



Human inborn errors of immunity underlying superficial or invasive candidiasis

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Abstract

Candida species, including *C. albicans* in particular, can cause superficial or invasive disease, often in patients with known acquired immunodeficiencies or iatrogenic conditions. The molecular and cellular basis of these infections in patients with such risk factors remained largely elusive, until the study of inborn errors of immunity clarified the basis of the corresponding inherited and “idiopathic” infections. Superficial candidiasis, also known as chronic mucocutaneous candidiasis (CMC), can be caused by inborn errors of IL-17 immunity. Invasive candidiasis can be caused by inborn errors of CARD9 immunity. In this chapter, we review both groups of inborn errors of immunity, and discuss the contribution of these studies to the deciphering of the critical mechanisms of anti-*Candida* immunity in patients with other conditions.

Introduction

The genus *Candida*, which contains about 200 different species, belongs to the phylum Ascomycota. *Candida* spp. are the most common cause of fungal infection in humans (Kullberg and Arendrup 2016; Pfaller and Diekema 2007), but only a few species (approximately 20) can cause disease. *Candida albicans*, *C. glabrata*, *C. tropicalis*, *C. parapsilosis*, and *C. krusei* account for about 90% of these diseases, and their prevalence depends on the geographic location, patient populations, and clinical settings (Turner and Butler 2014). *C. albicans* remains the major cause of invasive candidiasis, but *C. glabrata* (in northern Europe, USA, Canada) and *C. parapsilosis* (in southern Europe, Asia, Latin America) have emerged as important or even major pathogens (Horn et al. 2009; Pfaller et al. 2019; Klingspor et al. 2015; Leroy et al. 2009). *Candida* spp. have been reported to be the fourth most common nosocomial pathogen in the bloodstream, or at least within the top ten of such pathogens (Kullberg and

Arendrup 2016; Wisplinghoff et al. 2004). These *Candida* spp. are resident commensal yeasts in the oro-gastrointestinal and genitourinary tracts in healthy individuals. However, they can also act as pathogens in humans, causing superficial infections of the skin, scalp, nails, or oral and genital mucosae, or invasive, often life-threatening, systemic infections (candidemia) that may be disseminated to internal organs (leading to meningoenitis, brain abscesses, endophthalmitis, endocarditis, peritonitis, osteomyelitis, intra-abdominal abscesses, lung infections, etc.) (Kim and Sudbery 2011; Eggimann et al. 2011; Pappas et al. 2018). The infections they cause are a serious public health problem, with mortality often exceeding 40% (partly due to late diagnosis, the late initiation of antifungal therapies, and the emergence of resistance to antifungal drugs), and substantial costs associated with patient care and long hospital stays (Pappas et al. 2018; Chakrabarti and Singh 2011; Lass-Flörl 2009; Casadevall 2019; Jeffery-Smith et al. 2018; Cheng et al. 2005; Almirante et al. 2005; Gudlaugsson et al. 2003).

Various risk factors, iatrogenic or acquired, are known, such as HIV infection, mainly associated with oro-pharyngeal candidiasis (de Repentigny et al. 2004). Invasive candidiasis is mostly associated with organ transplantation, hemodialysis, parenteral nutrition, intravenous catheters, abdominal surgery, extensive burns, long-term stay in intensive care units, or the administration of broad-spectrum antibiotics or of immunosuppressive agents such as chemotherapy (Kullberg and Arendrup 2016; Ortega et al. 2011). In this context, invasive candidiasis is an increasing

