



Genetic susceptibility to aspergillosis in allogeneic stem-cell transplantation

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Genetic susceptibility to aspergillosis in allogeneic stem-cell transplantation

Short title: Polymorphisms in stem-cell transplantation and aspergillosis

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Abstract

Invasive aspergillosis (IA) is a major threat for the outcome of allogeneic stem-cell transplantation (allo-SCT). Despite presenting similar degrees of immunosuppression, not all individuals at-risk ultimately develop infection. Therefore, the traditional view of neutropenia as a key risk factor for aspergillosis needs to be accommodated within new conceptual advances on host immunity and its relationship to infection. Polymorphisms in innate immune genes, such as those encoding TLRs, cytokines and cytokine receptors, have recently been associated with susceptibility to IA in allo-SCT recipients. This suggests that understanding host–pathogen interactions at the level of host genetic susceptibility will allow the formulation of new targeted and patient-tailored antifungal therapeutics, including improved donor screening.

Introduction

Invasive infections by *Aspergillus* moulds are associated with high rates of morbidity and mortality, particularly among patients with hematological malignancies, prolonged neutropenia, treated with corticosteroids, or undergoing stem-cell or solid organ transplantation [1]. Although immunocompetent and nonatopic subjects are fairly resistant to *Aspergillus* infections, *A. fumigatus* is associated with a wide spectrum of diseases in humans, ranging from allergic syndromes to more severe forms of invasive disease [2]. These considerations imply that only certain host circumstances render the fungus pathogenic or innocuous to the host [3]. As a matter of fact, the exposure to *Aspergillus* is ubiquitous, and there is no evidence that isolates causing invasive infection are genetically or phenotypically distinct [4].

The most important risk factor for invasive aspergillosis (IA) has historically been neutropenia. However, it is not clear why some patients with comparable levels of apparent immunocompromise develop disease and others do not. Additionally, stem-cell transplant recipients have reduced rates of neutropenia-related infections and increased frequency of late-onset infections, concomitant with the occurrence of graft-versus-host disease (GVHD) [5]. These findings, together with the incidence of aspergillosis in non-neutropenic patients [2, 6], attest to the importance of specific defects in both innate and adaptive immune mechanisms to the pathogenesis of the infectious process [7-9].

Since allogeneic stem-cell transplantation (allo-SCT) dramatically impairs various layers of the immune system, subtle defects in the immune response could become clinically significant. On the contrary, in healthy individuals, the redundancy of the different immune pathways could easily camouflage such immune deficiencies. In this regard, over the last few years, significant advances into the genetic basis of IA occurring in the allo-SCT setting have been made (Table 1), being now clear that host

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3 genetic variants determine disparate immune responses to the fungus, ultimately
4 contributing to different degrees of susceptibility to infection [10].
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10 **The multi-faceted host immune response to *Aspergillus fumigatus***

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12 Although fungi are not mere passive bystanders in the infectious process, compelling
13 evidence points to the mammalian immune system as the most important determinant of
14 the host-fungus interaction. Host defense mechanisms against *Aspergillus* are numerous
15 and range from relatively primitive and constitutively expressed non-specific defenses
16 to sophisticated adaptive mechanisms induced specifically during infection [11]. These
17 two arms of the immune system are linked through a variety of cross-regulatory
18 pathways, the integration of which provides for the host the complex arsenal of effector
19 mechanisms for defense.
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32 Among the multiple effector mechanisms of the innate immune system, resident
33 alveolar macrophages have long been recognized as the first line of defense against
34 *Aspergillus*, preventing hyphal germination and the consequent activation of
35 inflammatory responses against the fungus [12]. In contrast, polymorphonuclear cells
36 (PMNs) are the predominant immune cells in the acute stage of infection. PMNs may
37 act as “double-edged swords”, as they are essential for pathogen eradication, but a
38 disproportionate release of oxidants and proteases may also be responsible for injury to
39 the lung [13]. This implies that tight regulatory mechanisms are required to balance
40 protection and immunopathology for efficient control of the fungus.
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54 The innate immune response to fungi is based on a restricted number of
55 receptors, the pattern recognition receptors (PRRs), which play important roles in
56 manipulating the immune response against the fungus, improving or decreasing the
57 intensity of the inflammatory reactions often intended to sterilize the host to avoid
58 infection. Among the signaling PRRs, the Toll-like receptor (TLR) family is
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3 undoubtedly involved in cell activation upon contact with pathogens [14]; specifically,
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5 TLR2, TLR4 and TLR9 have been implicated in host defense against *A. fumigatus* [13,
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7 15-18]. It is of interest that signaling through TLR2 and TLR4 in PMNs is associated
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9 with the induction of distinct activation programs, eventually culminating in the
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11 occurrence of different patterns of fungal clearance and inflammatory pathology [13,
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13 15]. On the other hand, *A. fumigatus* is also capable of subverting the host's
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15 inflammatory response through the attenuation of TLR2- and TLR4-mediated
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17 proinflammatory responses, therefore leading to an immunosuppressive effect
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19 eventually facilitating invasiveness [19].
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25 Although the signaling pathways elicited by TLRs are known to be essential in
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27 controlling fungal infection [15], recent studies have also highlighted the pivotal role of
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29 C-type lectin receptors, in particular dectin-1, in the immune response to *A. fumigatus*
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31 [20]. In fact, TLRs and dectin-1, alone or synergistically, can modulate the induction of
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33 Th1- and Th17-polarizing cytokines in response to the fungus [21], demonstrating that
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35 the involvement of innate immune receptors other than TLRs may also be required to
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37 promote adequate immune responses against *A. fumigatus*.
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43 **TLR4 deficiency triggers paradoxical effects in invasive aspergillosis**

