus* conidia and activate nuclear factor of activated T cells (NFAT) in response to non-conventional TLR9 signaling, which is transduced by Bruton's tyrosine kinase (Btk) rather than by MyD88 signaling. Btk activation drives phospholipase C (PLC)- $\gamma$ 2 activation, resulting in calcineurin and downstream NFAT activation (Figure 1). Calcineurin inhibition by FK506 diminishes macrophage and lung TNF expression, with smaller decreases in CXCL1, CXCL2, and CCL3 (MIP-1 $\alpha$ ) (Herbst et al, 2015). Earlier work has shown that TNF signaling is crucial in host defense against *A. fumigatus* through its regulation of neutrophil responses (Mehrad et al, 1999b; Schelenz et al, 1999). Thus, calcineurin activation downstream of TLR9 engagement contributes to host resistance to IA, a finding that is important in the management of solid organ and hematopoietic cell transplant patients maintained on calcineurin inhibitors.

### Biphasic neutrophil recruitment is necessary for host resistance to against IA

It is well established in both human patient populations and animal models that neutrophils are critical inflammatory cells necessary for host resistance against IA (Gerson, 1984, Mehrad, 1999, Bonnett, 2006). Early work demonstrated that anti-CXCR2 treated (Mehrad et al, 1999a) or *Cxcr2*<sup>-/-</sup> (Bonnett et al, 2006) mice are highly susceptible to IA. In mice, CXCR2 mediates chemotactic responses to CXCL1, CXCL2, and CXCL5, but the relative contribution of each of these ligands to CXCR2-dependent neutrophil trafficking has not been defined. Until recently, the precise inflammatory events regulating CXCR2-dependent recruitment of neutrophils to the lungs following *A. fumigatus* challenge remained ill defined. IL1RI/MyD88- and Card9-dependent signaling non-redundantly mediates optimal CXCR2-dependent recruitment of neutrophils to the lungs throughout the course of *A. fumigatus* infection in a murine model of *Aspergillus* bronchopneumonia (Jhingran et al, 2015) (Figure 2). Signaling by IL-1 cytokines is also critical in humans, because SNPs in the IL-1 gene cluster are associated with increased susceptibility to IPA (Wojtowicz et al, 2015)

Sainz et al, 2008). Additionally, Card9 defects in humans can result in spontaneous development of IA (M. Lionakis and colleagues, personal communication; manuscript under review at the *Journal of Allergy and Clinical Immunology*). IL1RI/MyD88 signaling is critical for neutrophil recruitment during *A. fumigatus*-induced keratitis (Leal et al, 2010) and bronchopneumonia (Caffrey et al, 2015; Jhingran et al, 2015; Shepardson et al, 2014). Following challenge with *A. fumigatus* the early expression of CXCR2 ligands, specifically CXCL1 and to a lesser extent CXCL5, was highly dependent on IL-1RI/MyD88 signaling in radioresistant, CC10-expressing lung epithelial cells (Caffrey et al, 2015; Jhingran et al, 2015). Exposure to *A. fumigatus* induces high levels of both IL-1 $\alpha$  and IL-1 $\beta$  protein early in the infection (Caffrey et al, 2015). Expression of the IL-1 $\alpha$  and IL-1 $\beta$  cytokines is partially dependent on HIF-1 $\alpha$  signaling in myeloid cells (Shepardson et al, 2014), likely alveolar macrophages (Bonnett et al, 2006) and CCR2<sup>+</sup> monocytes (Caffrey et al, 2015; Espinosa et al, 2014). HIF-1 $\alpha$  is stabilized after recognition of  $\beta$ -glucan by Dectin-1 (Cheng et al, 2014), which can regulate IL-1 expression (Leal et al, 2010; Steele et al, 2005). However, which IL-1 cytokine is responsible for signaling through IL-1RI to drive CXCR2 ligands is currently debated (Caffrey et al, 2015; Karki et al, 2015; Moretti et al, 2014).

Subsequently, Card9 signaling drives a second phase of CXCL1 and CXCL2 expression that occurs in a MyD88-independent manner, which functions to mediate a second wave of neutrophil recruitment to infected airways (Jhingran et al, 2015; Jhingran et al, 2012) (Figure 2). This Card9-dependent response depends on Card9 expression in radiosensitive cells, with the majority of CXCL2-expressing cells being neutrophils (Jhingran et al, 2015). Interestingly, Card9 signaling at this point appears to be independent of Dectin-1 and Dectin-2 (Jhingran et al, 2015). Beyond the Card9-coupled CLRs discussed above, Card9 integrates signals from multiple pattern recognition receptors including RIG-I/Mda5/MAVS (Poeck et al, 2010), Toll-like receptors (TLR) (Hara et al, 2007), or Nod2 (Hsu et al, 2007). Therefore, it is possible that CLR-independent mechanisms may contribute to Card9 activation following *A. fumigatus* challenge. More work elucidating this late interaction of *A. fumigatus* with the host respiratory tract is needed and may have particular relevance to chronic forms of the disease with significant hyphal growth and tissue damage. In this context, strain heterogeneity in response to these infection environments may significantly skew or alter the host inflammatory response and consequently drive changes to the therapeutic strategy needed to protect the host from damage.