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problem in elderly patients, with significantly higher mortality rates as compared to younger patients (Barchiesi et al. 2017; Wang et al. 2014a). Neonates are also at risk of invasive forms of candidiasis, such as the central nervous system (CNS) candidiasis reported in low-birth weight or preterm neonates (Barton et al. 2014; Fernandez et al. 2000; Huang et al. 1998; Pahud et al. 2009). These fungal diseases frequently strike individuals with many risk factors. As a result, their pathogenesis remains poorly understood at the molecular and cellular levels. The study of primary immunodeficiencies (PID) with “syndromic” candidiasis, whether superficial or invasive, and, more recently, that of inborn errors of immunity in otherwise healthy patients with “isolated” candidiasis, whether superficial or invasive, has progressively shed light on the mechanisms conferring protective immunity to *Candida* spp. (Drummond and Lionakis 2018; Li et al. 2017; Pilmis et al. 2016; Lanternier et al. 2013a; Antachopoulos et al. 2007; Corvilain et al. 2018; Okada et al. 2016; Puel et al. 2010a, 2012; Drummond et al. 2018). The elucidation of the pathogenesis of these fungal diseases in patients with inherited immunodeficiencies (ID) has important clinical implications for the patients and their families, with the possibility of genetic diagnoses and counseling, but should also facilitate the development of novel prophylactic or curative treatments with a rational basis, for PID patients and patients with other more common conditions (e.g. acquired ID). Research into the genetic basis of *Candida* diseases is important, given the high mortality associated with *Candida* diseases, despite the availability of antifungal drugs, and the increasing frequency of antifungal drug-resistant strains (Perfect 2017).

Chronic mucocutaneous candidiasis and inborn errors of IL-17 immunity

Mucocutaneous candidiasis is characterized by *Candida* spp. infections of the nails, skin, scalp, and/or oral and genital mucosae (Puel et al. 2010a; Glocker and Grimbacher 2010; Vazquez and Sobel 2002; Eyerich et al. 2008; Kirkpatrick 2001; Lilic 2002; Eyerich et al. 2010). Mucosal candidiasis, such as oral thrush, is relatively frequent in individuals on steroid or antibiotic treatments. Up to 75% of women present at least one episode of vulvovaginal candidiasis during their lifetime, and recurrent (> 1 episode) vulvovaginal candidiasis has been estimated to have a global annual prevalence of 3871 per 100,000 women (Denning et al. 2018). Chronic mucocutaneous candidiasis (CMC) is characterized by severe, persistent or recurrent (relapse upon discontinuation of treatment) disease (Eyerich et al. 2010). CMC, present as severe oropharyngeal candidiasis, is very common in AIDS patients (de Repentigny et al. 2004; Pirofski and Casadevall 2009). Similarly, in the context of PID, CMC is frequent

in patients with broad T-cell defects, such as combined or severe combined immunodeficiencies (CID or SCID, respectively) (Lanternier et al. 2013a; Antachopoulos et al. 2007; Vinh 2011; Picard et al. 2018; Tangye et al. 2020). This inherited form of CMC, usually referred to as CMC disease (CMCD), is rare, affecting approximately 1 in every 50,000 individuals. The CMC in affected patients is syndromic, as it is associated with many other clinical manifestations, mostly infectious and/or autoimmune. Syndromic CMC is also common in some PIDs without major global apparent T-cell deficiencies, albeit with milder clinical features. These PIDs include autosomal dominant (AD) STAT1 gain-of-function (GOF), a complex and heterogeneous PID in which CMC is one of the first features observed and is common to most patients, and often severe (Okada et al. 2016; Puel et al. 2012; Olbrich and Freeman 2018; Depner et al. 2016; Toubiana et al. 2016; Boisson-Dupuis et al. 2012; Engelhardt and Grimbacher 2012; Liu et al. 2011). It is frequently associated with other infectious diseases, typically mucocutaneous bacterial, viral, or fungal diseases, and less frequently with invasive infectious diseases, autoimmune manifestations, and oro-esophageal squamous cell carcinoma (Li et al. 2017; Lanternier et al. 2013a; Puel et al. 2010a, 2012; Eyerich et al. 2010; Depner et al. 2016; Toubiana et al. 2016; Boisson-Dupuis et al. 2012; Liu et al. 2011; van de Veerdonk et al. 2011). Another such PID is hyper-IgE syndrome (HIES), another complex PID characterized by severe skin and pulmonary staphylococcal disease, severe eczema, high serum IgE levels, and some developmental abnormalities (Olbrich and Freeman 2018; Zhang et al. 2018). It may be AD due to heterozygous-dominant negative mutations of the gene encoding the transcription factor STAT3 (Paulson et al. 2008; Minegishi 2009; Minegishi et al. 2007; Holland et al. 2007), or autosomal recessive (AR) due to bi-allelic loss-of-function (LOF) mutations of the gene encoding another transcription factor, Zinc Finger Protein (ZNF)341 (Frey-Jakobs et al. 2018; Beziat et al. 2018). About 80% of patients develop oral thrush, onychomycosis, and/or vaginal candidiasis. CMC is also frequent and the only infectious disease common to most patients with AR autoimmune polyendocrine syndrome type 1 (APS-1, also called APECED, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy). This syndrome is characterized by multi-organ autoimmunity due to bi-allelic mutations of the gene encoding the transcription factor *AIRE* (Husebye et al. 2009; Constantine and Lionakis 2019; Ferre et al. 2016). Other PIDs in which CMC is milder or less frequent (25–35%) include AR ROR γ / γ T deficiency, characterized by disseminated BCG diseases (Okada et al. 2015), AR IL-12p40 and IL-12R β 1 deficiencies, characterized by a selective predisposition to mycobacterial and *Salmonella* diseases (Rosain et al. 2019; Bustamante et al. 2014; Ouederni et al. 2014), and AR CARD9 deficiency, generally characterized by invasive