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45 There is now undeniable evidence that genetic variants within recognition molecules
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47 involved in innate immunity may account, in part, for the inherited differences in human
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49 susceptibility to infection [22]. Given the broad effect of TLRs on immunity [14], their
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51 function in human disease has been investigated largely by comparing the incidence of
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53 disease among individuals with different polymorphisms in genes that participate in
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55 TLR signaling. Accordingly, growing amounts of data suggest that the ability of certain
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57 individuals to properly respond to TLR ligands may be impaired by polymorphisms in
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59 TLR genes, resulting in an altered susceptibility to, or course of, infectious or
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inflammatory disease [23]. Most studies so far have focused on the highly polymorphic *TLR4* gene, in which two co-segregated missense polymorphisms – D299G and T399I – have been described to compromise the extracellular ligand-binding domain of TLR4 [24]. These variants have been linked with blunted airway [25] and systemic inflammatory responses [26] to inhaled lipopolysaccharide (LPS) in adults and attenuated LPS-induced responses in primary airway epithelial cells [25]. Interestingly, the D299G substitution was found to have a greater functional impact compared with the T399I genotype [25].

One of the first studies investigating the functional consequences of *TLR4* polymorphisms in aspergillosis described an increased frequency of the chronic form of pulmonary aspergillosis, chronic cavitary pulmonary aspergillosis (CCPA), among D299G carriers [27]. In CCPA patients, the fungus is able to grow in pre-formed lung cavities, therefore escaping immune surveillance. Considering that subjects harboring the D299G polymorphism have an additional defect in TLR4 function, the increased susceptibility observed is likely due to an extensive impairment in fungal recognition. Accordingly, Tlr4-deficient mice were also found to be highly susceptible to aspergillosis, in most part due to the inability to effectively clear the fungus [13].

In the stem-cell transplantation setting, the D299G polymorphism in *TLR4* was also found to increase susceptibility to IA in allo-SCT recipients from unrelated donors [28]. The fact that a previous study failed to associate the same donor polymorphism with IA in allo-SCT patients [29] further stresses that the contribution of the D299G polymorphism may depend on the type of transplant and associated clinical variables. In this regard, we have recently described an association between donor D299G and colonization by *A. fumigatus*, but not invasive disease, in a cohort of T-cell-depleted transplant recipients from related donors [30]. Therefore, fungal colonization may not predict susceptibility to infection in the presence of D299G, at least in this particular

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3 transplant setting. The contribution of this polymorphism to colonization by *A.*
4 *fumigatus* could be explained by the fact that an abnormal TLR4 extracellular domain
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6 could be hampering its function by disrupting microbial recognition, eventually leading
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8 to fungal escape from immune surveillance (Fig. 1). However, *TLR4* polymorphisms
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10 have also been shown to display a protective effect from hyper-inflammatory diseases,
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12 including atherosclerosis and related conditions [31]. Therefore, the failure to recognize
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14 the fungus may be compensated by the lack of an exuberant inflammatory response to it
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16 which may ultimately be harmful to the host. In this regard, we have found that a hyper-
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18 inflammatory state, more than the fungus itself, may contribute to susceptibility to
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20 aspergillosis and other fungal infections [32]. Thus, by limiting the inflammatory
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22 response to the fungus, the D299G polymorphism could contribute to resistance to
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24 aspergillosis, despite evidence of fungal growth. Interestingly, the D299G
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26 polymorphism was recently shown to have a unique distribution with high prevalence in
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28 Africa and low prevalence in Europe, with the authors arguing that the benefit from
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30 reduced inflammation during malaria in Africa might have been counter-selected due to
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32 lack of inflammation in response to bacterial infections [33].
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41 Although TLR4 has been representing the cornerstone of genetic variability to
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43 aspergillosis in the last few years, polymorphisms in other TLRs have also been linked
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45 with susceptibility to *Aspergillus*. In particular, a common polymorphism in the *TLR9*
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47 promoter (T-1237C) has been shown to predispose to the allergic form of pulmonary
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49 aspergillosis, allergic bronchopulmonary aspergillosis (ABPA) [27]. It is worth
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51 mentioning that we found this polymorphism to lead to an increase in *TLR9* gene
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53 expression in human mononuclear cells that could be further sustained upon TLR9
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55 engagement, presumably resulting in a gain-of-function of the receptor (Rodrigues F,
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57 unpublished data). This observation is consistent with a role for TLR9 in response to
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59 allergy since Tlr9-deficient mice have been shown to be more resistant to induced
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allergenic stimuli [34]. In addition, PMNs from these mice had an increased capacity to kill conidia and damage *Aspergillus* hyphae [13], therefore arguing for a detrimental role of this *TLR9* polymorphism and consequent enhancement of *TLR9* function in allergic aspergillosis.

