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DECLARATION

This thesis has been composed by myself and has not been used in any previous application for a degree. Throughout the text I use both 'I' and 'We' interchangeably.

All the results presented here were obtained by myself, except for:

1) *Human Leukocyte Antigen genotyping* (Figure 6: high-resolution HLA-DRB1 allele frequencies) *were performed in collaboration with Dr Benedetta Allegra Mazzi, Immunogenetics Laboratory, HLA & Chimerism, Department of Immunohematology & Blood Transfusion, IRCCS Ospedale San Raffaele Milan, Italy*

2) *Part of DNA extraction* (Figure 6: high-resolution HLA-DRB1 allele frequencies) *was performed in collaboration with Dr Lorena Citterio, Dr Laura Zagato, and Dr Elisabetta Messaggio, Research Unit on Genomics of Renal Diseases and Hypertension, IRCCS Ospedale San Raffaele Milan, Italy.*

3) *Part of the clinical data regarding patients' allergy history* (Figure 2: timing of onset of allergy in relation to SLE onset, Figure 3: onset of the first and second allergic reactions in patients with SLE, Table 3: allergy features in patients with SLE) *was collected by Dr. Andrea Sorce, Università Vita-Salute San Raffaele, Milan, Italy.*

All sources of information are acknowledged by means of reference.

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ABSTRACT

Systemic lupus erythematosus (SLE) is a multi-organ autoimmune disease characterised by protean clinical manifestations and a multifaceted pathogenic background. Allergic reactions and infectious events complicate the course of SLE, but their reciprocal correlations are poorly understood. Availability of accurate tools to stratify patients with homogeneous endo/phenotypes and guide personalised treatments is still an unmet need. Despite the potential pathogenic role of T cells in SLE, little is known about the quantitative and qualitative features of antigen-specific T cell responses. Based on clinical data demonstrating a tripartite association between disease flares, allergic and infectious events, a multi-step experimental plan was designed to seek and characterise antigen-specific T cells recognising histone-, Epstein-Barr virus (EBV)- and penicilloylated albumin-derived peptides in patients with SLE in comparison to patients with Takayasu's arteritis and healthy controls. Genetic studies confirmed that human leukocyte antigen (HLA)-DRB1*03:01 is a risk factor for SLE and revealed novel associations among DRB1*11:01, allergic and infectious events, and between DRB1*07:01 and infection protection. Stem-cell memory T cells (T_{SCM}) were expanded in patients with SLE possibly accounting for persisting inflammation. Using direct *ex vivo* visualisation of antigen-specific T cells stained with class II HLA tetramers through flow cytometry, histone-specific CD4⁺ T cells were selectively detected in patients with SLE and their accumulation in the peripheral blood associated with the presence of anti-DNA antibodies. Penicilloylated albumin-specific T cells identified patients with beta-lactam allergy. EBV-specific cells were detected as expected in patients and controls. Variations in the size of the three types of antigen-specific T cell populations were reciprocally correlated and cytokine responses to isolated epitopes revealed activation of multiple inflammatory pathways suggesting cross-contamination between antimicrobial, allergic and autoreactive responses. Histone-specific and EBV-specific effector memory T cells and T regulatory cells decreased during SLE flares, possibly reflecting peripheralization into target tissues and defective anti-inflammatory responses. EBV-specific T_{SCM} also decreased and EBV-induced cytokine responses were impaired during active phases of the disease possibly indicating mis-differentiation of precursors, and ineffective antiviral responses. These data support the existence of a multidirectional dysfunction of the

immune response, possibly traceable and targetable through T cell responses, as a pathophysiological and clinical hallmark of SLE.

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ACRONYMS AND ABBREVIATIONS

Acronym/abbreviation	Description
AAV	ANCA-associated vasculitides
aB2GPI	Anti-beta 2 glycoprotein I antibodies
aCL	Anti-cardiolipin antibodies
ACR	American College of Rheumatology
ADNA	Anti-(double-stranded)DNA antibodies
ANA	Anti-nuclear antibodies
ANCA	Anti-neutrophil cytoplasmic antibodies
APC	Allophycocyanin
aPL	Anti-phospholipid antibodies
APRIL	a proliferation inducing ligand (APRIL)
APS	Antiphospholipid syndrome
aRNP	Anti-ribonucleoprotein antibodies
aSm	Anti-Smith antigen antibodies
aSSA	Anti-SSA antibodies
aSSB	Anti-SSB antibodies
AZA	Azathioprine
BAFF	B cell activating factor
BILAG	British Isles Lupus Assessment Group
BCR	B cell receptor
CI	Confidence interval
CMV	Cytomegalovirus
COVID-19	SARS-CoV-2-related disease
DMSO	Di-methyl-sulfoxide
DVT	Deep vein thrombosis
ECLAM	European Consensus Lupus Activity Measure
GCA	Giant cell arteritis
HLA	Human leukocyte antigen
HR	Hazard ratio
IFN α	Interferon alpha
IFN γ	Interferon gamma

