

Immunogenetics of Disease-Causing Inflammation in Sarcoidosis

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Abstract Sarcoidosis is a systemic inflammatory disorder characterised by tissue infiltration by mononuclear phagocytes and lymphocytes with associated non-caseating granuloma formation. Originally described as a disorder of the skin, sarcoidosis can involve any organ with wide-ranging clinical manifestations and disease course. Recent studies have provided new insights into the mechanisms involved in disease pathobiology, and we now know that sarcoidosis has a clear genetic basis largely involving human leukocyte antigen (HLA) genes. In contrast to Mendelian-monogenic disorders—which are generally due to specific and relatively rare mutations often leading to a single amino acid change in an encoded protein—sarcoidosis results from genetic variations relatively common in the general population and involving multiple genes, each contributing an effect of varying magnitude. However, an individual may have the necessary genetic profile and yet the disease will not develop unless an environmental or infectious factor is encountered. Genetics appears also to contribute to the huge variability in clinical phenotype and disease behaviour. Moreover, it has been established that sarcoidosis granulomatous inflammation is a highly polarized T helper 1 immune response that starts with an antigenic stimulus followed by T cell activation via a classic HLA class II-mediated pathway. A complex network of lymphocytes,

macrophages, and cytokines is pivotal in the orchestration and evolution of the granulomatous process. Despite these advances, the aetiology of sarcoidosis remains elusive and its pathogenesis incompletely understood. As such, there is an urgent need for a better understanding of disease pathogenesis, which hopefully will translate into the development of truly effective therapies.

Keywords Sarcoidosis · Polymorphisms · HLA · Genetic predisposition · Genes · Phenotypes · Pathogenesis

Introduction

The existence of a genetic predisposition to sarcoidosis is supported by several lines of evidence: (1) monozygotic twins are more often concordant for the disease than dizygotic twins [1, 2]; (2) familial clustering of the disease occurs in approximately 5–16 % of patients [3]; and (3) there are striking differences in disease prevalence and clinical manifestations across different geographic areas and racial groups [4]. Linkage, candidate gene, and genome-wide association studies have identified a number of susceptibility loci with the human leukocyte antigen (HLA) class II alleles representing the main contributor to disease susceptibility across patients of different ethnicity [5]. Sarcoidosis is not a single-gene disease; instead, a multitude of genes are believed to be involved, each contributing an effect of varying magnitude. Genetics is also likely to contribute to the wide variety of clinical manifestations and prognosis observed in this disease (Fig. 1). In this regard, some believe that sarcoidosis is a “family” of different disorders, including among the others Löfgren’s syndrome, chronic/progressive lung disease, and granulomatous uveitis, each with potentially distinct genetic associations

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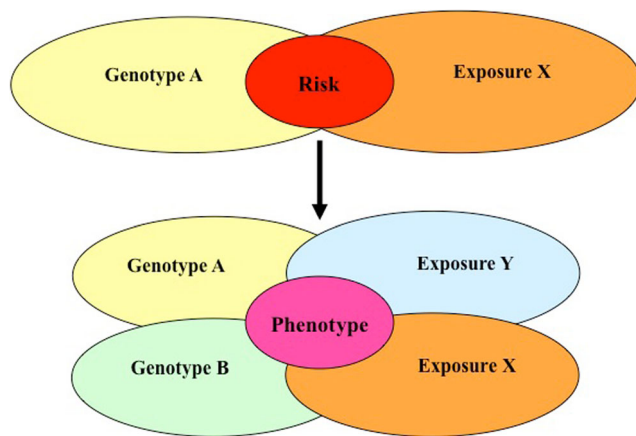


Fig. 1 Proposed model for the development of sarcoidosis. A variety of genetic variants may confer susceptibility to sarcoidosis, but the disease develops only in the context of a relevant exposure. Susceptibility genes contribute an effect of varying magnitude, depending on the function of their gene product and gene-gene interactions. The relevance of environmental exposures is likely to be influenced by their duration, intensity, timing or context. A similar model might also apply to disease phenotype

[6]. Chronic beryllium disease could also be considered as a subset of the broad grouping “sarcoidosis” and almost certainly was historically [7].

Antigen-Driven T Cell Response—the *Trimolecular Complex*

In order to elicit a granulomatous response, the sarcoid antigen/s must be processed by antigen presenting cells (APCs) (e.g. macrophages and dendritic cells), and a peptide fragment presented in the context of major histocompatibility complex (MHC) class II molecules, usually HLA-DR or HLA-DQ [8–10]. HLA molecules bind antigenic peptides within a groove composed of two α -helices and a floor of antiparallel β -strands to form a complex that is recognized by α/β^+ T cell receptor (TCR)-expressing T cells [11]. The antigen-binding properties of the MHC class II peptide-binding groove are determined by polymorphic amino acid residues that form pockets interacting with the antigenic peptide side chains. Contrary to class I molecules (HLA-A, HLA-B, and HLA-C), which present endogenous peptides of 8–10 amino acid length to CD8⁺ T cells, HLA class II molecules (HLA-DP, HLA-DQ, and HLA-DR) bind longer exogenous peptides (their peptide-binding groove is open-ended) for recognition by CD4⁺ T cells [12–14]. These peptides, which are largely derived from polypeptides that have been phagocytized or internalized by endocytosis by APCs, are loaded onto HLA class II molecules for display on the cell surface [15–17]. The MHC molecule/peptide/TCR (the “*trimolecular complex*”) [9] interaction provides the first activation signal for the antigen-specific T cells. When co-stimulatory

molecules, such as CD80 and CD86, provide a second signal, T cells are ready to orchestrate the immune response that culminates with granuloma formation [9, 18]. Indeed, lung T cells in sarcoidosis show numerous signs of (recent) activation, including reduced surface density of the CD3/TCR complex [19], IL-2 gene expression [20], spontaneous release of cytokines (e.g. interferon- γ [IFN- γ] and IL-2) [21, 22], as well as cell surface expression of HLA-DR and very late activation antigen-1 (VLA-1) [23].