IL-23 and IL-17 have a largely detrimental role in aspergillosis

Despite TLRs being proved to be crucial for detecting infection and activating the innate and adaptive immune systems, sustained TLR stimulation can result in chronic inflammation and is also associated with the development of certain autoimmune diseases [35]. In the last two decades, the immunopathogenesis of aspergillosis and associated inflammatory diseases has been explained primarily in terms of Th1/Th2 balance [11, 36]. Until recently, CD4⁺ Th1 cells were considered responsible for the development of inflammatory responses to *Aspergillus* that were mediated by IL-12p70, the key cytokine driving Th1-cell differentiation. The discovery of the IL-12 cytokine-family member IL-23 has led to a re-evaluation of this conceptual framework [37]. IL-23, although not directly involved in Th17 differentiation, plays an important role in maintaining Th17 effector function [38]. Several experimental studies and clinical investigations confirmed that IL-23-driven Th17 cells, rather than the Th1-cell subset, mediate the inflammatory responses of autoimmune or infectious origin [32, 39]. In addition, both IL-23 and the Th17 pathway correlate with disease severity and immunopathology in diverse infections [40-41], suggesting that IL-12 and IL-23 have distinct roles in promoting antimicrobial immune responses and diseases in vivo.

We have recently demonstrated that IL-17 has a largely detrimental role in aspergillosis in non-immunosuppressed mice, since it hampered neutrophil-mediated killing of *A. fumigatus* and the in vivo clearance of the fungus [41]. In addition, blockade of IL-23 and IL-17 greatly increased antifungal resistance, as judged by the

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3 decreased fungal growth in the relevant target organs and the ameliorated signs of
4 inflammation, both clinically and at the tissue level [41]. Thus, despite the important
5 role in regulating PMN homeostasis and recruitment [42], IL- 23 and IL-17, by
6 subverting the tolerogenic program of PMNs, may promote pathogen growth and
7 infection as a result of the induced inflammatory pathology. In this regard, in a mouse
8 model of chronic granulomatous disease, we have recently found that down-regulation
9 of IL-23 promoted by exogenous administration of pentraxin 3 (PTX3) restored
10 antifungal resistance and restrained the inflammatory response to the fungus through the
11 limited expansion of IL-17-producing $\gamma\delta$ T-cells and the emergence of Th1/Treg
12 responses with minimum pathology [43]. Altogether, these results may serve to
13 accommodate the paradoxical association of chronic inflammatory responses with
14 intractable forms of fungal infection, where fungal persistence occurs in the face of an
15 ongoing inflammation.

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The ability of IL-17 to promote fungal germination further stresses its potential
negative role in the immune responses against *A. fumigatus* [44]. Therefore, the function
of the Th17 pathway may go beyond its ability to promote inflammation and subvert
antimicrobial immunity by also having a direct action on fungal morphology and
virulence. This may translate in concomitant Th2 cell activation, known to be strictly
dependent on high levels of hyphal growth [45], and further prevent Th1 functioning.
Thus, the Th17 pathway may contribute to the pathogenesis of fungal infections,
occurring in a fungus-autonomous fashion at sites of infection.

Genetic impairment of IL-23 signaling protects from invasive aspergillosis

Polymorphisms in cytokine genes can influence immune responses and inflammation,
thereby affecting susceptibility to aspergillosis in allo-SCT recipients [46]. However,
the role of polymorphisms in genes from the IL-23/Th17 inflammatory pathway in