### Regulation of CXCR2 expression on neutrophils

Interestingly, patients with autosomal dominant Hyper-IgE syndrome (AD-HIES/Job's syndrome), a rare primary immunodeficiency due to mutations in STAT3, develop fungal pneumonias, including aspergillosis (Vinh et al, 2010). The molecular mechanism behind the increase in *Aspergillus* spp. infection in AD-HIES patients remains undefined, though AD-HIES neutrophils inhibit *A. fumigatus* hyphal growth and metabolism similar to control neutrophils (Vinh et al, 2010). The cytokine granulocyte colony-stimulating factor (G-CSF) drives STAT3 activation in immature bone marrow neutrophils, which increases CXCR2 expression and neutrophil mobilization (Nguyen-Jackson et al, 2010). Interestingly, leukocytes from AD-HIES patients express lower levels of the ELR<sup>+</sup> chemokine receptors, CXCR1 and CXCR2 (Mintz et al, 2010).



Recently, it has been observed that the phenotype and antifungal function of neutrophil found after sublethal *A. fumigatus* challenge are altered. Neutrophils in the airways express elevated levels of Dectin-1/Clec7a and CXCR2 beginning 3 days after sublethal *A. fumigatus* challenge (Savers et al, 2016). Elevated levels of neutrophil Dectin-1/Clec7a and CXCR2 expression could also be seen in the peripheral blood and bone marrow at 10 days post-challenge and were associated with enhanced secondary neutrophil responses and subsequent protection against lethal *A. fumigatus* challenge (Savers et al, 2016). These data suggest that the proinflammatory environment induced by *A. fumigatus* likely has long-term effects that may alter neutrophil differentiation or mobilization in the bone marrow, a process that has been shown to underlie G-CSF signaling (Nguyen-Jackson et al, 2010). However, the role of the G-CSF in host defense against aspergillosis has not been explored. Our data demonstrate that G-CSF expression is highly dependent on IL-1RI/MyD88 signaling following *A. fumigatus* challenge (Caffrey et al, 2015). Therapeutically, G-CSF administration to neutropenic mice has been shown to enhance peripheral blood leukocytes and host resistance to fungal infections (Polak-Wyss, 1991; Uchida et al, 1992). Thus, much still remains to be uncovered about the regulation of this pathway, including whether G-CSF/STAT3 signaling can regulate neutrophil mobilization and maturation for the prevention of IA.

## Regulation of neutrophil antifungal activity

In addition to the timely recruitment of neutrophils to the respiratory tract after *A. fumigatus* exposure, the appropriate activation of antifungal function is necessary for host resistance to IA. CGD patients have a defect in neutrophil NADPH oxidase activity and a 40% lifetime risk of IPA (Holland, 2010). Both *in vitro* and *in vivo* studies have shown that p47<sup>phox(-/-)</sup> neutrophils have decreased antifungal activity that is cell-intrinsic (Jhingran et al, 2012; Morgenstern et al, 1997; Pollock et al, 1995). Similarly, inflammatory monocytes and their descendant cells harness NADPH oxidase-dependent conidial clearance (Espinosa et al, 2014). Additionally, neutrophils from mice exposed to sub-lethal *A. fumigatus* inocula display enhanced reactive oxygen species formation, but the molecular mechanism behind this increase was not explored (Savers et al, 2016). During respiratory fungal challenge, neutrophil and monocyte NADPH oxidase activity is regulated in part by pulmonary granulocyte-macrophage colony-stimulating factor signaling (Kasahara et al, 2016). However, the mechanisms underlying the induction of antifungal effector activities against different *Aspergillus* morphotypes remain to be fully defined.

Neither Dectin-1 nor CARD9 are essential in a cell-intrinsic manner for conidial phagocytosis and killing by lung neutrophils and alveolar macrophages (Jhingran et al, 2015; Jhingran et al, 2012). Similarly, human neutrophils recognize *A. fumigatus* primarily via CD11b/CD18 rather than via Dectin-1 (Gazendam et al, 2016). In the lung, Syk signaling regulates neutrophil conidial uptake (Jhingran et al, 2012). Beyond CLRs, Syk coordinates the biological activities of CD11b/CD18 complexes (Mocsai et al, 2010). The CD11b/CD18 receptor contains a  $\beta$ -glucan binding site (Xia et al, 1999) and can also interact with pentraxin-3-opsonized conidia (Moalli et al, 2010), as described above. Furthermore, CD18 is essential for neutrophil NADPH oxidase activity via a Syk-dependent (and dectin-1-/CARD9-independent) signal transduction when neutrophils are challenged

with killed *A. fumigatus* hyphae (Boyle et al, 2011; Leal et al, 2012). In contrast, other groups have reported that peritoneal-elicited or bone marrow neutrophils utilize Dectin-1 signaling to regulate the respiratory burst following exposure to *A. fumigatus* and *C. albicans* fungal components, or to zymosan, a  $\beta$ -glucan-enriched fungal ghost particle (Li et al, 2011; Werner et al, 2009). Collectively, these findings likely highlight molecular redundancy involved in activating and coupling Syk-dependent fungal recognition to the induction of leukocyte effector functions (Huang et al, 2012; Jhingran et al, 2012).

In addition to its direct effects on fungal viability, NADPH oxidase fosters the recruitment of the autophagy protein LC3 to peripheral blood mononuclear cell phagosomes that contain swollen *A. fumigatus* conidia (Kymizi et al, 2013). In CGD patients, defective LC3 recruitment to *Aspergillus* phagosomes can be ameliorated by pharmacologic blockade of IL-1 receptor signaling with anakinra restoring phagocytic killing of the conidia (de Luca et al, 2014).