IL1, 2, 3...N	Interleukin 1, 2, 3...N
IQR	Interquartile range
IRF	Interferon regulatory factors
LAC	Lupus anticoagulant
MHC	Major histocompatibility complex
MMF	Mycophenolate mofetil
MTX	Methotrexate
NET	Neutrophil extracellular trap
OR	Odds ratio
PBS	Phosphate buffered saline
PDN	Prednisone
PE	Phycoerythrin
PerCP	Peridinin-chlorophyll-protein
PHA	Phytohaemagglutinin
PRR	Pattern recognition receptors
PTPN22	Protein tyrosine phosphatase N22
RR	Relative risk
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
SDI	SLICC/ACR damage index
SLE	Systemic lupus erythematosus
SLICC	SLE International Collaborating Clinics
TAK	Takayasu's arteritis
TCR	T cell receptor
TGF β	Transforming growth factor beta
TLR	Toll-like receptor

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INTRODUCTION

General premise

Systemic lupus erythematosus (SLE) is a complex inflammatory disease characterised by multi-organ damage and broad inter- and intraindividual variability both in terms of pathophysiology and clinical phenotypes (Arnaud & Tektonidou, 2020, Rahman & Isenberg, 2008). Autoimmune manifestations are usually regarded as the hallmark of the disease, whereas the potential role of coexisting immune dysfunction in terms of susceptibility to infections and allergy has less been explored. Despite being conventionally classified as a rare disease (OrphaNet code 536), SLE can affect up to 1.6 persons per 1,000 inhabitants (Danchenko, Satia et al., 2006) and, along with other immune-mediated disorders (Huscher, Merkesdal et al., 2006), might have a significant social impact due to disease- and drug-related morbidity (Scofield, Reinlib et al., 2008). Human and economic costs of this disease are in fact particularly high, especially since SLE preferentially affect young people, and specifically women of childbearing age. Furthermore, disease-related morbidity and costs increase with disease duration and are higher in disadvantaged populations and in subjects receiving suboptimal treatments, such as corticosteroid monotherapy or treatments without antimalarials (Barber & Clarke, 2017). This evidence can most likely be explained with higher accrual of chronic damage due to delayed diagnosis/treatment or inconstant disease monitoring leading to long-lasting uncontrolled disease activity. Nonetheless, even state-of-the-art care is insufficient to stably grant complete, drug-free remission to most patients with SLE. In fact, current diagnostic and treatment tools still lump patients with SLE into broad and non-specific categories and have a limited value in identifying clinically and prognostically relevant sub-phenotypes (Doria, Gatto et al., 2015). Developing translational models to describe SLE clinical variability along with biological correlates might therefore be crucial for the development of affordable prognostic markers and less toxic therapies. Antigen selectivity and coordination of long-term inflammatory responses constitute two intrinsic properties of T-lymphocytes and are increasingly exploited for the development of molecularly targeted diagnostic and therapeutic tools in multiple branches of human pathology (Milone, Xu et al., 2021, Oliveira, Ruggiero et al., 2015), while much less is known regarding the pathogenic role of T-cells and their potential medical applications in the setting of autoimmune/rheumatic diseases. Taking advantage of the nature of SLE

as a paradigm of immune dysfunction, this study aims to characterise antigen-specific T-cell responses in patients with SLE and correlate this evidence with clinical data.