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3 aspergillosis has only recently been addressed [47]. It has already been shown that the
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5 R381Q variant in *IL23R* confers protection against a number of immune-mediated
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7 diseases, such as inflammatory bowel disease [48] and psoriasis [49], but also against
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9 GVHD in recipients of hematopoietic cells from HLA-identical donors [50]. Although
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11 the genetic findings have been thoroughly replicated, much less is known about the
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13 functional consequences of this variant. A recent study demonstrated that the protective
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15 effects displayed by the R381Q polymorphism in *IL23R* were due to a deficient
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17 activation of IL-23-driven Th17 responses [51]. In vitro committed effector Th17 cells
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19 derived from subjects harbouring the R381Q protective allele stimulated with IL-23
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21 were shown to have impaired production of IL-17A compared to wild-type individuals
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23 [51]. Interestingly, IL-23 stimulation of highly purified naïve T-cells did not result in
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25 any difference whatsoever between R381Q genotypes [51], suggesting that the
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27 consequences of the polymorphism may be exclusively reflected in the function of
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29 already differentiated Th17 cells.
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36 In T-cell-depleted allo-SCT recipients, we found that donor R381Q was
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38 associated with strong protection from IA and patient R381Q with improved overall
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40 survival [47] (Fig. 2). Strikingly, none of the patients carrying the R381Q
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42 polymorphism enrolled in the study developed aspergillosis. These findings are
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44 consistent with the protective effects of IL-23 signaling attenuation in experimental
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46 aspergillosis [41]. However, a set of polymorphisms in the *IL17A* and *IL17F* genes were
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48 not associated with susceptibility to IA in allo-SCT recipients [47], a finding suggesting
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50 that further studies are needed to define cellular and molecular mechanisms by which
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52 protection from aspergillosis is conferred by the disruption of the IL-23/Th17 axis.
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58 The fact that donor R381Q also increased the risk of cytomegalovirus infection
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60 [47], while being consistent with the enhancing role of IL-23 of antiviral immunity [52],
indicates that *Aspergillus* more than viral infection may impact on survival, at least in

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3 the T-cell-depleted transplantation setting. Although the R381Q polymorphism could
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5 arguably influence survival by modifying the incidence of disease relapse or GVHD, no
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7 beneficial effects on relapse or GVHD were found at all [47].
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10 11 12 **Immunogenetics: from bench to bedside**

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14 Although the dissection of complex genetic traits modulating susceptibility to
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16 aspergillosis is complex, the contribution of host genetics may hold the key to elucidate
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18 new risk factors for these severe, often fatal diseases. In this sense, new conceptual
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20 advances on the knowledge of host immunity need to be accommodated also from an
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22 immunogenetic point of view.
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27 It is interesting that the genetic bases for susceptibility to human disease may
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29 also be evaluated by the screening of inbred murine strains. Recently, this approach was
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31 performed using an immunocompromised mice model of IA [53]. Through a haplotype-
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33 based computational genetic analysis of survival data, the gene encoding plasminogen
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35 (PLG) was recently identified as a suitable candidate for susceptibility to *Aspergillus*.
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37 Consequently, a functional polymorphism in human *PLG* was reported to affect the risk
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39 of developing IA in allo-SCT recipients [53]. Besides shedding light into the role of the
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41 fibrinolytic system in the pathogenesis of IA, this approach identified a novel,
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43 biologically plausible candidate gene, validating its future use in the identification of
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45 less obvious disease-related genes.
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51 Considering the key role played by many genetic polymorphisms at the host-
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53 fungus interface, further large-scale translational and clinical studies are needed to
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55 corroborate the data obtained from human cohorts. The modulation of host immune
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57 responses has been regarded as a potential therapeutic avenue with promising impact
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59 also on the treatment of fungal infections. We have recently reported that intranasal
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administration of a small interference RNA (siRNA) targeting the inflammatory

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3 PI3K/Akt/mTOR pathway rendered mice protection from experimental aspergillosis
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5 through attenuation of the inflammatory pathology [54]. The promising application of
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7 siRNA therapeutics, together with the awareness of the immunogenetic profile of each
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9 individual at-risk, including those subjected to allo-SCT, could prove useful to the
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11 design of fungal vaccines capable of targeting the appropriate signaling pathways and
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13 the development of therapeutics that target inflammation in aspergillosis.
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17 In conclusion, understanding host–pathogen interactions at the level of host
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19 genetic susceptibility, together with the molecular and cellular bases affected, will allow
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21 the identification of potential therapeutic targets and the design of prophylactic
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23 strategies exerting control over the outcome of immune pathways. The genetic
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25 screening of at-risk patients may ultimately be used to individualize treatments through
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27 the formulation of new targeted and patient-tailored antifungal therapeutics, which are
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29 likely to improve the management and outcome of aspergillosis, particularly in the
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31 stem-cell transplantation setting.
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58 **Disclosure of conflict of interest**

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60 No conflict of interest.

Figure legends

Fig.1 - The D299G polymorphism of *TLR4* triggers paradoxical effects in invasive aspergillosis following stem-cell transplantation.

Fig.2 - The genetic impairment of IL-23 signaling promoted by the R381Q polymorphism in *IL23R* protects from invasive aspergillosis.