fungal diseases (Corvilain et al. 2018; Glocker et al. 2009; Lanternier et al. 2013b; Alves de-Medeiros et al. 2016). A final group of patients displays early CMCD in an otherwise healthy context, with the exception of mucocutaneous staphylococcal disease in some patients. This condition is often referred to as isolated CMCD (see below).

Investigations of the molecular and cellular bases of PID with syndromic CMCD suggested that IL-17A/F-mediated immunity might protect against mucocutaneous candidiasis and that CMCD might result from inborn errors of IL-17A/F immunity (Puel et al. 2010a, 2012; Kisand et al. 2011; Korn et al. 2009; Miossec et al. 2009). Indeed, all of them are characterized by impaired IL-17A/F immunity, due to abnormally low levels of circulating IL-17A/F-producing T (Th17) cells, or to the presence of autoantibodies directed against IL-17 cytokines. Indeed, patients with AD STAT1 GOF have very low proportions of Th17 cells, both ex vivo or and after differentiation in vitro (Toubiana et al. 2016; Liu et al. 2011; van de Veerdonk et al. 2011; Hiller et al. 2018; Zhang et al. 2017; Ma et al. 2016). This Th17 cell deficiency may result from enhanced/overt STAT1 signaling downstream from the STAT3-dependent IL-6, IL-21, and IL-23 cytokines, which is critical for the development and maintenance of Th17 cells (Korn et al. 2009; Miossec et al. 2009; Louten et al. 2009), enhanced STAT1 signaling downstream from IFN- α/β , IFN- γ , and IL-27, which has been shown to inhibit the development of Th17 cells via STAT1 (Guo et al. 2008; Diveu et al. 2009; El-behi et al. 2009), or both these mechanisms (Liu et al. 2011; Hirahara et al. 2010). Patients with AD HIES also have very low proportions of ex vivo and in vitro differentiated Th17 cells (Minegishi et al. 2009; Milner et al. 2008; Ma et al. 2008; de Beaucoudrey et al. 2008), due to an impairment of STAT3-dependent signaling downstream from IL-6R, IL-21R, and IL-23R (Korn et al. 2009). Similarly, patients with AR HIES and ZNF341 deficiency also have abnormally low proportions of ex vivo and in vitro differentiated Th17 cells, due to the disruption of ZNF341-dependent STAT3 transcription and activity (Zhang et al. 2018; Frey-Jakobs et al. 2018; Beziat et al. 2018). As expected, patients with AR deficiencies of ROR γ/γ T, a master transcription factor of Th17 cells (Manel et al. 2008; Ivanov et al. 2006; Yang et al. 2008a; Zhu et al. 2010), also have barely detectable levels of Th17 cells (Okada et al. 2015), and patients with IL-12p40 and IL-12R β 1 deficiencies, in whom the production of and response to IL-23 and IL-12 are abolished, also have low levels of circulating Th17 cells (Ma et al. 2016; de Beaucoudrey et al. 2008). Most, but not all of the tested patients with deficiencies of CARD9, an adaptor transducing signals downstream from C-type lectin receptors following the recognition of fungal cell wall components, have low circulating levels of Th17 cells, probably due an impairment of the induction of pro-Th17 cytokines (e.g. IL-6, IL-23)