The TCRs contain highly specific antigen recognition sites. The huge TCR variety for specific antigens derives from rearrangement of germ line variable (V), diversity (D), junctional (J) and constant (C) region elements of the TCR genes ($\alpha\beta$ and $\gamma\delta$). Thus, antigen-specific responses result in the expansion of a limited number of T cells bearing specific TCRs (*clonal* or *oligoclonal* expansions). The expansion of T cells exhibiting a restricted repertoire of TCR $\alpha\beta$ or $\gamma\delta$ genes in the lung, blood and skin of sarcoidosis patients strongly suggests that a limited number of peptides are responsible for the selection and expansion of these particular T cells [24–29]. The most striking example of selective TCR usage in sarcoidosis was described by Grunewald and colleagues, who demonstrated a preferential accumulation of CD4⁺ T cells expressing the TCR AV2S3 gene segment in the lung of Scandinavian patients carrying the HLA-DRB1*0301 (DR-17) allele [25, 27, 30]. A preferential AV2S3 gene usage by CD4⁺ T cells has also been observed in sarcoidosis patients carrying the HLA-DRB3*0101 (i.e. DR52a) allele [25, 30]. The HLA-DRB1*0301 and HLA-DRB3*0101 alleles share identical amino acid sequences in the regions responsible for antigen binding and probably allow presentation of similar antigenic peptides and expansion of the same T cell population. The lung-accumulated AV2S3⁺ T cells show a higher degree of activation and differentiation than other bronchoalveolar lavage (BAL)-derived CD4⁺ T cells [31–33]. Of note, selective stimulation of AV2S3⁺ T cells has been correlated with sarcoidosis of acute onset and short duration, suggesting for these cells a protective role against the putative sarcoid antigen/s [34]. Investigations on the messenger RNA (mRNA) as well as protein level demonstrated that the AV2S3⁺ T cells have a very low expression of the T regulatory cell transcription factor forkhead box P3 (FoxP3), indicating that they are effector rather than regulatory cells [32, 33, 35]. This is confirmed by the demonstration that they produce T helper (Th) 1 cytokines [32]. Thus, they may act to eliminate a specific antigen, leading to disease resolution. After clinical recovery, the number of CD4⁺AV2S3⁺ cells in the BAL of sarcoidosis patients tends to normalise [36]. While the majority of studies have demonstrated overexpression of α/β TCR genes [37], an increased number of γ/δ^+ TCR T lymphocytes has also been observed in the blood and BAL from patients with sarcoidosis [38]. The γ/δ TCR is potentially relevant to sarcoidosis as γ/δ^+ T cells from normal individuals respond to mycobacterial heat shock

proteins, and mycobacterial products are thought to play a role in at least a subset of sarcoidosis cases [39]. In addition, V δ 1⁺ T cells are clonally expanded in pulmonary sarcoidosis consistent with the concept that the disease results from persistent, specific antigenic (exogenous and/or self) stimulation that induce a cell-mediated immune response [29].

The Early Years

Because of the highly polymorphic nature of the HLA genes and the requirement for HLA molecules in the presentation of antigens to T cells, the search for HLA associations with sarcoidosis has been the focus of several studies. Hedfors and Möller initially reported an increased frequency of HL-A7 (now HLA-B7) in sarcoidosis patients ($n=50$) compared to controls ($n=100$) [40]. This was in contrast to Kueppers and colleagues, who analysed 132 patients and 600 controls but found no significant associations between HL-A antigens and sarcoidosis [41]. However, a couple of years later, HLA-B7 was found to associate with sarcoidosis, this time in a South Carolina Black population (28 patients vs 80 controls) [42]. HLA-B7 is now known to belong to a haplotype common in Caucasians, i.e. HLA-A*0301: B*0702: Cw*0701: DRB1*1501: DQA1*0102: DQB1*0602, which has at least in part been found to associate with a more chronic form of sarcoidosis [43]. In 1981, Smith and colleagues identified a link between carriage of HLA-B8 and spontaneous resolution and suggested that inherited factors relating to the immune system may influence the clinical phenotype of sarcoidosis [44]. This concept was further substantiated in a study by Hedfors and Lindström, who HLA-typed 19 sarcoidosis patients with an acute onset, bilateral hilar lymphadenopathy, ankle joint arthritis, and (in seven of them) also erythema nodosum (this combination of signs and symptoms is commonly referred to as Löfgren's syndrome; Fig. 2). The authors found a strong association with HLA-B8/DR3 and concluded that such a strong association might be explained by an “immunogenetically determined handling of a postulated etiological antigen” [45]. Gardner and colleagues identified an association between B8/Cw7/DR3 and good prognosis in Caucasian but not black West Indian patients [46]. Krause and co-workers studied 42 sarcoidosis patients with arthritis and 134 ethnically matched controls and found a strong association with HLA-DR3 [47]. The authors proposed that genetic factors must be considered together with a postulated triggering antigen in sarcoidosis [47].

Modern Times

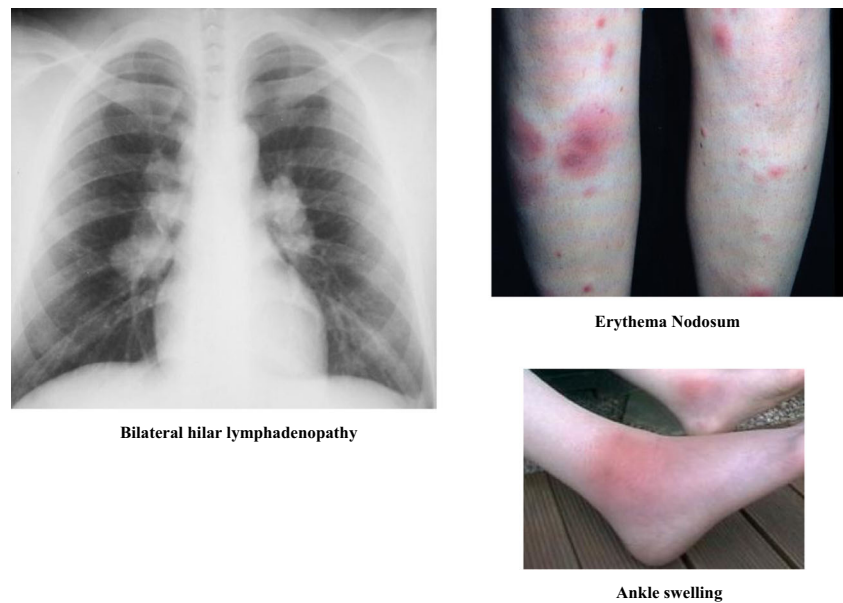
Although the HLA allele distribution significantly differs across ethnic populations, subsequent studies, using more

specific tools for HLA analysis and more rigorous disease definitions, have shown that certain HLA class II alleles associate with disease protection/risk across different populations. Specifically, HLA-DRB1*01 and DRB1*04 protect against disease in several Caucasian populations, while DRB1*03, DRB1*11, DRB1*12, DRB1*14 and DRB1*15 are risk factors for sarcoidosis [5, 7].

A number of studies have also confirmed the HLA-B8/DR3 association with Löfgren's syndrome (LS) [48]. In addition to displaying distinct clinical manifestations, patients with LS can be further characterized according to the carriage of DRB1*03. Among LS patients in Sweden (where two thirds of them carry the DRB1*03 allele), disease resolution (defined as disease duration <2 years) was reported to occur in 95 % of DRB1*03⁺ patients, but only in 49 % of DRB1*03⁻ [49]. Interestingly, a clustering of disease onset in January, April and May has been observed in DRB1*03⁺ but not DRB1*03⁻ patients, suggesting a key role for season-specific antigens in the development of LS. The mechanisms through which DRB1*03 influence disease behaviour in LS is unknown. However, DRB1*03⁺ patients display a less pronounced Th1-type immune response with reduced levels of IFN- γ and tumor necrosis factor (TNF)- α [50], yet they may be able to mount a more effective and specific immune response against the postulated antigen/s [32]. Such an efficacious immune response includes lung accumulation of Th cells with expression of a specific TCR (AV2S3) [27] and production of several Th1 cytokines when stimulated with a specific mycobacterial antigen (mKatG) [32].