References

1. Segal BH, Walsh TJ. Current approaches to diagnosis and treatment of invasive aspergillosis. *Am J Respir Crit Care Med* 2006; 173(7): 707-17.
2. Marr KA, Patterson T, Denning D. Aspergillosis. Pathogenesis, clinical manifestations, and therapy. *Infect Dis Clin North Am* 2002; 16(4): 875-94, vi.
3. Stergiopoulou T, Meletiadiis J, Roilides E, *et al.* Host-dependent patterns of tissue injury in invasive pulmonary aspergillosis. *Am J Clin Pathol* 2007; 127(3): 349-55.
4. Gravelat FN, Doedt T, Chiang LY, *et al.* In vivo analysis of *Aspergillus fumigatus* developmental gene expression determined by real-time reverse transcription-PCR. *Infect Immun* 2008; 76(8): 3632-9.
5. Garcia-Vidal C, Upton A, Kirby KA, Marr KA. Epidemiology of invasive mold infections in allogeneic stem cell transplant recipients: biological risk factors for infection according to time after transplantation. *Clin Infect Dis* 2008; 47(8): 1041-50.
6. Denning DW, Follansbee SE, Scolaro M, *et al.* Pulmonary aspergillosis in the acquired immunodeficiency syndrome. *N Engl J Med* 1991; 324(10): 654-62.
7. Cenci E, Mencacci A, Fe d'Ostiani C, *et al.* Cytokine- and T helper-dependent lung mucosal immunity in mice with invasive pulmonary aspergillosis. *J Infect Dis* 1998; 178(6): 1750-60.
8. Roilides E, Katsifa H, Walsh TJ. Pulmonary host defences against *Aspergillus fumigatus*. *Res Immunol* 1998; 149(4-5): 454-65; discussion 523-4.
9. Romani L, Fallarino F, De Luca A, *et al.* Defective tryptophan catabolism underlies inflammation in mouse chronic granulomatous disease. *Nature* 2008; 451(7175): 211-5.
10. Carvalho A, Cunha C, Pasqualotto AC, *et al.* Genetic variability of innate immunity impacts human susceptibility to fungal diseases. *Int J Infect Dis* 2009.
11. Romani L. Immunity to fungal infections. *Nat Rev Immunol* 2004; 4(1): 1-23.
12. Latge JP. *Aspergillus fumigatus* and aspergillosis. *Clin Microbiol Rev* 1999; 12(2): 310-50.
13. Bellocchio S, Moretti S, Perruccio K, *et al.* TLRs govern neutrophil activity in aspergillosis. *J Immunol* 2004; 173(12): 7406-15.
14. Akira S, Uematsu S, Takeuchi O. Pathogen recognition and innate immunity. *Cell* 2006; 124(4): 783-801.

15. Bellocchio S, Montagnoli C, Bozza S, *et al.* The contribution of the Toll-like/IL-1 receptor superfamily to innate and adaptive immunity to fungal pathogens in vivo. *J Immunol* 2004; 172(5): 3059-69.
16. Bretz C, Gersuk G, Knoblauch S, *et al.* MyD88 signaling contributes to early pulmonary responses to *Aspergillus fumigatus*. *Infect Immun* 2008; 76(3): 952-8.
17. Chignard M, Balloy V, Sallenave JM, Si-Tahar M. Role of Toll-like receptors in lung innate defense against invasive aspergillosis. Distinct impact in immunocompetent and immunocompromized hosts. *Clin Immunol* 2007; 124(3): 238-43.
18. Ramirez-Ortiz ZG, Specht CA, Wang JP, *et al.* Toll-like receptor 9-dependent immune activation by unmethylated CpG motifs in *Aspergillus fumigatus* DNA. *Infect Immun* 2008; 76(5): 2123-9.
19. Chai LY, Kullberg BJ, Vonk AG, *et al.* Modulation of Toll-like receptor 2 (TLR2) and TLR4 responses by *Aspergillus fumigatus*. *Infect Immun* 2009; 77(5): 2184-92.
20. Werner JL, Metz AE, Horn D, *et al.* Requisite role for the dectin-1 beta-glucan receptor in pulmonary defense against *Aspergillus fumigatus*. *J Immunol* 2009; 182(8): 4938-46.
21. Ferwerda G, Meyer-Wentrup F, Kullberg BJ, Netea MG, Adema GJ. Dectin-1 synergizes with TLR2 and TLR4 for cytokine production in human primary monocytes and macrophages. *Cell Microbiol* 2008; 10(10): 2058-66.
22. Garantziotis S, Hollingsworth JW, Zaas AK, Schwartz DA. The effect of toll-like receptors and toll-like receptor genetics in human disease. *Annu Rev Med* 2008; 59: 343-59.
23. Lasker MV, Nair SK. Intracellular TLR signaling: a structural perspective on human disease. *J Immunol* 2006; 177(1): 11-6.
24. Rallabhandi P, Bell J, Boukhvalova MS, *et al.* Analysis of TLR4 polymorphic variants: new insights into TLR4/MD-2/CD14 stoichiometry, structure, and signaling. *J Immunol* 2006; 177(1): 322-32.
25. Arbour NC, Lorenz E, Schutte BC, *et al.* TLR4 mutations are associated with endotoxin hyporesponsiveness in humans. *Nat Genet* 2000; 25(2): 187-91.
26. Michel O, LeVan TD, Stern D, *et al.* Systemic responsiveness to lipopolysaccharide and polymorphisms in the toll-like receptor 4 gene in human beings. *J Allergy Clin Immunol* 2003; 112(5): 923-9.
27. Carvalho A, Pasqualotto AC, Pitzurra L, *et al.* Polymorphisms in toll-like receptor genes and susceptibility to pulmonary aspergillosis. *J Infect Dis* 2008; 197(4): 618-21.
28. Bochud PY, Chien JW, Marr KA, *et al.* Toll-like receptor 4 polymorphisms and aspergillosis in stem-cell transplantation. *N Engl J Med* 2008; 359(17): 1766-77.
29. Kesh S, Mensah NY, Peterlongo P, *et al.* TLR1 and TLR6 polymorphisms are associated with susceptibility to invasive aspergillosis after allogeneic stem cell transplantation. *Ann N Y Acad Sci* 2005; 1062: 95-103.
30. Carvalho A, Cunha C, Carotti A, *et al.* Polymorphisms in Toll-like receptor genes and susceptibility to infections in allogeneic stem cell transplantation. *Exp Hematol* 2009; 37(9): 1022-9.
31. Kiechl S, Lorenz E, Reindl M, *et al.* Toll-like receptor 4 polymorphisms and atherogenesis. *N Engl J Med* 2002; 347(3): 185-92.
32. Romani L, Puccetti P. Controlling pathogenic inflammation to fungi. *Expert Rev Anti Infect Ther* 2007; 5(6): 1007-17.
33. Ferwerda B, McCall MB, Alonso S, *et al.* TLR4 polymorphisms, infectious diseases, and evolutionary pressure during migration of modern humans. *Proc Natl Acad Sci U S A* 2007; 104(42): 16645-50.