by phagocytes after activation by fungal ligands (Corvilain et al. 2018; Glocker et al. 2009; Lanternier et al. 2013b; Wang et al. 2014b) (Fig. 1). Finally, APS1 patients, who suffer from multiple autoimmune endocrinopathies due to LOF mutations of the gene encoding AIRE, a transcription factor involved in the removal of self-reactive T cells (Finnish-German AC 1997; Nagamine et al. 1997), frequently harbor high levels of antibodies against various self-antigens (Meyer et al. 2016), including neutralizing autoantibodies directed not only against cytokines such as IFN- α and IFN- ω (Ferre et al. 2016; Meager et al. 2006) in particular, but also against Th17 cytokines, such as IL-17A, IL-17F, and IL-22 (Kisand et al. 2010, 2011; Puel et al. 2010b). These studies have paved the way for the identification of inborn errors of IL-17-mediated immunity conferring CMC in otherwise healthy individuals, or in individuals with mucocutaneous *Staphylococcus aureus* infections (Okada et al. 2016; Puel et al. 2010a, 2012).

A candidate approach identified AD IL-17F and AR IL-17RA deficiencies, each in a single family, in 2011, as the first genetic etiologies of isolated CMCD (Li et al. 2017; Puel et al. 2011). Indeed, a heterozygous private missense variation of *IL17F*, predicted to be deleterious, was identified in five relatives from an Argentinian multiplex family with early-onset CMC. The index patient had also had recurrent upper respiratory tract infections, asthma, and recurrent episodes of furunculosis since infancy. In these patients, the proportions of ex vivo IL-17A- and IL-22-producing T cells were within the control ranges, but IL-17F levels were not evaluated. The mutation was shown to impair the binding of IL-17F to its receptor, which consists of IL-17RA/IL-17RC, on the surface of control fibroblasts. Studies with control fibroblasts and keratinocytes revealed an impairment not only of the responses to mutant IL-17F homodimers, but also of that to heterodimers containing the mutant protein (IL-17A/mutant IL-17F, wild type IL-17F/mutant IL-17F), showing that the mutant IL-17F was hypomorphic and exerted a dominant-negative effect on IL-17A- or wild-type IL-17F-mediated responses (Puel et al. 2011). A second family of Tunisian-German origin has since been reported, in which a woman and her son carrying a heterozygous mutation of *IL17F* both presented CMC with an onset in early childhood, with no other infectious phenotype; the causal effect of the variant in this family has yet to be characterized (Bader et al. 2012). In parallel, AR complete IL-17RA was reported in a patient born to consanguineous Moroccan parents (Puel et al. 2011). This patient suffered from early-onset CMC and cutaneous *S. aureus* infection, and was homozygous for a nonsense mutation affecting the extracellular part of IL-17RA. Additional homozygous nonsense, missense, frameshift, splice site, and large deletion mutations have since been found in a total of 23 patients with AR IL-17RA deficiency, from 13 unrelated kindreds