HLA-B8/DR3 is known to be part of the so-called 8.1 ancestral haplotype (HLA A*0101: B*0801: Cw*0701: DRB1*0301: DQA1*0501: DQB1*0201) which is quite common in Caucasians. Besides HLA, this haplotype includes or is linked to a large number of non-HLA genes of critical importance for the immune system. Sarcoidosis associations with class I genes were originally considered to be caused by linkage disequilibrium (LD) (e.g. the tendency for genetic variants located close to each other on the same chromosome to be associated within a population more often than if they were unlinked) with class II genes [7]. However, multiple logistic regression analysis revealed that both HLA-B7 and HLA-B8 increase the risk of sarcoidosis independently of class II genes [43]. Moreover, patients with the common allele combination HLA-A*3, B*07, DRB1*15 have been shown to be at significantly higher risk of developing chronic disease. Another common haplotype (HLA-A*01, B*08, DRB1*03), which is present in approximately 20 % of Swedish sarcoidosis patients, is associated almost invariably with resolving disease in Sweden [43] as well as with LS in Croatian sarcoidosis patients [51]. HLA class I alleles may thus have more influence on disease susceptibility and behaviour than previously thought (43, 51; Fig. 3). As seen above, HLA-DQB1 alleles are also linked to various HLA-DRB1 alleles, and in African

Fig. 2 Clinical manifestations of Löfgren's syndrome



Americans, HLA-DQB1 alleles were suggested to be more important for sarcoidosis associations than DRB1 alleles [52]. In particular, carriage of HLA-DQB1*0201 was found to be protective against the disease, while DQB1*0602 was linked to radiographic progression [10].

Pockets

The peptide-binding groove of the HLA class II molecule consists of two α -helices, making up the walls of the groove, and a β -pleated sheet that constitutes the floor of the groove. Depending on the amino acids within the groove, different peptides will be bound. As such, certain amino acids at distinct positions may have a greater influence in antigen binding than others. In chronic beryllium disease, for example, there is a strong association between glutamic acid (Glu) at position 69, found primarily on HLA-DPB1*0201, and reactivity against beryllium and subsequently disease [53, 54]. The nature of the peptide(s) that in addition to beryllium binds to the HLA-DP molecule has recently started to be investigated [55, 56]. In the peptide-binding groove of the HLA molecule, a number of pockets are formed (P1, P4, P5, P7 and P9). Side chains of the amino acids may dig into the HLA molecule to improve anchoring of the peptide. In sarcoidosis, pockets number 4, 6 and 7 appear to be important for interacting with potential sarcoidosis-associated peptides. Foley and colleagues described that the protective DRB1*01 and DRB1*04 molecules have in common small hydrophobic residues at position 11 of antigen binding pocket 6, while non-protecting DRB1 molecules had instead hydrophilic residues at the same position [8]. Position 11 contains the only variable

amino acid in pocket 6 and may influence substantially the binding capacity of the pocket. In a similar approach, Voorter and co-workers studied 149 Caucasian patients to search for distinct amino acids within the antigen-binding parts of DRB1 and DQB1 molecules and their associations with sarcoidosis risk. The patients were divided into those with a good prognosis (i.e. chest radiographic stage I) and those at risk for a more chronic disease (i.e. chest radiographic stage II–IV) [57]. The authors found the DRB1 residues Pro11, Arg13, Ser37 and Ala71 associated with both disease overall and chronic disease. Interestingly, all four residues are found on DRB1*1501. In addition, Ala71, which is part of the peptide binding pocket 4, allows preferential binding of non-charged aromatic residues and thereby specifically influences the HLA-bound peptide repertoire. Moreover, a HLA-DR Arg74 residue was found significantly more often in patients with radiographic stage I and good prognosis. DR Arg74 is also part of pocket 4 and is found almost exclusively on DRB1*0301, which is associated with good prognosis [58]. Arg74 determines the preferential binding of aspartic acid in pocket 4 of the DR molecule. Interestingly, DRB1 pocket 4 was also shown to be a common denominator for two different HLA molecules, both with a unique association with lung accumulated T cells expressing the AV2S3 TCR, further indicating specific antigenic peptide recognition by these cells in the lungs of sarcoidosis patients [30]. Pocket 7 has also been suggested to be important for association with sarcoidosis and for binding of specific peptides. In the US ACCESS study, HLA-DRB1 amino acid residue at position 47 (F⁴⁷), which is located in pocket 7, appeared to independently contribute to the risk of sarcoidosis in white American patients [59]. Of note, HLA-DRB1-F⁴⁷ was present on the three alleles most