In monocytes and macrophages, the formation of a complex that consists of VPS34, a class III phosphatidylinositol-4,5-bisphosphate 3-kinase, Beclin 1, UVRAG, and Rubicon, results in sustained PIP<sub>3</sub> deposition in the early phagosomal membrane and initiates LC3-associated phagocytosis (Martinez et al, 2015). The ensuing recruitment of NOX2 (i.e. the catalytic p91 subunit of NADPH oxidase) into the NADPH oxidase complex and its activation ensures that both PIP<sub>3</sub>- and ROS-dependent signals facilitate the assembly of an ATG5/ATG12/ATG16L complex that in turn promotes ATG7- and ATG3-dependent lipidation and insertion of LC3 (i.e., LC3-II) into the phagosomal membrane (Martinez et al, 2015; Yang et al, 2012a). The newly formed LC3-associated phagosomes can fuse with LAMP1-containing lysosomes and undergo maturation (Figure 1).

Bone marrow-derived macrophages that lack Beclin-1, Rubicon, or ATG7 expression display defective *A. fumigatus* conidial clearance *in vitro*. Similarly, Rubicon<sup>-/-</sup> or conditional myeloid Beclin-1 or ATG7 (i.e., Beclin-1<sup>LysM</sup> and ATG7<sup>LysM</sup>) knockout mice exhibit slowed conidial clearance in the lung (Martinez et al, 2015). In addition to its role in mediating LC3-associated autophagy, Rubicon acts as a feedback inhibitor of CARD9-dependent signaling by disassembling the CARD9/BCL10/Malt1 complex (Yang et al, 2012b).

Conditional deletion of Atg5 in hematopoietic cells increases murine susceptibility to *A. fumigatus* challenge in an immune compromised pulmonary challenge model (Akoumianaki et al, 2016). Conidial melanins partially inhibit LC3-associated phagocytosis by impeding the assembly of a functional NADPH oxidase complex (Akoumianaki et al, 2016). This finding may partially explain the loss of virulence observed in conidial melanin mutants.

Despite the important fungicidal role of phagocyte NADPH oxidase, the majority of CGD patients are not diagnosed with IA during their lifetimes, implying the existence of alternate clearance mechanisms. Consistent with this observation, alveolar macrophages have the capacity to kill conidia effectively in the absence of detectable products of NADPH oxidase *in vivo* (Cornish et al, 2008). Human lactoferrin, an iron chelator, can act in a fungistatic manner and inhibit fungal germination in an NADPH oxidase-independent manner *ex vivo*



(Zarembler et al, 2007). Neutrophil-derived lipocalin-1 can sequester fungal siderophores and limit hyphal extension in the fungal keratitis model (Leal et al, 2013). Interleukin-6 controls the synthesis of host-derived iron chelators, heme- and siderophore-binding proteins that limit *A. fumigatus* iron acquisition in ocular tissues (Leal et al, 2013). Neutrophil calprotectin (a heterodimer of S100A8/S100A9 subunits) is an abundant cytoplasmic protein that contributes to nutritional immunity by sequestering essential ions (i.e.,  $Zn^{++}$ ,  $Mn^{++}$ ) via chelation. Calprotectin limits extracellular hyphal growth in the eye in an ocular challenge model, but is dispensable for conidial killing in the lung following intratracheal conidial challenge (Clark et al, 2016). The role of nutrient sequestration may be less pronounced in the pulmonary immune response to *A. fumigatus* conidia, in part due to relative differences in attenuating conidial versus hyphal growth.

Neutrophil extracellular traps (NETs) can be observed in the murine lung when mice are challenged with pre-swollen conidia (Bruns et al, 2010), but are rarely observed when resting conidia, the infectious propagules, are administered to mice. The release of NETs depends on the size of encountered fungal particle(s) and phagocytosis of individual, small fungal cells (e.g., *C. albicans* blastoconidia or *A. fumigatus* conidia) directs neutrophil elastase and CD63 localization to the phagosome, temporally coincident with NADPH oxidase assembly on the phagosomal membrane (Branzk et al, 2014). The process of fungal cell phagocytosis activates Dectin-1 and this signaling pathway acts as a negative regulator of NETosis (Branzk et al, 2014). In contrast, large fungal particles that do not enter phagosomes trigger the nuclear translocation of neutrophil elastase. This process enables the proteolytic processing of histones that precedes chromatin decondensation required for NETosis. The role of NETosis in anti-*Aspergillus* defense in vivo remains controversial and is supported largely by circumstantial evidence (Bianchi et al, 2011). Ex vivo studies of conidial and hyphal killing by human neutrophils suggest that NETosis does not contribute fungistatic activity against either morphotype (Gazendam et al, 2016), though these experiments do not account for the inflammatory and tissue context found within the respiratory tract.