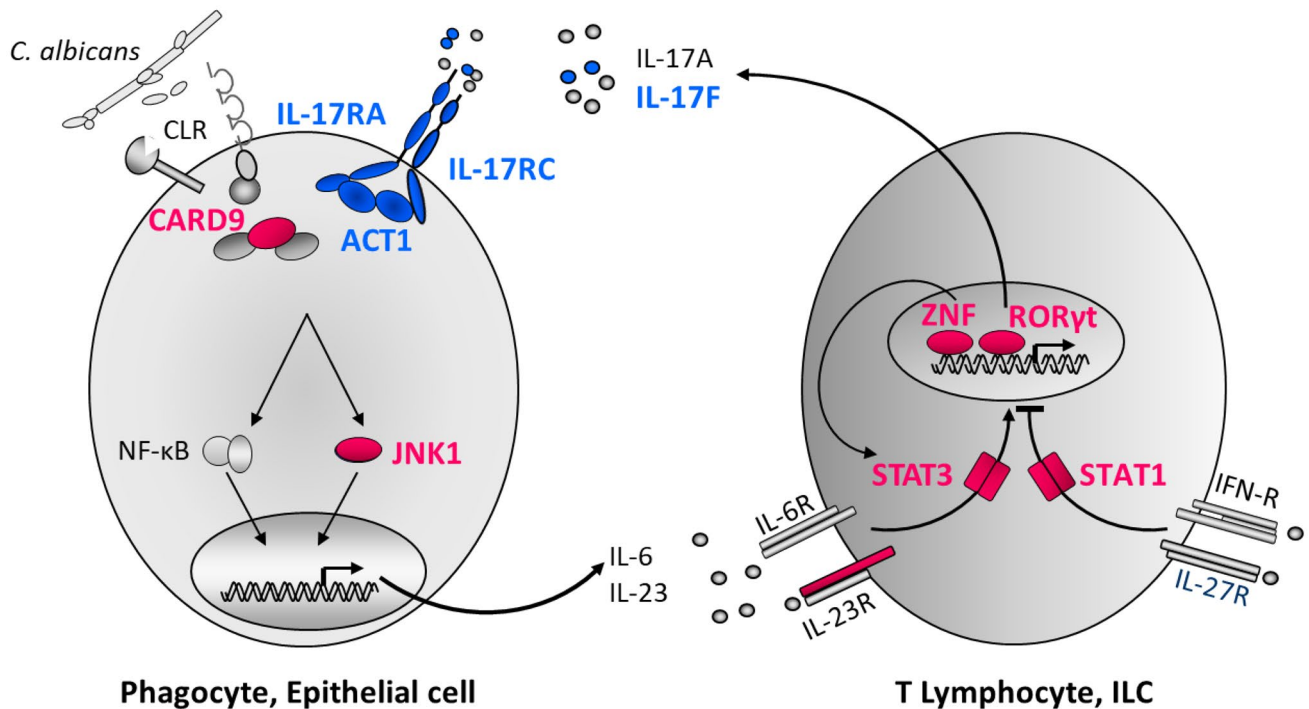


Fig. 1 Inborn errors of IL-17 immunity in patients with isolated or syndromic CMCD. Schematic representation of IL-17A/F immunity and cooperation between cells recognizing *C. albicans* and responding to IL-17A/F (phagocytes and epithelial cells), and cells producing IL-17A/F (T and innate lymphocytes). Human IL-17A/F immunity is crucial for protective mucocutaneous immunity against *C. albicans*. Proteins for which mutations in the corresponding genes underlie CMCD are shown in blue or red. Monoallelic LOF mutations of

IL17F and of *MAPK8* (encoding JNK1), and bi-allelic LOF mutations of *IL17RA*, *IL17RC* and *ACT1* impair IL-17A/F responses. Bi-allelic LOF mutations of *IL12RB1*, *RORC* (encoding RORγ/RORγT), *ZNF341*, monoallelic LOF mutations of *STAT3* and monoallelic GOF mutations of *STAT1* impair IL-17A/F production. Mutations of *IL17F*, *IL17RA*, *IL17RC* and *ACT1* underlie isolated CMCD (blue), whereas mutations of *CARD9*, *MAPK8*, *IL12RB1*, *STAT1*, *STAT3*, *ZNF341* and *RORC* underlie syndromic CMCD (in red)

originating from Morocco, Turkey, Japan, Saudi Arabia, Algeria, Argentina, and Sri Lanka (Li et al. 2017; Fellmann et al. 2016; Levy et al. 2016). All patients displayed early-onset CMC. About 70% of these patients also presented staphylococcal skin diseases, and 40% developed recurrent bacterial infections of the respiratory tract (Li et al. 2017; Puel et al. 2011; Fellmann et al. 2016; Levy et al. 2016). AR complete IL-17RC deficiency was subsequently identified by whole-exome sequencing in three unrelated patients with early-onset CMC in the absence of any other infectious phenotype, including staphylococcal disease in particular; these patients were born to consanguineous families originating from Turkey and Argentina (Ling et al. 2015). AR ACT1 deficiency is the fourth genetic defect responsible for isolated CMCD. It was identified in two siblings, born to consanguineous Algerian parents, with early-onset CMC and recurrent skin and scalp *S. aureus* disease (Boisson et al. 2013). Both patients were found to carry a homozygous missense mutation of *TRAF3IP2* encoding ACT1, which is a key downstream adapter in the IL-17 response pathway (Qian et al. 2007; Chang et al. 2006; Linden 2007). The fibroblasts of all IL-17RA-, IL-17RC-, and ACT1-deficient