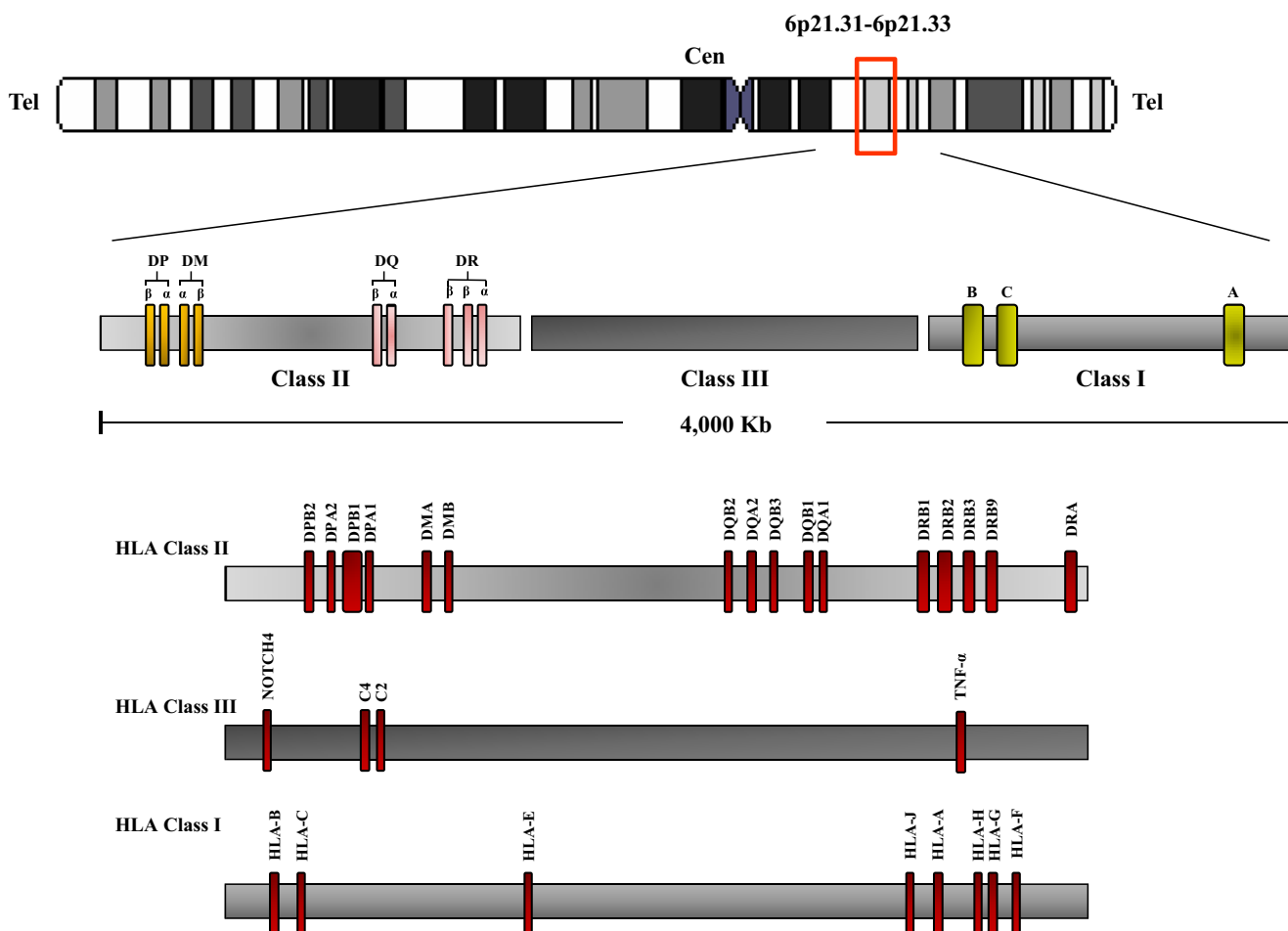


Fig. 3 Gene map of the human leukocyte antigen (HLA) region. The HLA region spans approximately 4×10^6 nucleotides on chromosome 6p21.31–6p21.33, with class II, class III and class I genes located from the centromeric (Cen) to the telomeric (Tel) end. HLA class I molecules mediate immune responses against *endogenous*, whereas class II

molecules are involved in the presentation of *exogenous* antigens to T helper cells. The HLA class III region contains a number of genes involved in immune response regulation, including tumour necrosis factor (TNF)- α and complement proteins (C2, C4)

strongly associated with sarcoidosis, namely DRB1*1101, DRB1*1201 and DRB1*1501 [59].

Studies of Today

Wennerström and colleagues recently studied 188 patients and 224 controls in Finland and confirmed DRB1*1501 to be a risk factor for and DRB1*0101 to be protective against sarcoidosis [60]. While in contrast to previous studies DRB1*15 was not found to associate with persistent disease in Finnish patients, the authors confirmed a strong association between DRB1*0301 and good prognosis, particularly in patients without extra-pulmonary manifestations. Detailed analysis of HLA class II pockets revealed specific amino acid residues in pockets 4, 7 and 9 to associate with disease course; in particular, the amino acid at residue 71 of pocket 4 associated with disease prognosis.

Sato and colleagues studied 340 UK, 139 Dutch and 163 Japanese patients, and 354, 218 and 168 matched controls, respectively. In common for all three populations was the protective effect of HLA-DRB1*01 with a similar tendency for DRB1*04 in the Caucasian populations [61]. In addition, DRB1*12 associated with disease in UK and Dutch patients with a similar trend observed in Japanese patients, whereas DRB1*14 associated with disease only in Caucasian patients. Uveitis associated with DRB1*0803 in the Japanese population and with DRB1*04 in the UK population, while it was too rare amongst Dutch patients to provide meaningful results. In the Japanese cohort, DRB1*0803 was also significantly associated with neurosarcoidosis. The Dutch cohort was the only one that included a substantial proportion of patients with LS, again strongly associating with DRB1*03, as shown before in several reports [58]. The authors however found no particular amino acid position to associate with overall disease, pulmonary disease, LS or uveitis. More recently, Suzuki and colleagues studied 237 Japanese patients and

287 matched controls for any DRB1 or DQB1 allele associations; DRB1*0803 and DRB1*0901 were identified as risk alleles, irrespective of disease onset or phenotype [62]. Zhou and co-workers have recently reported in a study of 131 Chinese Han patients and 122 controls an association between HLA-DRB1*11 and disease risk, while DRB1*07 and HLA-B*13 were protective [63]. Of note, DRB1*11 confers susceptibility to sarcoidosis also in Indian [64] and Japanese patients [65]. Moreover, in the ACCESS study the HLA-DRB1*1101 allele associated with disease in both black and white American patients [59]. Finally, it is noteworthy that HLA-DRB1*11 has been found to associate with antigen presentation of distinct mycobacterial derived antigens ESAT-6 and mKatG [66], which have been proposed as sarcoidosis antigens [67].

HLA-Type in Relation to Phenotypes

Some HLA-DRB1 alleles influence clinical phenotype and disease behaviour. The best example is probably Löfgren's syndrome, which in several reports has been shown to associate with a benign disease course [45, 49, 51]. In Sweden, the influence of DRB1*03 on disease course is so strong that it is now used as a biomarker of good prognosis [68]. On the other hand, HLA-DRB1*15 has been suggested to predispose to a chronic form of the disease [69–71]. Sarcoidosis uveitis has been shown to associate with DRB1*0401 in the ACCESS study, in both black and white Americans [59]. Similarly, DRB1*0401 is a risk factor for uveitis in Japanese and UK subjects [61], as well as in Scandinavian patients in whom DRB1*0401 homozygosity confers a substantially increased risk for uveitis [72]. Although very few, patients with Heerfordt's syndrome—characterized by fever, parotid or

salivary gland enlargement, cranial nerve palsy and uveitis—were also shown to associate with DRB1*0401 [72]. On the other hand, lung-predominant sarcoidosis was found to associate with DRB1*12 and DRB1*14 [57]. Cardiac sarcoidosis is associated with HLA-DQB1*0601 in Japanese patients [73]. Finally, HLA-DQB1*0602, which is in strong LD with DRB1*1501, has been shown to associate with splenomegaly in Japanese patients [74], and with small fibre neuropathy in Caucasians [75]. HLA associations with sarcoidosis are summarized in Table 1.

Conflicting results with regard to HLA associations have many plausible explanations, besides the well-known interethnic differences between study populations. Patient sampling and other methodological aspects may also affect the results and complicate data evaluations. Further, it is likely that a diagnosis of “sarcoidosis” covers several distinct disease entities, each with their own separate genetic association and exposure history.

Other Genetic Associations with Sarcoidosis

A number of non-HLA genes have also been associated with risk of disease or phenotype (5, 7; Table 2). One example is the finding of a sarcoidosis risk variant within the *butyrophilin-like 2 (BTNL2)* gene [62, 80, 85–92]. BTNL2 is structurally similar to the co-stimulatory molecule CD80 (B7-1) but in contrast to CD80 it is believed to act as an inhibitory molecule for T cells. Accordingly, defective BTNL2 function might result in an exaggerated T cell activation. Another example is *annexin A11 (ANXA11)* [80–84]. The functional relevance of the risk variant detected in sarcoidosis patients is not known, but it has been proposed that it may affect the survival of inflammatory cells. Other reported genetic associations