Dynamics of T cell-responses in health and disease

Physiology

T lymphocytes lie at the apex of the adaptive immune response and coordinate the flow of antigen information from innate immune cellular and humoral sensors to effector T and B cells as well as back to innate effectors to promote threat recognition and neutralisation, besides maintaining tolerance to self structures. Two main subsets of T lymphocytes are defined based on their main biological function: CD4⁺ (helper) T cells and CD8⁺ (cytotoxic) T cells. Aberration in T cell function are associated with immunodeficiency, allergy and autoimmunity. Under physiological conditions, double positive (CD4⁺, CD8⁺) T cells residing in the thymus undergo a two-step process of selection and maturation into single positive (CD4⁺ or CD8⁺) naïve T cells, based on the affinity of their T cell receptor (TCR) for an array of self antigens presented through the major histocompatibility complex (MHC) repertoire of each individual. Failure of optimal negative and positive T cell selection in the thymus due to genetic defects such as those involving the AIRE (Autoimmune Regulator) gene are associated with multidirectional immune dysfunction with coexisting immunodeficiency and autoimmunity. After antigen encounter through antigen presenting cell presentation, naïve CD4⁺ and CD8⁺ cells further differentiate into increasingly committed T cell populations, which can in turn be classified based on stemness capacity and biological activity. Stem-cell memory T cells (T_{SCM}) are minimally differentiated antigen-experienced CD4⁺ or CD8⁺ T cells with the ability to repopulate a whole set of downstream antigen-specific T cell subpopulations (Gattinoni, Speiser et al., 2017). Monitoring antigen-specific T_{SCM} counts after haematopoietic stem cell transplantation is crucial for prognostic stratification in terms of variety and robustness of regained immunological competence (Cieri, Oliveira et al., 2015, Oliveira et al., 2015). Central memory T cells (T_{CM}) are supposed to constitute the step following T_{SCM} in terms of stemness. Within the CD4⁺ lineage, T_{CM} might constitute the memory reservoir of follicular helper and germinal centre follicular helper T cells (T_{FH} and _(GC)T_{FH}, respectively). Similarly, effector memory T cells (T_{EM}) lie downstream T_{CM} in the

differentiation cascade of T cells and constitute the memory counterpart of proper effectors. Effector cells (T_{EFF}) are in charge of the bulk production of cytokines characterising a given inflammatory event and expand following sustained stimulation with a trigger antigen (Ruterbusch, Pruner et al., 2020).

Polarisation within the $CD4^+$ lineage might in turn vary considerably according to the nature of the inciting stimuli and constitutes an overlapping layer of complexity within T cell classification. Accordingly, distinct subpopulations of T_{FH}/T_{CM} and T_{EFF}/T_{EM} might arise from different inflammatory environments (Ruterbusch et al., 2020). A T helper 1 (Th1) environment arises under high-IL12 conditions and is characterised by enhanced production of interferon gamma ($IFN\gamma$), recruitment and activation of innate immunity and cellular responses towards viruses and intracellular pathogens. Conversely, a T helper 2 (Th2) environment, leading to the generation of T_{FH2} and T_{EFF2} subsets, typically promotes B-cell differentiation, eosinophil-mediated responses and tissue fibrosis following stimulation by parasites, venoms and other environmental antigens (Ruterbusch et al., 2020). A Th2 environment involves the release of IL4, IL5, IL13 and IL33. T helper 17 cells (Th17) differentiate in response to a cytokine milieu characterised by abundance of IL6, IL23 and transforming growth factor beta ($TGF\beta$) and constitute a standalone third type of inflammatory environment (Sallusto, 2016). Th17 secrete an array of cytokines including the prototypical IL17A and IL17F, which in turn are responsible for neutrophil activation and potentiation of multiple cytokine release from epithelial, endothelial and innate immune cells (Acosta-Rodriguez, Rivino et al., 2007). Besides the three main branches of T helper cell differentiation (Th1, Th2, Th17) additional Th cell subtypes with peculiar functional specialisations have been progressively discovered, including plastic populations of Th1/Th2, Th1/Th17 and Th2/Th17 cells (Sallusto, 2016). IL9-secreting Th9 cells constitute a distinct population of Th cells within the Th2 biological spectrum, with potential non redundant function in the response to selected parasites. Similarly, Th22 cells arise under Th17-like conditions being however unable to release IL17 and may have a role in controlling pathogens affecting the skin. Non-classic Th1 cells or Th1-star ($Th1^*$) cells constitute a recently defined subset within the spectrum of Th17 responses, showing a potential specialisation in contrasting infections due to intracellular pathogens (such as *Mycobacteria*) and a limited role in viral infections (Sallusto, 2016). $Th1^*$ cells are characterised by the

expression of both Th1-specific and Th17-specific surface markers such as CXCR3 and CCR6.