Finally, it is well established that transendothelial migration of neutrophils can enhance their effector functions (Kolaczowska & Kubes, 2013; Swain et al, 2002). *In vitro*, human neutrophils that cross chemotactic gradients of N-formyl-methionyl-leucyl-phenylalanine (fMLP), leukotriene B4 (LTB<sub>4</sub>), or IL-8 have increased anti-*Aspergillus* activity compared to neutrophils that were exposed to a uniform concentration or not exposed at all (Jones et al, 2015). In murine neutrophils, we observed that bone marrow neutrophils isolated from *Il1r1*-deficient mice displayed decreased activity against *A. fumigatus* in an *in vitro* hyphal damage assay (Caffrey et al, 2015). Moreover, neutrophils that reached the airways of *Myd88*-deficient mice had decreased anti-conidial activity on a per cell basis early after *A. fumigatus* challenge, but this effect was dependent on neutrophil-extrinsic MyD88 expression (Jhingran et al, 2015). Interestingly, the decreased antihyphal activity of bone marrow neutrophils isolated from *Il1r1*-deficient mice is rescued by treatment with recombinant CXCL1 (Caffrey et al, 2015), suggesting exposure to a chemotactic signal enhances the antihyphal activity of murine neutrophils. It has also been demonstrated that airway neutrophils in *Card9*<sup>-/-</sup> mice and *Syk*<sup>-/-</sup> → C57BL/6 chimeric mice exhibit defects in antifungal activity (Jhingran et al, 2012). Thus, there is an integral connection between

neutrophil migration to infected airways and the induction and magnitude of their antifungal effector functions. Recent work strongly suggests that migrating leukocytes are exposed to oxygen and nutrient gradients that can significantly impact their antimicrobial functions. In the ensuing section, we turn to the potential impact of the host microenvironment on effector cell functions.

## Consequences of a Dynamic Infection Microenvironment on Fungal Immunity

While our understanding of *Aspergillus* immune recognition and immune effector cell recruitment has moved forward, the contribution of the tissue inflammatory microenvironment in promoting and regulating these responses represents a new frontier with significant therapeutic potential. Inflammatory responses are strongly associated with decreases in oxygen availability that contribute to decreases in pH and to significant alterations in the availability of micronutrients (e.g., iron) and macronutrients (e.g., glucose) (Eltzschig & Carmeliet, 2011; Naquet et al, 2016; Nizet & Johnson, 2009). Consequently, immune competent hosts have robust regulatory mechanisms to deal with this physiological bacchanal in response to microbes such as *A. fumigatus*. These responses are critical to prevent inhibition of cellular and tissue functions, yet are underexplored in the context of invasive fungal infections. Moreover, how specific immunomodulatory drugs alter the tissue microenvironment and the critical physiological regulatory mechanisms that are essential to prevent host damage remains an important area of investigation.

Evidence for the importance of maintaining a tissue environment conducive to robust and beneficial immune effector cell function is illustrated by recent elegant studies in bacterial pathogenesis, rheumatoid arthritis, inflammatory bowel disease, various cancers, and acute lung injury. For example, Campbell et al. observed that a neutrophil-driven hypoxic microenvironment in the GI tract is essential for resolution of colitis (Campbell et al, 2014). Depletion of neutrophils or their respiratory burst eliminated the protective response. Intriguingly, pharmacological stabilization of the transcription factor HIF-1 $\alpha$  restored protection. These data strongly suggest a critical role for HIF-1 $\alpha$  in regulating tissue microenvironment homeostasis to promote beneficial immune system function that prevent or mitigate host damage.

Recently, the role of HIF-1 $\alpha$  in response to *A. fumigatus* murine airway challenge was reported (Shepardson et al, 2014). It was observed that treatment of mice with a high corticosteroid dose resulted in a significant decrease in HIF-1 $\alpha$  mRNA and nuclear protein levels in lung homogenates compared to untreated animals. Thus, in a clinically relevant murine model that is conducive to massive fungal proliferation and host mortality, lung HIF-1 $\alpha$  levels and activation are reduced. These data suggest a potential role for HIF-1 $\alpha$  in mediating resistance to *A. fumigatus* pulmonary challenge. In support of this hypothesis, immune competent mice lacking HIF-1 $\alpha$  in the myeloid compartment (i.e., HIF-1 $\alpha$ <sup>LysM</sup>) challenged with *A. fumigatus* displayed severe IA characterized by substantial fungal proliferation that ultimately led to mortality (Shepardson et al, 2014).

With regard to the underlying mechanism of HIF1 $\alpha$ -mediated fungal resistance, a seminal study on HIF-1 $\alpha$ 's role in innate immunity revealed a significant decrease in macrophage-mediated killing of group B *Streptococcus* in the absence of HIF-1 $\alpha$  (Cramer et al, 2003). Subsequent studies revealed a role for HIF-1 $\alpha$  in macrophage-mediated killing of group A *Streptococcus* (GAS) and *Pseudomonas aeruginosa*. Similar results with neutrophil bactericidal activity against GAS have been reported. Thus, it was reasonable to hypothesize that HIF-1 $\alpha$  mediated macrophage and/or neutrophil antifungal activity as well. Surprisingly, loss of HIF-1 $\alpha$  did not alter macrophage, monocyte, or neutrophil *A. fumigatus* conidiacidal activities *in vitro*, *ex vivo*, and *in vivo* (Shepardson et al, 2014). Thus, current data suggest that during infection with *A. fumigatus*, myeloid HIF-1 $\alpha$  activity is not critical for early antifungal effector mechanisms.