Table 1 Summary of HLA associations with sarcoidosis

Gene	Association	References
HLA-A3, HLA-B7	Risk factor for disease and associates with prolonged disease	[42, 43]
HLA-A1, HLA-B8	Risk factor for disease and associates with arthritis and with good prognosis	[43–46]
HLA-DRB1*01	Protective against disease	[8, 58, 61]
HLA-DRB1*0301 ^a	Risk factor for disease and associates with Löfgren's syndrome and good prognosis	[42, 45–47, 49, 51, 70, 76–78]
HLA-DRB1*04	Protective against disease and associates with ocular sarcoidosis and Heerfordt's syndrome	[58, 61, 69, 76, 79]
HLA-DRB1*0803	Risk factor for disease and associates with ocular sarcoidosis (in Japanese patients)	[61]
HLA-DRB1*1101	Risk factor for disease	[58, 59]
HLA-DRB1*12	Risk factor for disease	[59, 61]
HLA-DRB1*14	Risk factor for disease and associates with prolonged disease	[58, 69]
HLA-DRB1*15 ^b	Risk factor for disease and associates with prolonged disease	[59, 70]
HLA-DRB3*1501	Risk factor for disease and associates with Löfgren's syndrome	[59, 71]
HLA-DRB3*0101	Risk factor for disease and associates with disease progression	[77]

^a In strong LD with HLA-DQB1*0201

^b In strong LD with DQB1*0602

Table 2 Selected non-HLA candidate gene associations with sarcoidosis

Candidate gene, location	Variant	Association	References
ANXA11, 10q22.3-q23.1	rs1049550	Susceptibility to sarcoidosis	[80–84]
BTNL2, 6p21.3	rs2076530 A/G	Susceptibility to sarcoidosis	[62, 80, 85–92]
CCDC88B, 11q13.1	rs479777	Susceptibility to sarcoidosis	[93]
CCL5/RANTES, 17q.12	5' Flanking region between nucleotide -513 and -378	Organ involvement (≥ 3 organs)	[94]
CCR5, 3p21.31	Haplotype HHC	Female-specific association with Löfgren's syndrome	[95]
CD14, 5q31.1	-159 C/T (rs2569190)	Susceptibility to sarcoidosis and milder disease	[96]
C10ORF67, 10p12.31	rs1398024	Susceptibility to sarcoidosis	[97]
GREM1, 15q13-q15	rs1919364 C/G	Risk factor for pulmonary fibrosis	[98]
IL7R, 5p13	rs10213865 A/C	Susceptibility to sarcoidosis; similar trend observed in patients with Löfgren's syndrome	[99]
IL23R, 1p31.3	rs11209026 G/A; rs7517847 G/T; rs11465804 T/G	Susceptibility to chronic sarcoidosis; susceptibility to sarcoidosis and sarcoid uveitis	[100, 101]
ITGAE, 17p13.3-13.2	-1088 A/G (rs2891)	Susceptibility to sarcoidosis and risk factor for pulmonary fibrosis	[102]
MMP9, 20q11.2-q13.1	-1702 T/A	Susceptibility to sarcoidosis	[103]
MRC1/CD206, 10p12.33	rs691005 T/C	Susceptibility to sarcoidosis	[104]
MyD88, 3p22	-938 C/A (rs4988453)–1944 C/G (rs4988457) haplotype	Susceptibility to sarcoidosis	[105]
NOTCH4, 6p21.3	rs715299	Susceptibility to sarcoidosis	[80]
OS9, 12q13.3-q14.1	rs1050045	Susceptibility to sarcoidosis	[106]
PTGS2/COX2, 1q25.2-q25.3	-765 G/C (rs6681231)	Susceptibility to sarcoidosis and risk factor for pulmonary fibrosis	[107–109]
RAB23, 6p11	rs1040461	Susceptibility to sarcoidosis	[80, 109]
TGF- β 1, 19q13.1	-509 C/T (rs1800469), codon 10 T/C (rs1982073)	Sarcoidosis severity	[110]
TGF- β 2, 1q41	rs1891467 A/G	Acute/self-limiting disease (vs. patients with chronic disease)	[111]
TGF- β 3, 14q24	4875 G/A (rs3917165)	Risk factor for pulmonary fibrosis	[112]
TLR10-TLR1-TLR6, 4p14	Common haplotype encompassing the TLR10-TLR1-TLR6 gene cluster	Protection from chronic sarcoidosis	[113]
TLR9, 9q33.1	-1237 T/C (rs5743836)	Risk factor for chronic sarcoidosis	[114]
TNF- α , 6p21.3	-308 G/A (TNFA1/TNFA2; rs1800629), -857 C/T (rs1799724)	Susceptibility to Löfgren's syndrome and erythema nodosum; susceptibility to sarcoidosis	[115–119]
VDR, 12q13.11	BB/Bb/bb genotypes	Susceptibility to sarcoidosis	[120]
VEGFA, 6p12	813 C/T (rs3025039)/VEGFA haplotype	Protection from sarcoidosis; susceptibility to acute disease	[121–123]
VEGFR1, 13q12	VEGFR1 haplotypes	Susceptibility to sarcoidosis	[123]
VEGFR2, 4q11-q12	VEGFR2 haplotypes	Acute and chronic disease course	[123]

This table only includes either validated associations or positive associations awaiting confirmation

ANXA11 annexin A11, *BTNL2* butyrophilin-like 2, *CCDC88B* coiled-coil domain containing 88B, *C10ORF67* chromosome 10 open reading frame 67, *GREM1* gremlin 1, *ITGAE* integrin alpha(E)beta[7], *MMP9* metalloproteinase 9, *MRC1* mannose receptor gene 1, *MyD88* myeloid differentiation marker 88, *NOTCH4* neurogenic locus notch homolog protein 4, *OS9* osteosarcoma amplified 9, *PTGS2* prostaglandin-endoperoxide synthase 2, *RAB23* Ras-related protein Rab-23, *RANTES* regulated on activation, normal T cell expressed and secreted, *TGF- β 1* transforming growth factor β 1, *TLR* Toll-like receptor, *TNF- α* tumor necrosis factor- α , *VDR* vitamin D receptor, *VEGFA* vascular endothelial growth factor A, *VEGFR* vascular endothelial growth factor receptor

include, amongst others, the cytokines TNF and transforming growth factor (TGF)- β , and the IL-23 receptor, as well as different Toll-like receptor (TLR) genes (Table 2). Several of these gene variants are not unique to sarcoidosis, but associate also with other inflammatory disorders [6].