Regulatory T cells constitute an additional branch of the CD4⁺ T lymphocyte lineage and play a crucial role in immunosuppression and maintenance of tolerance. Regulatory cell subsets have also been described within the CD8⁺ T and B cell lineages (Grant, Liberal et al., 2015)

Allergy

T lymphocytes contribute to the promotion of hypersensitivity reactions both of immediate and delayed type. In the setting of atopy, molecular diagnostics has revolutionized the allergy practice and has disclosed novel opportunity for T cell studies exploiting protein antigens with known, selective immunogenicity. Inhalant or food allergen-specific CD4⁺ T cells are readily and selectively detectable in the blood of allergic subjects and show a Th2-skewed phenotype consistent with enhanced IgE responses (Archila, Jeong et al., 2015, Kwok, Roti et al., 2010, Macaubas, Wahlstrom et al., 2006). Furthermore, allergen-specific T cell phenotype varies with immunomodulatory therapies (Wambre, DeLong et al., 2012). In contrast to atopy, the molecular bases of immediate- and delayed-type hypersensitivity reactions to drugs have less been defined (Adam, Pichler et al., 2011). In the setting of penicillin allergy, some authors employed penicilloylated peptides to induce and measure T cell responses (Azoury, Fili et al., 2018, Nhim, Delluc et al., 2013, Padovan, Bauer et al., 1997). Penicilloylated peptides have been shown to bind effectively to several HLA-DRB1 molecules and to elicit detectable IFN γ responses as measured by ELISpot assays (Azoury et al., 2018, Nhim et al., 2013). Interestingly, effective anti-penicillin responses have consistently been detected in cells from healthy donors, possibly suggesting that potential sensitisation to beta-lactams is common in the general population with tolerance being mostly due to regulatory mechanisms (Azoury et al., 2018). No study has so far employed direct *ex vivo* techniques for T cell visualisation such as MHC multimers to characterise anti-beta lactam responses in allergic individuals, preventing dissection of non-specific or artificially skewed T cell responses due to cell stimulation protocols from natural mechanisms of allergic inflammation.

Autoimmune diseases

Systemic vasculitides

Inflammation of the large, medium and small blood vessels occurs in a multitude of conditions including infectious and autoimmune diseases. In this latter setting, systemic vasculitides can develop as a complication of other rheumatologic disorders or as primary immune-mediated diseases. The clinical-pathophysiological nomenclature by the Chapel Hill Consensus Conference identifies four major disease groups (small, medium, large and variable vessel vasculitides), besides three other special categories (single-organ vasculitides, vasculitides associated with probable aetiology and vasculitides associated with systemic diseases) (Jennette, Falk et al., 2013).

Extensive evidence from clinical observations and animal models supports a view of large vessel vasculitides as T cell-dependent diseases (Brack, Geisler et al., 1997, Weyand, Schonberger et al., 1994). T cells orchestrate the downstream inflammatory and hyperplastic response causing disruption of the vessel wall architecture and the subsequent formation of vessel stenosis and/or aneurysms. In giant cell arteritis (GCA), the inflammatory response is centripetal: T-cell infiltration of the vessel wall occurs through the adventitial vasa vasorum and is modulated by the local inflammatory niche, including vessel residing dendritic cells (Wen, Shen et al., 2017). Activation of CD4+ T cells prevails in GCA and is more prominently skewed towards a Th1/Th17 phenotype, consistent with the granulomatous nature of the disease (Brack et al., 1997, Deng, Younge et al., 2010). Th17-biased responses in GCA appear to account for systemic symptoms and vessel wall remodelling due to a direct correlation with local matrix metalloprotease expression. Th17 cells are also more susceptible to corticosteroid treatments which constitute the mainstay of therapy in this disorder. Th1-driven responses are instead more resistant and might account for glucocorticoid-refractory cases (Deng et al., 2010). Takayasu's arteritis (TAK) is a large vessel vasculitis with distinct clinical and pathophysiological features compared to GCA. From a clinical point of view TAK affects young women (in contrast to the elderly-skewed demographics of GCA) causing occlusion or aneurysmatic deformation of the upper and lower aorta and its major branches including coronary arteries. Similar to GCA, TAK is associated with selected HLA profiles (Carmona, Coit et al., 2017, Dong, Kimura et al., 1992, Lv, Wang et al., 2015) and with enhanced Th1 and Th17 responses.