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- 2
- 3 34. Ramaprakash H, Ito T, Standiford TJ, Kunkel SL, Hogaboam CM. Toll-like
- 4 receptor 9 modulates immune responses to *Aspergillus fumigatus* conidia in
- 5 immunodeficient and allergic mice. *Infect Immun* 2009; 77(1): 108-19.
- 6
- 7 35. Hurst J, von Landenberg P. Toll-like receptors and autoimmunity. *Autoimmun*
- 8 *Rev* 2008; 7(3): 204-8.
- 9
- 10 36. Romani L, Puccetti P. Protective tolerance to fungi: the role of IL-10 and
- 11 tryptophan catabolism. *Trends Microbiol* 2006; 14(4): 183-9.
- 12 37. Langrish CL, Chen Y, Blumenschein WM, *et al.* IL-23 drives a pathogenic T
- 13 cell population that induces autoimmune inflammation. *J Exp Med* 2005; 201(2): 233-
- 14 40.
- 15 38. Korn T, Bettelli E, Oukka M, Kuchroo VK. IL-17 and Th17 Cells. *Annu Rev*
- 16 *Immunol* 2009; 27: 485-517.
- 17
- 18 39. Dong C. Diversification of T-helper-cell lineages: finding the family root of IL-
- 19 17-producing cells. *Nat Rev Immunol* 2006; 6(4): 329-33.
- 20 40. Happel KI, Dubin PJ, Zheng M, *et al.* Divergent roles of IL-23 and IL-12 in host
- 21 defense against *Klebsiella pneumoniae*. *J Exp Med* 2005; 202(6): 761-9.
- 22 41. Zelante T, De Luca A, Bonifazi P, *et al.* IL-23 and the Th17 pathway promote
- 23 inflammation and impair antifungal immune resistance. *Eur J Immunol* 2007; 37(10):
- 24 2695-706.
- 25
- 26 42. Smith E, Zarbock A, Stark MA, *et al.* IL-23 is required for neutrophil
- 27 homeostasis in normal and neutrophilic mice. *J Immunol* 2007; 179(12): 8274-9.
- 28 43. D'Angelo C, De Luca A, Zelante T, *et al.* Exogenous pentraxin 3 restores
- 29 antifungal resistance and restrains inflammation in murine chronic granulomatous
- 30 disease. *J Immunol* 2009; 183(7): 4609-18.
- 31 44. Zelante T, Bozza S, De Luca A, *et al.* Th17 cells in the setting of *Aspergillus*
- 32 infection and pathology. *Med Mycol* 2009; 47 Suppl 1: S162-9.
- 33 45. Mencacci A, Spaccapelo R, Del Sero G, *et al.* CD4+ T-helper-cell responses in
- 34 mice with low-level *Candida albicans* infection. *Infect Immun* 1996; 64(12): 4907-14.
- 35 46. Weissinger EM, Dickinson AM. Immunogenomics and proteomics in
- 36 hematopoietic stem cell transplantation: predicting post-hematopoietic stem cell
- 37 transplant complications. *Cancer Treat Res* 2009; 144: 1-35.
- 38 47. Carvalho A, Cunha C, Di Ianni M, *et al.* Prognostic significance of genetic
- 39 variants in the IL-23/Th17 pathway for the outcome of T cell-depleted allogeneic stem
- 40 cell transplantation. *Bone Marrow Transplant*.
- 41 48. Duerr RH, Taylor KD, Brant SR, *et al.* A genome-wide association study
- 42 identifies IL23R as an inflammatory bowel disease gene. *Science* 2006; 314(5804):
- 43 1461-3.
- 44 49. Cargill M, Schrodi SJ, Chang M, *et al.* A large-scale genetic association study
- 45 confirms IL12B and leads to the identification of IL23R as psoriasis-risk genes. *Am J*
- 46 *Hum Genet* 2007; 80(2): 273-90.
- 47 50. Elmaagacli AH, Koldehoff M, Landt O, Beelen DW. Relation of an interleukin-
- 48 23 receptor gene polymorphism to graft-versus-host disease after hematopoietic-cell
- 49 transplantation. *Bone Marrow Transplant* 2008; 41(9): 821-6.
- 50 51. Meglio PD, Cesare AD, Laggner U, *et al.* F.15. A Gene-to-Function Analysis of
- 51 IL-23R Arg381Gln Polymorphism Reveals Impaired IL-17A Production in Th17 Cells.
- 52 *Clinical Immunology* 2009; 131(Supplement 1): S97-S97.
- 53 52. Kohyama S, Ohno S, Isoda A, *et al.* IL-23 enhances host defense against
- 54 vaccinia virus infection via a mechanism partly involving IL-17. *J Immunol* 2007;
- 55 179(6): 3917-25.
- 56 53. Zaas AK, Liao G, Chien JW, *et al.* Plasminogen alleles influence susceptibility
- 57 to invasive aspergillosis. *PLoS Genet* 2008; 4(6): e1000101.
- 58
- 59
- 60