Immunopathogenesis of Sarcoidosis Granulomatous Inflammation

Granuloma formation is regarded as a means of defending the host from persistent irritants of either exogenous or endogenous origin. In fact, the causative agent is walled off and sequestered

by cells of macrophage lineage allowing it to be contained, if not destroyed altogether [124]. However, these cells may also prime the adaptive immune system by displaying foreign antigens on the surface of MHC class I or II molecules. Depending on both pathogen and host factors, the adaptive immune response is usually dominated by either a type 1 T helper (Th1), Th2 or Th17 cell response [125, 126]. Sarcoidosis is mediated by a predominantly Th1 immune response in which a complex network of lymphocytes, macrophages, cytokines and chemokines mount an immune response that culminates with granuloma formation ([127]; Table 3). In experimental models, granulomatous inflammation is downregulated with clearance of antigen [128]. Conversely, if the antigen persists, continuing activation of T cells leads to further accumulation of macrophages, which can give rise to epithelioid cells (large cells with a pale nucleus and

abundant cytoplasm) or fuse to form giant multinucleated cells [129]. Macrophages are integral in both formation of granuloma and in promoting a Th1 immune response. The initial triggering of macrophages occurs via activation of so-called pattern-recognition receptors, recognizing evolutionary conserved molecular patterns of different classes of pathogens. The best characterized family of such receptors are TLRs. Enhanced or altered responses to TLR2 stimulation have been observed in cells from the lung and blood of sarcoidosis patients [130–132]. TLR2 has also been demonstrated to have a role in granuloma formation, both in animal models [130, 132] and in a human in vitro model of mycobacterial granulomas [133]. A critical role for aggregates of the acute-phase reactant serum amyloid A (SAA) to regulate granuloma formation in sarcoidosis has been proposed by Moller and colleagues; they found SAA to be expressed to a much

Table 3 Characteristics of cytokines and chemokines involved in sarcoidosis granulomatous inflammation

Cytokine name	Source	Biological role
Interferon- γ (IFN- γ)	Th1 cells	Activator of macrophages; inducer of differentiation of naive CD4 ⁺ lymphocytes toward a Th1 phenotype; regulator of granuloma induction; inhibitor of fibroblast proliferation
Tumor necrosis factor- α (TNF- α)	Macrophages, but also T cells, natural killer (NK) cells, and neutrophils	Adhesion molecule up-regulator; inducer of CD4 ⁺ T cell proliferation and survival; mediator of granuloma formation and maintenance
Transforming growth factor- β (TGF- β)	Several cell types, including macrophages	Inhibitor of lymphocyte activation and cytokine release by macrophages
Interleukin (IL)-1 β	Macrophages, but also dendritic cells and endothelial cells	T cell chemoattractant; activation cofactor following antigen presentation; adhesion molecule up-regulator; modulator of Treg function
IL-2	Th1 cells	Autocrine inducer of T cell proliferation and survival
IL-6	Mononuclear phagocytes, endothelial cells, fibroblasts	Inducer of B cell differentiation and antibody secretion; inhibitor of regulatory T cell differentiation
IL-12	Macrophages, B cells	Inducer of Th1 differentiation and IFN- γ production; mediator of granuloma formation
IL-15	Epithelial cells, fibroblasts, monocytes	Inducer of T cell proliferation; mediator of granuloma formation and maintenance
IL-18	Macrophages and dendritic cells	Inducer of Th1 differentiation and IFN- γ production
IL-27	Macrophages and dendritic cells	Inducer of T cell differentiation and activation and IFN- γ production (in synergy with IL-12)
Granulocyte macrophage colony-stimulating factor (GM-CSF)	Alveolar macrophages, but also T cells, mast cells, NK cells, endothelial cells and fibroblasts	Inducer of alveolar macrophage proliferation and differentiation. Inducer of the fusion of alveolar macrophages to multinucleated giant cells
Chemokine name	Receptor	Target cells
CCL2 (monocyte chemoattractant protein 1 (MCP-1))	CCR2	Monocytes
CCL3 (macrophage inflammatory protein 1 α (MIP-1 α))	CCR1, CCR5	Neutrophils and monocytes
CCL5 (regulated on activation, normal T cell expressed and secreted (RANTES))	CCR1, CCR3, CCR5	T cells, eosinophils
CCL19 (macrophage inflammatory protein 3 β (MIP-3 β))	CCR7	Dendritic cells
CXCL8 (IL-8)	CXCR1, CXCR2	Neutrophils
CXCL9 (monokine induced by IFN- γ (MIG))	CXCR3	Th1 cells
CXCL10 (IFN-inducible protein-10 (IP-10))	CXCR3	Th1 cells

higher degree in sarcoid granulomas than in granulomas in other diseases [130]. The same study also demonstrated that SAA stimulated BAL cells from sarcoidosis patients to a higher degree of cytokine release than cells from control subjects, partly by interaction with TLR2, and also promoted experimental Th1-mediated granulomatous inflammation. Macrophages exert their effects mainly by producing a number of chemokines and cytokines, such as CCL2 (monocyte chemotactic protein 1 (MCP1)), CCL3 (macrophage inflammatory protein-1 α (MIP-1 α)), CCL4 (macrophage inflammatory protein-1 β (MIP-1 β)), CCL5 (regulated on activation, normal T cell expressed and secreted (RANTES)), IL-8, IL-12, IL-15 and IP-10 [134]. In addition, macrophages produce IL-1, IL-15 and TNF- α , which induces endothelial cell-T cell interaction by up-regulating the expression of adhesion molecules on the endothelium [135]. TNF- α is a critical mediator of granuloma formation and maintenance through induction of CD4⁺ T cell proliferation and survival. In active pulmonary sarcoidosis, alveolar macrophages spontaneously release TNF [136], and higher levels of this cytokine have been observed in patients with severe/progressive disease compared with those with inactive disease [137]. The mechanisms responsible for the evolution of sarcoid granulomas to fibrosis are poorly understood but abnormal apoptotic-signalling pathways, loss of regulatory response as well as the development of a more Th2-like environment are likely to be involved (136; Table 4).

Table 4 Key stages in granuloma formation

- Initial activation of macrophages by ligand binding to pattern-recognition receptors, such as Toll-like receptors (TLRs), followed by release of soluble mediators
- Recognition of MHC class II bound antigen on antigen-presenting cells (APC) by T cells and subsequent activation of the CD4⁺ lymphocyte subset via the T cell receptor (TCR)
- Oligoclonal proliferation of CD4⁺ T cells with expression of Th1 cytokine profile (e.g. IL-2 and IFN- γ)
- Macrophage/T cell interaction via antigen presentation by macrophages to T cells and intercellular signalling (such as T-cell-derived IFN- γ further activating macrophages) leading to proliferation, activation and spontaneous cytokine release by both cell lines at sites of inflammation
- Amplified release of macrophage-derived cytokines TNF- α , IL-1, IL-6, IL-12, IL-15; chemokines IL-8, CCL5 (regulated on activation, normal T cell expressed and secreted (RANTES)), CCL2 (monocyte chemotactic protein (MCP-1)), CCL3 (macrophage inflammatory protein-1 α (MIP-1 α)), and granulocyte-macrophage colony-stimulating factor (GM-CSF)
- Fibrosis associated with shift to Th2 cytokine profile, up-regulation of macrophage-derived fibrogenic cytokines (TGF- β , PDGF and IGF-1), and increased production of neutrophil protease products
- Disturbance of programmed cell death (apoptosis) by dysregulation of the TNF-L/TNF-R superfamily, abnormal expression of oncogene products and change in Th1/Th2 ratio

IFN: interferon; IGF: insulin-like growth factor; MHC: Major Histocompatibility Complex; PDGF: platelet-derived growth factor; TGF: transforming growth factor; TNF: tumor necrosis factor