Further highlighting the importance of the timing of effector cell recruitment, loss of HIF-1 $\alpha$  in myeloid cells resulted in a significant decrease in neutrophil numbers in the airways and lung parenchyma (Shepardson et al, 2014). Rescue of pulmonary neutrophil recruitment to wild-type levels through exogenous provision of CXCL1, a CXCR2 ligand, restored full protection of myeloid HIF-1 $\alpha$ -deficient mice to challenge with *A. fumigatus*. These data suggest a critical role for HIF-1 $\alpha$  in contributing to the induction of cytokines and chemokines needed for optimal neutrophil recruitment and possibly cell survival at the site of infection (Figure 1). Besides CXCL1, other known pro-inflammatory cytokines were also reduced in the airways of myeloid HIF-1 $\alpha$  deficient mice, suggesting a critical role for myeloid HIF-1 $\alpha$  in regulating proinflammatory cytokine production in response to *A. fumigatus* challenge. In further support of these data, Fliesser and colleagues observed marked reductions in the mRNA levels of proinflammatory cytokine encoding genes in HIF-1 $\alpha$  silenced human dendritic cells compared to controls (Fliesser et al, 2015). Moreover, a strong reduction in IL-1 $\alpha$  protein levels were observed in the HIF-1 $\alpha$  silenced human dendritic cells exposed to *A. fumigatus* and hypoxia. Examination of HIF-1 $\alpha$  protein levels in DCs with reduced levels of Dectin-1 revealed an important partial Dectin-1 dependency for maintaining HIF-1 $\alpha$  protein levels in the face of *A. fumigatus* challenge under the examined *in vitro* conditions.

Though clearly much remains to be learned about HIF-1 $\alpha$ -mediated resistance to *A. fumigatus*, the initial reports suggest that augmenting HIF-1 $\alpha$  activity in specific immune compromised patient populations may help improve IA outcomes. Ongoing efforts to therapeutically target HIF-1 $\alpha$  are ongoing in other pathosystems (Bhandari and Nizet 2014). However, the underlying mechanism of the striking fungal-mediated murine mortality in the myeloid HIF-1 $\alpha$ -deficient mice remains unclear. Defining this mechanism is an important research direction to tap the potential of targeting HIF-1 $\alpha$  for antifungal therapeutic benefit. For example, high-dose steroid treatment in the IA murine model did not seem to dramatically alter total HIF-1 $\alpha$  protein in the lungs, rather, HIF-1 $\alpha$  nuclear localization was strongly reduced via an unknown mechanism. Therefore, if this observation holds true in steroid-treated patient populations at risk for IA, inducing nuclear HIF-1 $\alpha$  localization may be an important therapeutic target rather than increasing HIF-1 $\alpha$  levels per se.

With regard to HIF-1 $\alpha$  downstream effectors, recent genome-wide association studies in humans have identified mutations in a HIF-1 $\alpha$  transcriptional target gene, vascular

endothelial growth factor (VEGF), that are associated with increased risk for IA in specific transplant patient populations (Lupianez et al, 2015). VEGF is a critical signaling protein involved in angiogenesis and is strongly induced by hypoxia. *A. fumigatus* produces secondary metabolites such as gliotoxin that can directly inhibit angiogenesis (Ben-Ami et al, 2009). However, promotion of angiogenesis in murine models of IPA can improve outcomes through inhibition of the fungal mediated anti-angiogenic mechanisms and enhanced neutrophil recruitment (Ben-Ami et al, 2013). In further support of a critical role for HIF-1 $\alpha$ -mediated signaling in microvascular remodeling, angiogenesis, and tissue damage homeostasis, von-Hippel-Lindau (VHL) haplodeficient mice were observed to be remarkably resistant to *A. fumigatus* proliferation (Jiang et al, 2013). VHL haplodeficient endothelial cells had increased angiogenic activity and were resistant to serum deprivation induced cell death. VHL directly controls levels of HIF-1 $\alpha$  and is critical for hypoxia signaling and angiogenic responses (Ivan et al, 2001; Jaakkola et al, 2001). Taken together, myeloid HIF-1 $\alpha$  signaling likely plays roles beyond the regulation of effector cell recruitment that mediate protection against IA that remain to be fully defined. Moreover, these results present a seminal example for how manipulation of the infection microenvironment, through understanding of basic molecular mechanisms, can potentially be harnessed therapeutically to improve IPA outcomes.

### **Aspergillus strain variation and the innate immune response**

The impact of different *A. fumigatus* strains on host defense is an emerging area of great interest, particularly in the context of considering the specific fungal-host interaction to optimize IA patient care. Do all strains of *A. fumigatus* require the same host defense mechanisms for protection? Data suggest the answer to this question is no; the *A. fumigatus* strain matters. For example, it remains an open question why there are different observations on the dependency of IL-1 $\alpha$  or IL-1 $\beta$  to initiate IL-1RI/MyD88 signaling. One possibility is that different *A. fumigatus* strains under investigation preferentially induce one IL-1 cytokine over the other, since the inflammatory response differs rather dramatically between strains (Amarsaikhan et al, 2014; O'Dea et al, 2014; Rizzetto et al, 2013). While the extent of *A. fumigatus* strain variability on the host immune response remains unknown, these initial reports strongly suggest that more work (elucidating the role of *Aspergillus* spp. strain variation on host interactions and infectious outcomes) in this area is warranted. What fungal effectors and mechanisms drive these responses is unclear and their identification could yield novel therapeutic approaches. For example, strain variation may include differential expression of fungal immunomodulatory factors that are detected by the host immune system. For example, the polysaccharide galactosaminogalactan (GAG), a recently uncovered virulence factor in *Aspergillus* spp., can modulate the host inflammatory response. Purified GAG has been shown to be sufficient to induce the IL-1 antagonist, IL-1RA, which enhances the *A. fumigatus* pathogenesis and correlates with decreased neutrophil accumulation in the lungs (Gresnigt et al, 2014). More recent work demonstrates that while GAG overexpression in *Aspergillus nidulans* increases its virulence; this finding was not the result of altering neutrophil recruitment to the lungs through modulating IL-1Ra or IL-1 $\beta$  levels (Lee et al, 2015). The extent to which GAG production and secretion varies within a single or different *Aspergillus* species remains unclear but almost certainly varies.