1
2
3 54. Bonifazi P, D'Angelo C, Zagarella S, *et al.* Intranasally delivered siRNA
4 targeting PI3K/Akt/mTOR inflammatory pathways protects from aspergillosis. *Mucosal*
5 *Immunol*; 3(2): 193-205.
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Table 1. Human genetic association studies evaluating polymorphisms in immune genes and susceptibility to invasive aspergillosis in allogeneic stem-cell transplant recipients.

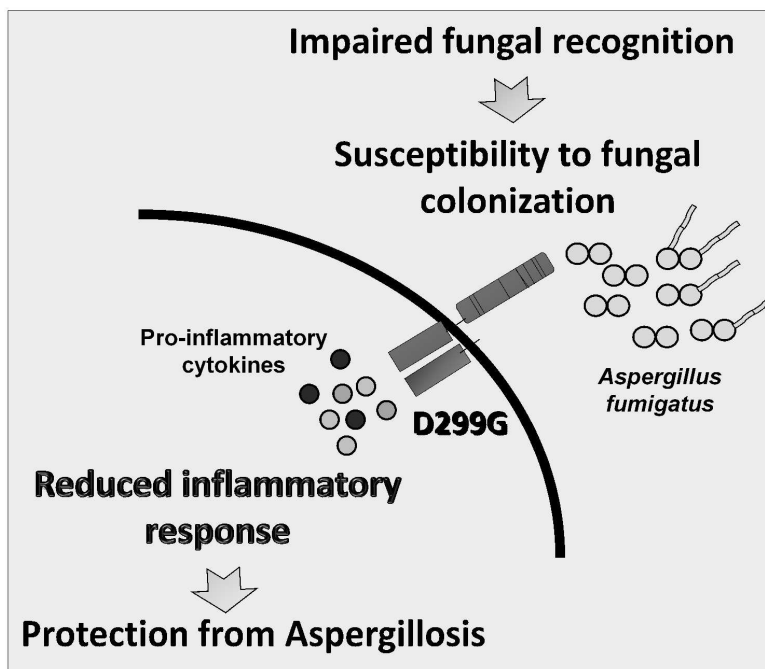
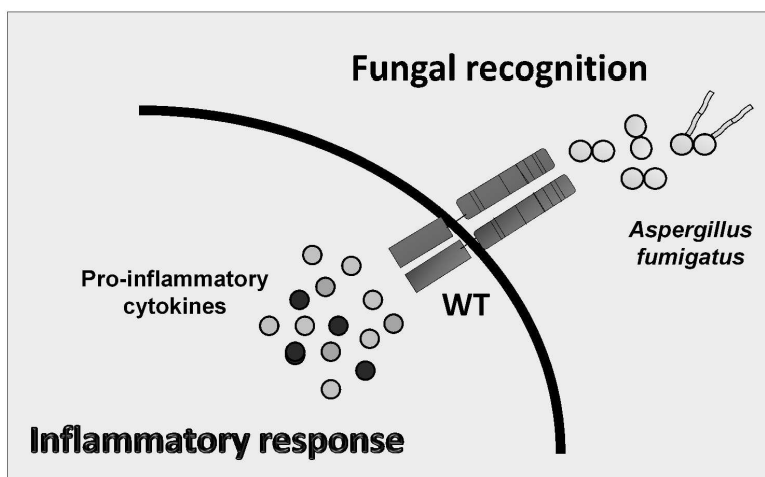
Reference	Gene	Polymorphism/Haplotypes	Relevant findings
Bochud et al.	<i>TLR4</i>	D299G and T399I (S4 haplotype)	An association between donor S4 haplotype and risk of IA was observed, especially if combined with CMV positivity (n=103 IA cases)
Carvalho et al.	<i>TLR4</i>	D299G *	Donor D299G was associated with fungal colonization (n=58), while susceptibility to IA was instead decreased among pre-colonized patients (n=34)
Carvalho et al.	<i>IL23R</i>	R381Q	Donor R381Q displayed a protective effect from IA (n=25 IA cases)
Granell et al.	<i>MBL2</i>	O/O or LXA/O †	Donor MBL-low genotype (38% vs. 12%) was associated with a higher probability of IA (n=106 donor-patients sibling pairs)
Granell et al.	<i>MASP2</i>	D105G	Recipient D105G (67% vs. 14%) was associated with a higher probability of IA (n=106 donor-patient sibling pairs)
Kesh et al.	<i>TLR1</i> and <i>TLR6</i>	R80T, N248S and S249P	<i>TLR1</i> R80T or combination of <i>TLR1</i> N248S and <i>TLR6</i> S249P from the recipient were associated with IA (n=22 IA cases)
Mezger et al.	<i>CXCL10</i>	C+11101T, C+1642G and A-1101G	Donor <i>CXCL10</i> polymorphisms were associated with IA (n=81 IA cases)
Seo et al.	<i>IL10</i>	-1082A/-819C/-592C	Recipient ACC haplotype had a protective role from IA (n=105 patients; 9.9% IA cases)
Zaas et al.	<i>PLG</i>	D472N	Risk of IA at day >40 after transplant was 5.6-fold higher in N/N vs. D/D recipients (n=83 IA cases)