Genetically determined and acquired alterations of T cell function constitute a characteristic feature of patients with small-vessel vasculitides such as anti-neutrophil cytoplasmic antibody (ANCA)-associated vasculitides (AAV). Specifically, patients with AAV frequently bear polymorphisms in key genes for T cell activation and co-stimulation control such as protein tyrosine phosphatase N22 (PTPN22) and cytotoxic T lymphocyte antigen 4 (Alberici, Martorana et al., 2014), besides selected HLA variants. Patients with AAV are also characterised by enhanced Th1/Th17 responses, which might be selectively triggered by exposure of key autoantigens such as proteinase 3 (Abdulahad, Stegeman et al., 2008, Kallenberg, 2011). A recent study also identified a shared B and T cell myeloperoxidase epitope and, by the use of MHC multimer staining techniques, identified circulating anti-myeloperoxidase-specific CD4⁺ T cells with a Th17 phenotype in patients with AAV (Free, Stember et al., 2019). Consistent with similar evidence in other disease settings, circulating T_{EFF}/T_{EM} cells decrease during active disease, reflecting their re-localisation into target tissues. Patients with AAV and active nephritis are in fact characterised by enhanced urinary concentration of T_{EM} cells in contrast to the circulating blood (Abdulahad, Kallenberg et al., 2009). Deficit of T regulation have also been advocated to contribute to the pathogenesis of AAV (Abdulahad, Stegeman et al., 2007).

Rheumatoid arthritis

Rheumatoid arthritis is a frequent autoimmune disease characterised by prominent symmetric involvement of small joints and potential extra-articular complications. Although clearly distinct in terms of demographics, clinical presentation and general pathophysiology, rheumatoid arthritis and GCA share a common HLA-DR risk allele. Similar to GCA, rheumatoid arthritis is characterised by a crucial role of Th17 cells for progression and maintenance of the inflammatory response. Specifically, Th17 cells promote TNF α -driven joint inflammation and B cell activation. Persisting inflammation leads to tissue damage with enhanced exposure of aberrantly edited self antigens, such as citrullinated peptides. This in turn, leads to the development of the hallmark anti-citrullinated peptides and chronicisation of the inflammatory status. Anti-citrullinated peptide T cell immunity plays a crucial role in initiating this process. Consistently, HLA-DRB1*04:01-restricted citrullinated peptides bound to MHC multimers allowed direct *ex vivo* visualisation of antigen- and disease-specific CD4⁺ T cells from the circulating

blood (James, Rieck et al., 2014), synovial fluid and tissue of patients with rheumatoid arthritis (Pieper, Dubnovitsky et al., 2018). Interestingly, arthritogenic antigen-specific CD4⁺ T cells from patients with rheumatoid arthritis are characterised by a memory phenotype with prominent expansion of the T_{SCM} compartment and respond to tumour necrosis factor alpha (TNF α) modulation mirroring the clinical phenotype (Cianciotti, Ruggiero et al., 2019, James et al., 2014, Pieper et al., 2018).

Systemic lupus erythematosus

Epidemiology

Multiple studies attempted to estimate SLE prevalence in the general population. A 2006 meta-analysis by Danchenko and colleagues suggests that SLE affects up to 159 persons for every 100,000 inhabitants, with significant regional and ethnical variations (Danchenko et al., 2006). More recent data indicate that this figure might be underestimated (Cortes Verdu, Pego-Reigosa et al., 2020, Pablos, Abasolo et al., 2020). SLE prevalence in Italy is supposed to range from 51 to 71 cases per 100,000 inhabitants according to at least three studies (AMRER (Associazione Malati Reumatici Emilia-Romagna), 2015, Benucci, Del Rosso et al., 2005, Govoni, Castellino et al., 2006). These figures are roughly higher than the average expected prevalence of SLE in Europe (Danchenko et al., 2006).