Another possible mechanism for how different *A. fumigatus* isolates induce different host responses is the generation of unique microenvironments within the respiratory tract. Following challenge with *A. fumigatus* there is significant induction of hypoxia and its intensity differs in models of neutropenia-induced and corticosteroid-mediated immunosuppression (Grahl et al, 2011b), but whether hypoxia quantitatively and temporally differs due to the infecting *A. fumigatus* isolate has not been addressed. Hypoxia dramatically alters cell death pathways and the local redox status of the tissue microenvironment. Hypoxia-induced conditions may favor the release of one effector cytokine over another, as discussed below for IL-1 $\alpha$  and IL-1 $\beta$ . The mechanisms of IL-1 $\alpha$  and IL-1 $\beta$  secretion differ substantially depending on the type of cell death, cellular redox status, and protease activation. IL-1 $\alpha$  release depends on necrotic cell death (England et al, 2014), calpain activity (Zheng et al, 2013), and increased oxidative stress (i.e., high intracellular H<sub>2</sub>O<sub>2</sub> levels) (McCarthy et al, 2013), but the exact events that stimulate its release following *A. fumigatus* challenge remain undefined. In contrast, IL-1 $\beta$  release is dependent on pyroptotic cell death and on caspase-1 and/or caspase-8 activation, typically via multisubunit inflammasomes (Lamkanfi & Dixit, 2014). *A. fumigatus* is known to activate NLRP3- (Karki et al, 2015; Moretti et al, 2014; Said-Sadier et al, 2010) and AIM2- (Karki et al, 2015) containing inflammasomes in order to mature and secrete IL-1 $\beta$ . Hypoxia reduces the local pH within the pulmonary tract, which is also known to modulate the activity of the NLRP3 inflammasome and IL-1 $\beta$  release (Torres et al, 2014).

With regard to the fungal hypoxia response, growth in hypoxic conditions is essential for virulence (Chung et al, 2014; Grahl et al, 2012a; Grahl et al, 2011a; Grahl et al, 2012b; Shepardson et al, 2013; Willger et al, 2008). An underappreciated point is that tissue hypoxia can alter fungal production of immunomodulating polysaccharides that in turn promote inflammation and host damage. For example, *A. fumigatus* strains exposed to low oxygen conditions increase the thickness of their cell wall and expose higher levels of  $\beta$ -glucan (Shepardson et al, 2013). This observation is also observed in *Candida albicans* strains (Marakalala et al, 2013). Thus, significant work elucidating the interactions between *A. fumigatus* and the host respiratory tract is needed to understand how *A. fumigatus* proliferates within the airways, alters the local microenvironment, and modulates host immunity.

## Conclusions and Future Directions

Many exciting advances in our understanding of immune mediated protection against *A. fumigatus* have occurred in the last few years, highlighted by robust animal model studies and new genetic associations in human populations. A major challenge moving forward remains how to harness these advances for therapeutic development. In this regard, fungal and host genetic variability is a daunting challenge that is now being fully appreciated. Moreover, the diversity of underlying disease conditions that predispose individuals to IA remains a significant challenge. Subtle changes in the infection microenvironment, unique to each fungal-host interaction, may prove to significantly impact infection outcomes. Consequently, much more research is needed to understand, in specific patient populations, which key immune defense mechanisms are perturbed, and why, in order to develop new therapeutic strategies. In this regard, with any proposed new intervention, the impact on

fungal virulence must also be taken into consideration. Thus, exciting opportunities exist to further our knowledge of *A. fumigatus* host interactions driven by rapid advances in technology that are opening up the proverbial black box of the fungal-host interaction in a given patient. As precise mechanisms of the host-pathogen interaction are more fully appreciated, one can envision full genotypic and phenotypic analyses of invading pathogen and patient in combination with infection microenvironment profiling to design optimum therapy for positive outcomes. The vision is bold but achievable with increased research efforts and collaboration between scientists, physicians, patients, and funding agencies.