Sarcoidosis Antigens

A mycobacterial aetiology of sarcoidosis has long been proposed, based on clinical and histological similarities with tuberculosis. Evidence for the presence of mycobacteria in sarcoidosis lesions have been obtained by PCR, and a meta-analysis of 31 such studies found that the odds of detecting mycobacterial nucleic acids were at least ten times higher in sarcoidosis tissues compared to control tissues [138]. Using a mass spectrometry approach to analyse sarcoidosis tissues, a specific mycobacterial protein, catalase-peroxidase (mKatG), was found to be present in a majority of sarcoidosis samples and to be the target of B cell responses in half of the patients [67]. Other studies have also found evidence of specific mycobacterial proteins in sarcoidosis tissue [139, 140]. Sarcoidosis patients have been found to harbour blood and lung T cell responses to mycobacterial proteins, including mKatG, ESAT-6, antigen-85A and heat shock proteins [141–144]. A preferential stimulation by mKatG of the TCR AV2S3⁺ T cells which accumulate in the lungs of HLA-DRB1*03⁺ patients has been reported (32; Fig. 4). Propionibacterial aetiology has also been proposed, although it remains more controversial. In support of this aetiopathogenetic hypothesis is the presence of propionibacterial DNA in sarcoidosis tissues [145] and cellular immune responses to *Propionibacterium acnes* in a subset of sarcoidosis patients [146]. It is plausible that there is not one single aetiological agent in sarcoidosis, but that different environmental agents, including non-organic substances, may lead to sarcoidosis granulomatous inflammation [147]. In an effort to directly identify the antigenic peptides presented by HLA molecules on antigen-presenting cells in the lungs of sarcoidosis patients, Wahlström and colleagues analyzed by liquid chromatography-mass spectrometry BAL cells from 16 HLA-DRB1*0301⁺ sarcoidosis patients and identified a number of peptides bound to the HLA-DR molecules, including peptides derived from well-known autoantigens such as vimentin and ATP synthase [148]. In a follow-up study, a prominent T cell response to vimentin was found in peripheral blood of a subset of patients having the same HLA type [149]. Thus, at least in some patients, autoimmunity may contribute to the inflammation in sarcoidosis. One possible explanation for such responses, which may be chronic or transient, is “molecular mimicry” with pathogen-derived molecules breaking tolerance to self-antigens.

Th1 Polarization

An established immunologic feature of sarcoidosis is that the CD4⁺ lymphocytes that trigger granuloma formation are strongly Th1 polarized. Indeed, the expression of both IFN- γ —a cytokine produced by Th1 cells—and a number

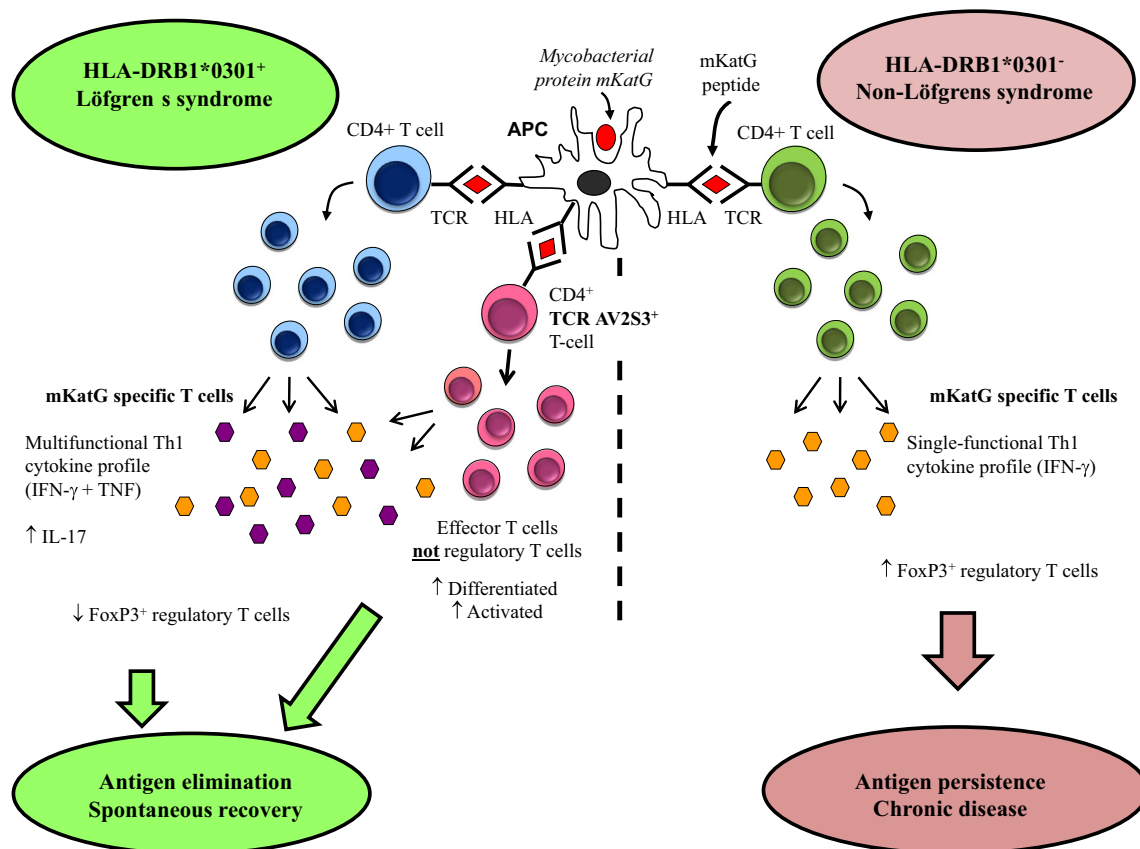


Fig. 4 Proposed model of how qualitative differences in T cell responses to the mycobacterial protein mKatG may promote distinct clinical outcomes in patient subgroups. In HLA-DRB1*0301⁺ patients, mKatG-specific T cells have the ability to produce a multifunctional Th1 cytokine profile (IFN- γ and TNF). Reduced expression of T regulatory cell transcription factor FoxP3 in AV2S3⁺ T cells suggests an effector rather than a regulatory function for this T cell subset, leading to eradication of

the inciting antigen and disease resolution. Conversely, in HLA-DRB1*0301⁻ patients, mKatG-specific T cells produce a single-functional Th1 cytokine profile (IFN- γ), which together with increased FoxP3⁺ regulatory T cells leads to antigen persistence and chronic disease. This figure is based on the results reported in references 25, 27, 31–34, 141 and 144 (courtesy Maria Wikén)

of Th1-promoting cytokines, such as IL-12, IL-15, IL-18 and IL-27—is up-regulated at sites of sarcoidosis granulomatous inflammation [150–153]. In addition, a study of cytokine expression in lymph nodes has demonstrated a spatial rearrangement of cytokine-producing cells, with IL-1 β , TNF- α and IFN- β being localized to the granuloma itself, and other cytokines, such as IL-1 α , IL-2 and IL-6 being distributed more randomly [154].