Women with SLE are nine times more frequent than men, consistent with the inflammatory effect of oestrogens and with the role of X-inactivation escape in enhancing innate immune responses (see below). Ultraviolet light, viral infections, low vitamin D, selected drugs and polymorphisms in a multitude of genetic loci constitute additional risk factors for the development of SLE (Simard & Costenbader, 2015). The peak incidence of the disease occurs during the III decade of life, although juvenile or late-onset cases may also develop, usually with less evidence of disproportion among female and male patients. Early-onset disease is usually more aggressive and shows a relatively higher prevalence of renal and neuropsychiatric involvement (Ambrose, Morgan et al., 2016, Artim-Esen, Sahin et al., 2017, Ramirez, Tejera-Segura et al., 2018). Furthermore, the first months following overt disease onset are usually characterised by a more aggressive course, while a relatively low frequency of disease flares is observed in longstanding disease (Gerosa, Ramirez et al., 2020, Holmqvist, Simard et al., 2015, Lim, Pullenayegum

et al., 2018, Nossent, Cikes et al., 2007, Piga, Floris et al., 2017, Scalzi, Hollenbeak et al., 2010). As anticipated, SLE can have a major impact on patients' quality of life, and social and economic balance. On the other hand, social and economic disparities have a role in SLE prognosis and might be more significant than genetics and disease-related variables in affecting the course of the disease (Joseph, Prasad et al., 2021, Ugarte-Gil, Pons-Estel et al., 2016). Long-term disability and mortality related to SLE have significantly decreased over time thanks to the introduction of immunosuppressive treatments, improved and more diffuse awareness of the disease in the general population and medical community and adoption of personalised approaches for patient care (Banchereau, Hong et al., 2016, Lever, Alves et al., 2020, Nossent et al., 2007). Despite the fall of acute inflammatory events as causes of SLE-related mortality, chronic complications due to prolonged smouldering activity, progressive damage accrual and drug-related effects, such as cardiovascular diseases and metabolic disorders still represent major mortality-related factors for patients with SLE. These considerations further support the need for novel tools to dissect the pathophysiological events deploying in each individual patient to early intercept potential drivers of long-term complications.

Clinical features

Inflammatory manifestations

The spectrum of clinical manifestations attributable to SLE is very broad and might vary significantly among patients and in the same subject during the course of the disease, according to the modulatory effect of the environment and of treatments (Agmon-Levin, Mosca et al., 2012, Banchereau et al., 2016).

Cutaneous and musculoskeletal manifestations constitute the most frequent features of SLE and might present both as a definite clinical cluster (Terao, Yamada et al., 2014) or as part of more complex combination of symptoms. Skin manifestations are reported in up to 85% of patients and the word lupus itself is a medieval medical term standing for face skin inflammation. In fact, photosensitivity is a hallmark of the disease and is particularly frequent in most exposed skin regions, such as face, upper trunk and limbs. Malar rash, classically described to spare the light-protected rhino-labial region, constitute the most typical manifestation of photosensitivity. According to the clinical-pathological Düsseldorf classification (Kuhn & Landmann, 2014, Sontheimer, 2004),

acute rash due to ultraviolet light-induced inflammation is usually opposed to subacute (SCLE) and chronic (CCLE) cutaneous lupus. Subacute lesions usually present as erythematous papules with a polycyclic appearance and also tend to occur more frequently in photosensitive areas. Discoid lupus, consisting of violaceous to brownish infiltrated plaques evolving into fibrotic and discoloured lesions, constitute the most frequent manifestations of CCLE. Additional CCLE lesions include mucous manifestations (oral and nasal ulcers), lupus panniculitis (also known as lupus profundus) and chilblains lupus. This latter sign is part of a broader spectrum of manifestations due to small vessel dysfunction and/or damage, encompassing Raynaud's phenomenon and cutaneous vasculitis. Alopecia is another frequent and invalidating skin manifestation of SLE. Cutaneous lupus (especially SCLE) is usually associated with positive anti-SSA(Ro)/SSB(La) antibodies (aSSA, aSSB respectively) and has a particularly strong association with HLA-DRB1*03 (Diaz-Gallo, Oke et al., 2021). Histologically it is characterised by prominent inflammation of the epidermal/dermal border (interface dermatosis) with variable degrees of lymphocyte infiltration and deposition of immunoglobulins and/or complement (evident as the so-called lupus band on immunofluorescence assays). The likelihood of developing scars and chronic skin damage is higher in patients with CCLE than in patients with SCLE and ACLE. Conversely, association with extracutaneous manifestations is more frequent in acute forms.