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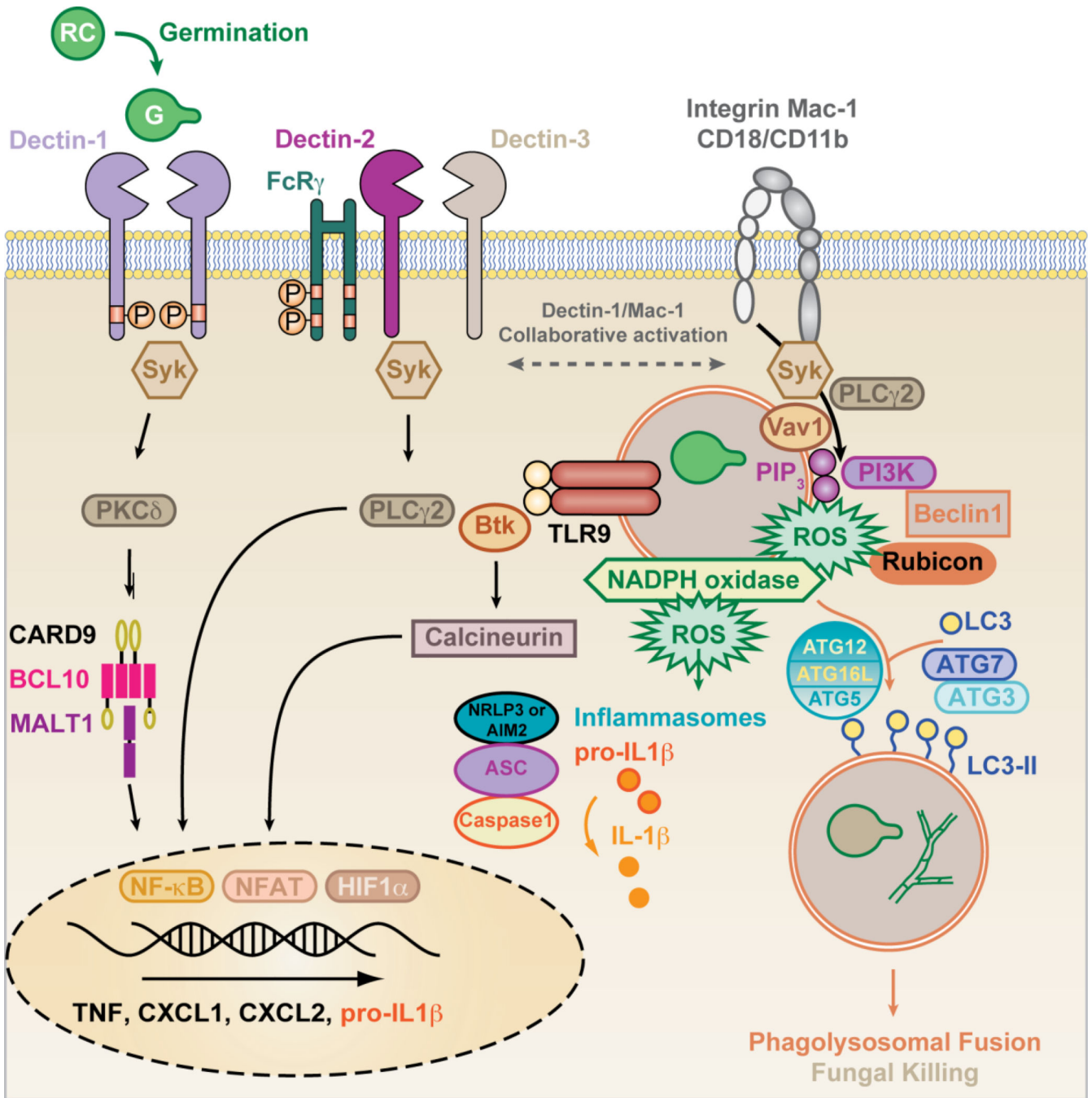
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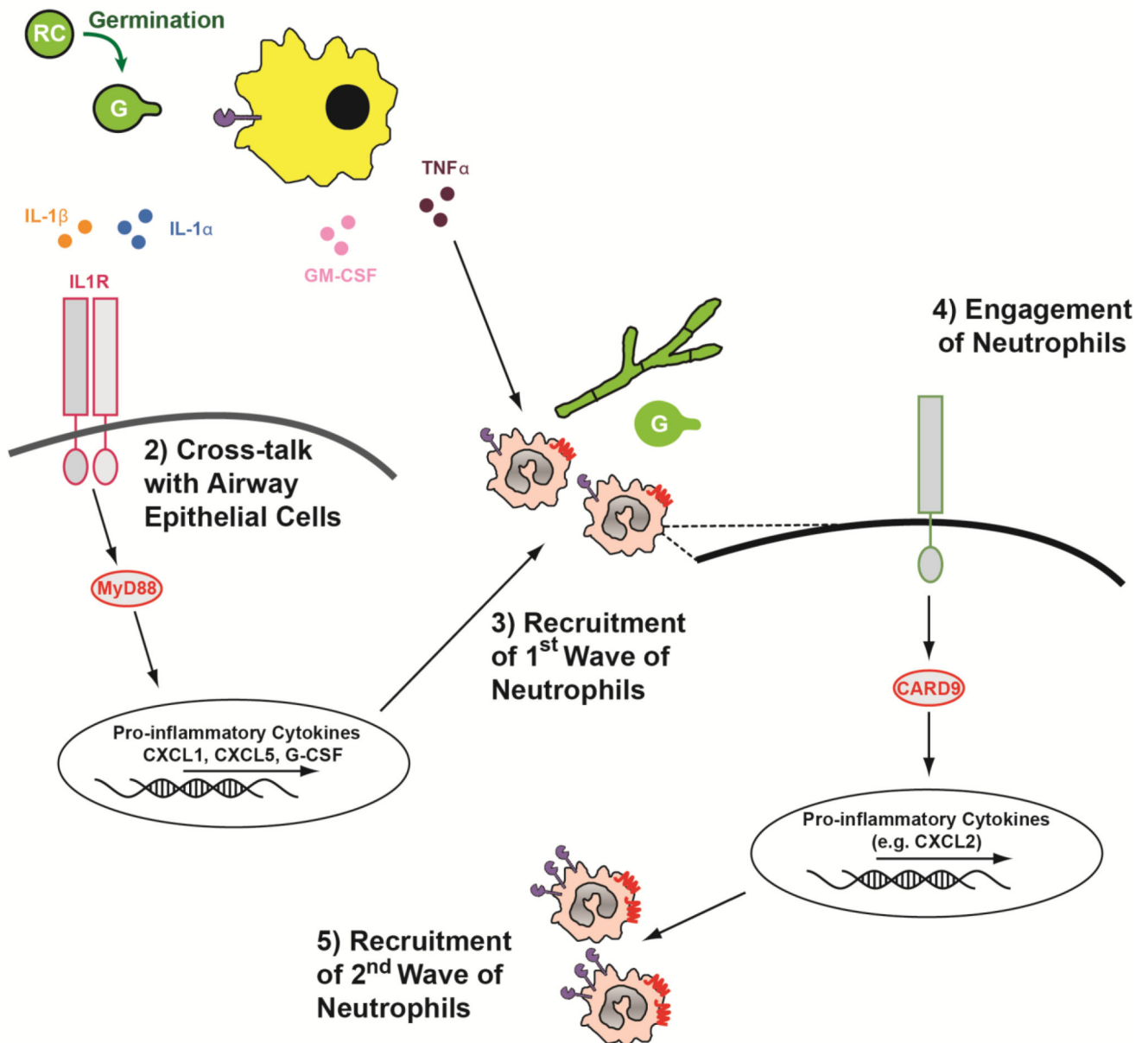
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**Figure 1. Model of fungus-induced signaling and activation of effector systems in myeloid cells**  
 Germinating *A. fumigatus conidia* (*SC*, swollen conidia) expose primarily surface  $\beta$ -glucan as well as other ligands that can activate Syk via CLRs (i.e., Dectin-1 with a hemi-ITAM in the receptor tail), FcR $\gamma$ -coupled (i.e., Dectin-2 that complexes with Dectin-3), and integrin receptors, i.e. Mac-1 (CD11b/CD18). Downstream PKC $\delta$  and CARD9 activation is critical for caspase-1 and -8 activity, NF- $\kappa$ B activation, and cytokine production. Syk-dependent PLC $\gamma$ 2 activation is linked to NADPH oxidase assembly in neutrophils. Following phagocytosis, *A. fumigatus* triggers macrophage TLR9-Btk signaling that is transduced into