IA – invasive aspergillosis; CMV – cytomegalovirus; MBL – mannose-binding lectin.

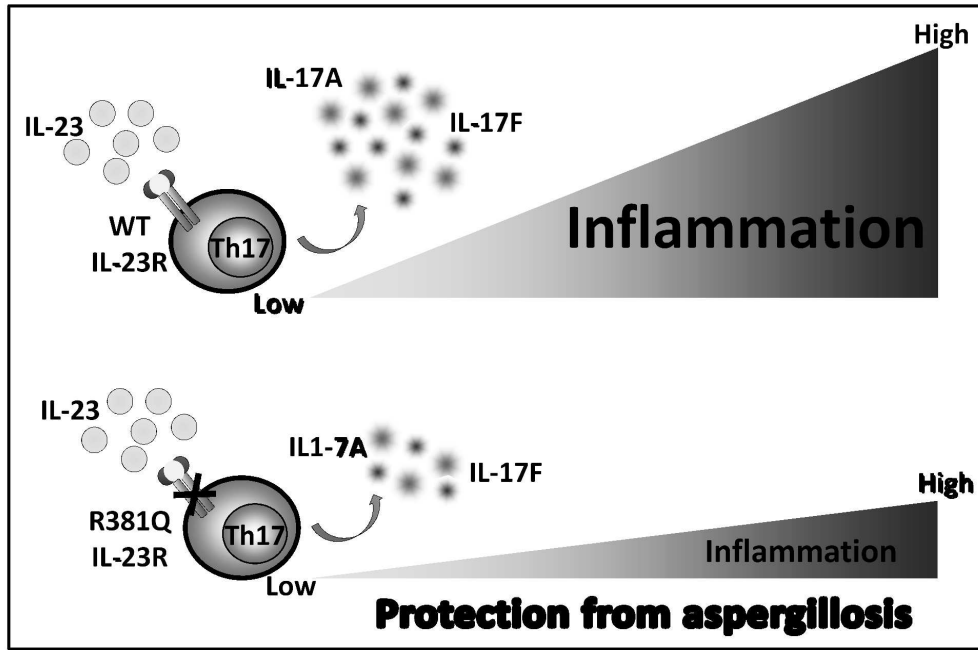
* D299G and T399I were always co-segregated.

† O/O and LXA/O are MBL-low haplotypes. LX represents an MBL promoter haplotype. Variants D, B and C are collectively named O, while A indicates the wild-type.

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The D299G polymorphism of TLR4 triggers paradoxical effects in invasive aspergillosis following stem-cell transplantation.
131x195mm (600 x 600 DPI)



The genetic impairment of IL-23 signaling promoted by the R381Q polymorphism in IL23R protects from invasive aspergillosis.
164x110mm (600 x 600 DPI)