patients failed to respond to IL-17A and IL-17F homodimers and heterodimers (Puel et al. 2011; Fellmann et al. 2016; Levy et al. 2016; Ling et al. 2015; Boisson et al. 2013). In addition, IL-17RA- and ACT1-deficient PBMCs, unlike PBMCs from patients with AR IL-17RC deficiency, failed to respond to IL17E/IL-25 (Levy et al. 2016; Boisson et al. 2013), which signals through IL-17RA/IL-17RB in an ACT1-dependent manner (Gaffen 2009). An AD deficiency of JNK1, a component of the MAPK signaling pathway (Johnson and Nakamura 2007; Hotamisligil and Davis 2016), was recently identified in a multiplex family originating from France with syndromic CMCD, in which three individuals from three generations presented early-onset CMC, mucocutaneous *S. aureus* infections, and a complex connective tissue disorder (Li et al. 2019). In vitro studies showed that the private *MAPK8* c.311+1G>A identified in the three patients was a loss-of-expression variant. JNK1 is involved in various signaling pathways, including the IL-17 pathway in particular (Van der Velden et al. 2012; Chang and Dong 2011; Gaffen et al. 2014). Accordingly, the fibroblasts of heterozygous patients displayed impaired cellular responses to IL-17A and IL-17F. JNK1 also acts

downstream from TGF β 1, which has been shown to participate in human Th17 differentiation in vitro (Manel et al. 2008; Volpe et al. 2008; Yang et al. 2008b). The proportions of ex vivo and in vitro differentiated Th17 cells were indeed low for these patients. This study reported a fifth genetic disorder in the IL-17 response pathway, underlying AD CMCD by haploinsufficiency, with impaired cellular responses to IL-17A/F and impaired IL-17A/F production (Fig. 1). Altogether, these five human genetic disorders demonstrate the essential role of IL-17A- and IL-17F-mediated immunity in mucocutaneous protection against *Candida* and, to a lesser extent, as found in IL-17RA-, ACT1- and JNK1-deficient patients, against disease caused by *S. aureus*. They also suggest that IL-17A- and IL-17F-dependent immunity is otherwise redundant for protection against fungi other than *Candida*, bacteria other than *S. aureus*, viruses, or even against invasive candidiasis or staphylococcal disease.

Invasive candidiasis and inborn errors of CARD9 immunity

Invasive candidiasis (IC) is defined as infections of the bloodstream (candidemia) or as deep-seated infections caused by *Candida* spp. and it ranks among the most frequent healthcare-associated bloodstream infections (Kullberg and Arendrup 2016; McCarty and Pappas 2016). Unlike CMC, patients with broad T-cell disorders are not particularly prone to IC. Furthermore, very few patients with CMC display IC, and vice versa. This suggests that T-cell dependent immunity is not essential for protection against IC and that different mechanisms are involved in immunity to superficial and invasive candidiasis. In IC, phagocytes, neutrophils in particular, but probably also, to a lesser extent, based on mouse studies, monocytes, macrophages and dendritic cells, are essential for protective immunity (Pappas et al. 2018). Indeed, IC is classically described in patients with acquired profound qualitative or quantitative disorders of neutrophils and monocytes/macrophages (Wisplinghoff et al. 2004). IC is relatively rare among patients with PID, and has been reported only occasionally in this context. Patients with severe congenital neutropenia (SCN), and mutations of *ELA2*, *HAX1*, or other genes, may develop syndromic IC. For example, IC was reported in 2% ($n=486$) of the patients from the French SCN registry (Lanternier et al. 2013a). A few patients with AR leukocyte adhesion disorder type-1 (LAD-1), due to CD18 deficiency resulting from bi-allelic mutations of *ITGB2* and leading to the impaired endothelial adhesion and transmigration of neutrophils into infected tissues, may display IC (Kuijpers et al. 2007; Fischer et al. 1988; Mellouli et al. 2010). In both cases, IC probably results from impaired neutrophil accumulation at the site of infection. Some patients with complete AR

myeloperoxidase (MPO) deficiency and concomitant diabetes, or with X-linked or AR chronic granulomatous disease (CGD) caused by mutations of genes encoding NADPH oxidase subunits and impaired oxidative burst-dependent *Candida* killing by phagocytes, may also display syndromic IC (Winkelstein et al. 2000; Lehrer and Cline 1969). Cases of deep-seated organ candidiasis have been reported in CGD patients, with central nervous system (CNS), soft tissue, lymph node, or liver diseases, and enhanced susceptibility to *C. lusitanae*, a *Candida* spp. rarely disease-causing in non-CGD patients (Estrada et al. 2006; Levy et al. 2002; Segal et al. 2000). Finally, in a large international study of patients with STAT1 GOF ($n=274$), 3.6% were reported to have syndromic IC (Toubiana et al. 2016).