IL-12, one of the most potent Th1-promoting cytokines, induces Th1 differentiation from naive T cells and Th1 proliferation. BAL cells from sarcoidosis patients display enhanced (spontaneous) expression of IL-12 protein and mRNA [155], with higher levels observed in individuals with active disease compared with both those with inactive disease and healthy controls [156–158]. IL-15 is a cytokine with functions similar to IL-12, and its secretion from BAL and peripheral cells is significantly higher in patients with active sarcoidosis compared with those with inactive disease and healthy controls [159]. IL-18 is essential for optimal induction of IFN- γ expression in T cells and natural killer (NK) cells [160]. IL-18

and IL-18R expression is increased in the lung of sarcoidosis patients and is associated with higher expression of IFN- γ and IL-2 as well as local T cell activation [152, 160]. IL-27, a cytokine involved in T cell activation and induction of IFN- γ , is also overexpressed in sarcoidosis [153]. In turn, IFN- γ enhances macrophage accessory functions, and thereby synergizes with other pro-inflammatory cytokines, such as TNF- α , to facilitate cellular trafficking and recruitment to disease sites [161]. In addition, IFN- γ up-regulates the expression of co-stimulatory molecules, which optimize T cell activation, and increases TNF- α release from appropriately triggered macrophages [162]. The role of IFN- γ in granulomatous inflammation is supported by the observation that granulomas do not develop in IFN- γ knockout mice exposed to thermophilic bacteria [163]. The notion of Th1 polarization as a key feature of sarcoidosis is substantiated further by the occurrence of new onset or recrudescence of disease following treatments with biologic agents that promote a Th1 response (e.g. IFN- α and IFN- γ) [164, 165] as well as by the observed down-regulation of several cytokines, chemokines and

chemokine receptors associated with Th2 responses at disease sites in patients with sarcoidosis [155, 166]. IFN- γ is a likely contributor to the Th1-type cytokine profile in sarcoidosis by suppressing the Th2 lymphocyte response [167].

Th17 Cells

Th17 cells, i.e. T cells producing IL-17 as their signature cytokine, were found to constitute a separate lineage 10 years ago and have been implicated in several inflammatory and autoimmune diseases. They have also been shown to be essential for pulmonary granuloma formation in response to mycobacterial infection in mice [168, 169]. This prompted investigations in sarcoidosis patients, where a couple of studies found Th17 cells in increased frequencies in blood and in BAL fluid, and also to be present in the granuloma [170–172]. Th17 cells specific for the mycobacterial protein ESAT-6 were found to be present in blood and BAL of sarcoidosis patients [172], while another study found that IL-17 responses to the mycobacterial protein mKatG were higher in BAL cells from sarcoidosis patients with Löfgren's syndrome compared to non-Löfgren's patients [173]. The same study also demonstrated the highest levels of IL-17 in BAL fluid of HLA-DRB1*03⁺ Löfgren's patients, i.e. patients with a very good prognosis. The frequencies of Th17 cells producing IFN- γ , an example of "hybrid" T cells combining characteristics of two lineages, have also been compared between sarcoidosis patients and healthy controls, however with conflicting results [172, 174].

Regulatory T Cells

Regulatory T cells (Tregs) maintain immune homeostasis by inhibiting APCs and effector T cell function [175]. Both natural constitutive (nTregs) and adaptive (antigen-specific) induced (iTregs) forms of Tregs have been described, which overall represent about 5–10 % of circulating CD4⁺ T cells in healthy subjects [176]. However, there is no marker allowing nTregs or iTregs to be analysed separately. Most Tregs express FoxP3, which is regarded as a "master regulator" of Treg differentiation, as well as high levels of CD25. In sarcoidosis, tissue-, blood- and BAL-derived FoxP3⁺ T cells appear to exhibit an impaired ability to suppress TNF- α , IFN- γ and IL-2 production and are not effective in inhibiting granuloma formation *in vitro* [177, 178]. At the same time, peripheral Treg cells exert powerful antiproliferative activity that may account for the "immune paradox of sarcoidosis" [177] (e.g. extensive granulomatous inflammation and cytokine secretion associated with a state of anergy as indicated by

the lack of reaction to skin antigen tests and *ex vivo* exposure to common recall antigens in peripheral blood) [179, 180]. However, another study found sarcoidosis Tregs to have a reduced ability to suppress proliferation [181]. Moreover, Idali and colleagues have reported a reduced expression of FoxP3 in CD4⁺FoxP3⁺ BAL T cells of sarcoidosis patients consistent with a reduced function of Tregs [35]. Decreased BAL Treg numbers have been associated with both a favourable prognosis and a chronic (active) disease course [33, 182], suggesting that further studies are needed to elucidate the role of dysfunctional Tregs in the pathogenesis of sarcoidosis.

CD1d-restricted natural killer T (NKT) cells represent another important regulatory T cell subset. Ho and colleagues have shown that NKT cells are absent or significantly reduced in the peripheral blood of patients with classical sarcoidosis (but not in those presenting acutely with features of Löfgren's syndrome) [183]. Notably, there was no difference in the proportion of CD1d-restricted NKT cells between peripheral blood and lungs, suggesting that the peripheral blood deficiency is not due to sequestration of these cells in the lungs. Furthermore, CD1d expression on APC of patients was normal; thus, the deficiency of CD1d-restricted NKT cells is not due to abnormal CD1d expression. The results of a follow-up study by the same group suggest that the deficiency in NKT cells may lead to reduced IL-10 production by monocytes, resulting in an exaggerated T cell proliferation [184].

Progression to Fibrosis

Chronic granulomatous inflammation can lead to fibrosis of the lung, heart and liver in patients with sarcoidosis. Fibrosis requires the recruitment and proliferation of fibroblasts, leading to extracellular deposition of collagen matrix products [185]. Excessive chemokine production has been associated with progressive pulmonary fibrosis [186]. Indeed, a number of mediators that are found at sites of sarcoid granulomatous inflammation (e.g. fibronectin) are chemoattractant for fibroblasts, whereas macrophage-produced transforming growth factor- β (TGF- β), insulin growth factor-1 (IGF-1) and platelet-derived growth factor (PDGF) induce fibroblast proliferation and collagen matrix deposition [187, 188]. The Th1-defining cytokine IFN- γ , which is highly expressed at disease sites, has direct antifibrotic effects [189], whereas Th2 cytokines, such as IL-4 and IL-13, promote fibrogenesis [190]. Accordingly, it has been suggested that a local shift from Th1 to Th2 cytokine predominance may favour progression to chronic, fibrotic disease [191, 192]. However, the relevant pathways involved in the fibrotic outcome in sarcoidosis remain uncertain [193, 194].

Concluding Remarks

While the search for the sarcoidosis antigen/s continues, it seems inevitable that the development of the disease is determined by a complex interplay between host/genetic factors and the antigen/s. In addition, genetic abnormalities that confer disease risk are likely to be largely separate from those that influence specific disease manifestations. Therefore, if sarcoidosis genetics is to move forward, it is imperative that meticulous databases of phenotypically well-defined patients continue to be constructed. Some of the genes that could potentially affect an individual's susceptibility to disease and the course of any established disease have been identified. Much work remains to be done, but a fuller understanding of the genetic basis of sarcoidosis is likely to open up new therapeutic avenues, both for the treatment of this and other granulomatous disorders.

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Compliance with Ethical standards

Conflict of Interest Paolo Spagnolo serves as consultant for Roche and has received consulting fees from Boehringer Ingelheim. Johan Grunewald, Jan Wahlström and Anders Eklund declare that they have no conflict of interest.

Research involving Human Participants and/or Animals N/A

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