calcineurin-dependent NFAT activation. HIF-1 $\alpha$  cooperates with NF- $\kappa$ B and NFAT to regulate inflammatory cytokine production (e.g., CXCL1) in myeloid cells. Macrophage phagosomes that contain swollen conidia recruit Rubicon-, Beclin-1, UVRAG-, and VPS34-containing complexes that result in phosphatidylinositol-3-phosphate (PIP<sub>3</sub>) deposition and the assembly of functional NADPH oxidase. PIP<sub>3</sub> and ROS mediate the assembly of ATG12/ATG5/ATG16L-dependent conjugation systems that facilitate ATG3- and ATG7-dependent lipidation of LC3. Lipidated LC3 inserts into phagosomal membrane and regulates the phagolysosomal fusion. The relative contribution of NADPH oxidase versus LC3-associated autophagy to fungal killing in myeloid cells has not been clearly defined *in vivo*. Rubicon not only associates with the class III phosphatidylinositol-3-kinase (i.e. VPS34 complex), but also stabilizes the NADPH oxidase complex, and negatively regulates CARD9-dependent NF- $\kappa$ B signal transduction. Please see text for additional detail.

## 1) Initial Recognition by Tissue Resident Macrophages



**Figure 2. Biphasic neutrophil recruitment to the lungs in response to *Aspergillus fumigatus*** (1) Upon entry into the airway resting *Aspergillus* conidia (RC) rapidly begin germination. Upon swelling and germ tube emergence (G) tissue resident monocytes and macrophages recognize *Aspergillus* exposed carbohydrate cell wall components through an array of pattern-recognition receptors. These activated monocytes and macrophages secrete numerous inflammatory cytokines, including IL-1 $\alpha$ , IL-1 $\beta$ , GM-CSF, and TNF- $\alpha$  into the surrounding tissue to initiate neutrophil recruitment. TNF- $\alpha$  may directly enhance neutrophil recruitment to the lung, while (2) IL-1 $\alpha$  and IL-1 $\beta$  will mediate cross-talk with airway epithelial cells that express the IL-1RI. Through IL-1RI/MyD88-dependent signaling events airway

epithelial cells produce CXCL1, CXCL5, and G-CSF. (3) These pro-inflammatory mediators drive the first wave of CXCR2-dependent neutrophil recruitment to the lungs. (4) Upon entry into the lungs neutrophil interact with the *Aspergillus* germ tubes, which results in Card9-dependent, but Dectin-1 and Dectin-2 independent, signaling which results in the expression of CXCL2 by neutrophils. (5) Finally, CXCL2 drives the accumulation of a second wave of neutrophils to the lungs through a CXCR2-dependent mechanism. Neutrophils found in the lungs at later time-point also express higher levels of the CXCR2 receptor and Dectin-1.