Since its discovery in 2009, in a large multiplex consanguineous family from Iran with CMC and possible brain disease caused by *Candida* spp. (Glocker et al. 2009), AR CARD9 (C-type lectin receptor adaptor caspase recruitment domain-containing protein 9) deficiency has emerged as the only known inborn error of immunity conferring a selective susceptibility to fungal diseases in otherwise healthy individuals, with no other infectious or noninfectious manifestations (Corvilain et al. 2018; Drummond et al. 2018; Drummond and Lionakis 2016). Over 70% of patients with CARD9 deficiency have developed IC, with a strong tropism for the CNS. Indeed, about 80% of patients with probable or proven IC have CNS diseases, such as meningoencephalitis, brain abscesses, masses mimicking metastasis, or a combination of these manifestations (Corvilain et al. 2018; Glocker et al. 2009; Alves de-Medeiros et al. 2016; Drewniak et al. 2013; Gavino et al. 2014; Lanternier et al. 2015; Herbst et al. 2015; Gavino et al. 2016; Drummond et al. 2015; Celmeli et al. 2016; Cetinkaya et al. 2018). Strikingly, these patients present no concomitant diseases of the kidney, liver, or spleen, as typically seen in CARD9-expressing (but usually strongly immunosuppressed) infected patients, probably as a result of CARD9-independent mechanisms of protective immunity (Drummond et al. 2015). Gastrointestinal tract, bone, eye, intra-abdominal organ (liver and mesenteric LNs), or mucocutaneous surface involvement may also occur, as some patients have been reported to have severe colitis, osteomyelitis, endophthalmitis, intra-abdominal candidiasis, or CMC (Glocker et al. 2009; Lanternier et al. 2013b, 2015; Alves de-Medeiros et al. 2016; Gavino et al. 2016; Drummond et al. 2015; Rieber et al. 2016; Jones et al. 2016; Gavino et al. 2018). The onset of invasive disease is particularly variable, with a substantial proportion of CARD9-deficient patients presenting with IC as adults, with a mean age of 21.9 years [median age: 17.5 years; range (3.5–58.0 years)]. CARD9-deficient patients with CMC and/or IC have been identified in nine countries around the world (Algeria, Morocco, Iran, Turkey, Pakistan, Canada, Italy, El Salvador, and South Korea), and one patient was of mixed European origin. Of all

Candida spp., *C. albicans* is the most frequently involved in infections. It has been detected in 93% of patients, the other *Candida* spp. detected, *C. glabrata* and *C. dubliniensis*, each being found in a single patient (Corvilain et al. 2018).

CARD9, which is part of the CARD9/BCL10/MALT1 (CBM) complex, is mainly expressed in phagocytic cells, and transduces signals downstream from C-type lectin receptors (CLRs), including Dectin-1 (*CLEC7A*), Dectin-2 (*CLEC6A*), Dectin-3 (*CLEC4D*), and Mincle (*CLEC4E*), which are specific for β -glucans (Dectin-1), α -mannans (Dectin-2 and Dectin-3), and glycolipids (Mincle) from the fungal cell walls (Shiokawa et al. 2017; Perez de Diego et al. 2015). In humans, upon receptor stimulation and SYK activation, the CBM complex activates the NF- κ B, MAPK, and ERK pathways, thereby stimulating the transcription of genes encoding pro-inflammatory cytokines and chemokines, such as IL-2, IL-10, IL-12, tumor necrosis factor (TNF)- α , pro-Th17 cytokines (IL-1 β , IL-6, IL-23), granulocyte-macrophage colony-stimulating factor (GM-CSF), and CXCL1 or CXCL2 (Roth and Ruland 2013).

CARD9-deficient patients have no overt immunological phenotype: they have normal leukocyte counts; when tested, T-cell proliferation in response to mitogen or antigens is mostly normal, and the phagocyte oxidative burst, tested in vitro in the dihydrorhodamine (DHR) assay, is also normal. However, high eosinophil counts, high serum IgE levels, or both, have been observed in several CARD9-deficient patients, and the reasons for this remain unknown (Corvilain et al. 2018). CSF samples were analyzed in some patients and revealed hyperproteinorrachia, and hypoglycorrachia and pleocytosis, mostly with mononuclear cells (lymphocytes and/or monocytes) and eosinophils, but, remarkably, no neutrophils (Drummond et al. 2015) [by contrast to patients with *Candida* meningitis wild-type for CARD9, for whom neutrophils generally predominate in the CSF (Drummond et al. 2015)]. IL-17-mediated immunity was evaluated in about half the CARD9-deficient patients (with candidiasis or other fungal diseases), and was impaired in two-thirds of those tested, with no clear correlation between impaired or normal IL-17 immunity and the presence or absence of CMC (Corvilain et al. 2018). PBMCs, monocytes, and in vitro monocyte-derived macrophages or DCs tested in vitro upon stimulation with heat-killed *C. albicans* displayed impaired responses in terms of pro-inflammatory cytokine or chemokine production (Corvilain et al. 2018). A selective defect of the killing of unopsonized (but not opsonized) *C. albicans* yeasts but not hyphae by neutrophils has been reported in vitro and has been suggested to contribute to *Candida* CNS disease, due to the lower levels of opsonization in the CNS (Corvilain et al. 2018; Drewniak et al. 2013). However, a lack of neutrophil recruitment to infection sites (e.g. CNS), consistent with the absence of neutrophils from the CSF fluids of CARD9-deficient patients

with *Candida* CNS infections, contrasting with their blood neutrophil counts within the normal range, appears to be the major CARD9-dependent mechanism underlying IC in these patients (Drummond and Lionakis 2016, 2018; Drummond et al. 2015). Recently, based on *Card9*^{-/-} mouse studies, abnormally low levels of IL-1 β -dependent CXCL1 production by microglial cells following stimulation with the fungal toxin candidalysin were proposed as an explanation for the defective recruitment of neutrophils to the *Candida*-infected CNS, and impaired CNS *Candida* clearance (Drummond et al. 2015, 2019).

Conclusion

The investigation of patients with PID and syndromic CMC or IC, or of otherwise healthy patients with CMC or IC provides us with a unique opportunity to elucidate the molecular and cellular bases of these diseases and to gain insight into the pathophysiological mechanisms underlying them. The knowledge gained in the context of PID can be applied to other settings, such as hematological malignancies or AIDS, for example. The spectrum of inborn errors underlying CMC and, to a lesser extent, IC, is expanding and has already provided important insight into the role of specific immune pathways in anti-*Candida* host defense. Indeed, IL-17-mediated immunity has emerged over the last 10 years as crucial against CMC and, to a lesser extent, mucocutaneous *S. aureus* diseases. However, it seems to be redundant against IC, invasive staphylococcal diseases, and other common microbes (including fungi and bacteria). Inherited CARD9 deficiency is a genetic etiology of CMC and IC. Remarkably, *Candida* diseases can occur at any age, from early childhood to late adulthood. The adult onset seen in several CARD9-deficient patients is an uncommon feature of inborn errors of immunity and should lead clinicians to consider CARD9 deficiency in adults presenting with unexplained *Candida* diseases. Next-generation sequencing in patients with CMC or IC without inborn errors of the IL-17 pathway or CARD9 will probably reveal new genetic defects that may further elucidate the pathogenesis of *Candida* infections in patients with inborn errors of IL-17 immunity or CARD9. The comprehensive genetic dissection of *Candida* diseases (in patients with syndromic PID or in otherwise healthy individuals) should shed new light on the molecular and cellular mechanisms conferring protective immunity to *Candida* spp., and should pave the way for more rational therapies based on a better understanding of the underlying pathophysiological mechanisms. The clinical implications extend well beyond patients with fungal diseases due to inborn errors of immunity to patients with fungal diseases due to other causes.

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