Joint involvement is also frequent in patients with SLE, especially in late-onset subsets (Ambrose et al., 2016), with an estimated prevalence of up to 90% (Petri, 2007). Non-erosive synovitis or tenosynovitis is usually regarded as the typical pattern of joint disease in SLE, as opposed to the erosive pattern of rheumatoid arthritis. However, overlap syndromes encompassing seropositive rheumatoid arthritis and SLE (rhumus) might also occur. In addition, erosive features are increasingly recognised in the absence of rheumatoid serology (namely anti-citrullinated antibodies and/or rheumatoid factor) and even in patients with Jaccoud's arthropathy, a reducible joint deformity of ill-defined pathophysiology, usually regarded as SLE-specific (Di Matteo, Smerilli et al., 2021). Novel evidence also challenges the paradigm of SLE selectivity for the synovial tissue, suggesting that enthesitis might further expand the heterogeneous spectrum of SLE phenotype and correlate with general disease activity (Di Matteo, Filippucci et al., 2018).

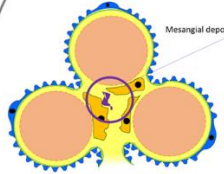
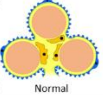
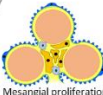
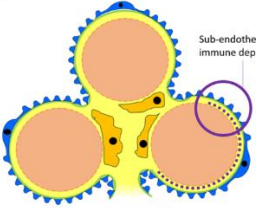
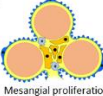
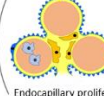
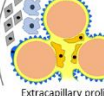
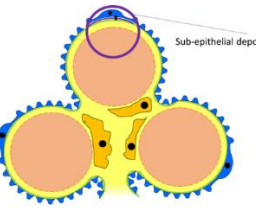

Data from multiple studies also indicate that subclinical joint inflammation might be particularly frequent, leading to chronic damage despite clinical monitoring, in the absence of serial imaging (Piga, Gabba et al., 2016, Tani, Carli et al., 2018).

Constitutional symptoms constitute a frequent but elusive aspect of SLE clinical spectrum. Fatigue is the commonest symptom in this category, as it may affect more than 80% of patients. Its clinical course is often uncoupled from general disease activity and might be related to multiple mechanisms including systemic inflammation, abnormal iron metabolism or alterations in brain connectivity and emotional input processing (Cleanthous, Tyagi et al., 2012, Harboe, Greve et al., 2008, Moroni, Mazzetti et al., 2021, Wincup, Sawford et al., 2021, Wiseman, Bastin et al., 2017). Enhanced activation of the reticuloendothelial system is also common, especially in patients of younger age and can manifest as low-grade to high fever and diffuse lymph-node enlargement. These manifestations can further evolve or be complicated by the development of haemophagocytic lymphohistiocytosis or Kikuchi-Fujimoto's disease. Distinguishing florid inflammation from haematological malignancies is often challenging both at a clinical and histological level (Gavand, Serio et al., 2017, Henter, Horne et al., 2007, Kim, Kwok et al., 2012, Petri, Kawata et al., 2013).

Lupus nephritis constitutes the main cause of SLE-related morbidity and affects about 40% of patients during their disease course. A histopathological classification identifies six patterns of glomerular involvement in terms of immune deposits and/or proliferation (**Figure 1**). Class I and II glomerulonephritis correspond to the presence of minimal mesangial deposits (I) and/or proliferation (II), with no or isolated mild urinary sediment abnormalities as clinical correlates. Class III and IV are characterised by sub-endothelial deposits and hypercellularity at the level of either mesangial, endocapillary, and/or extracapillary spaces due to proliferation of resident cells and/or infiltration by circulating leukocytes. Class IV affects 50% or more of the glomeruli, in contrast to class III, and is further sub-classified into segmental (class IV-S) or global (class IV-G) forms in case of lesions in less than 50% vs 50% or more of each glomerular tuft. Class III and IV are also classified according to the presence of active and/or chronic lesions. Class III and IV constitute the most frequent and aggressive forms of lupus nephritis and usually present with nephritic syndromes with abnormal proteinuria, active urinary sediment, with or without hypertension and reduced filtration rates. Class V glomerulonephritis refers to

membranous nephropathy with or without coexistent proliferation. This form usually presents with nephrotic manifestations, is less aggressive and rapidly evolving than class III and IV and shows an overall better prognosis despite being less affected by immunosuppression (Farinha, Pepper et al., 2020). Class VI corresponds to irreversible renal failure with loss of functional glomeruli and diffuse sclerosis.

Figure 1: histopathological classification of glomerular involvement in SLE.

Immune deposits	Proliferation	% Glomeruli	Class
 Mesangial deposits	 Normal		I
	 Mesangial proliferation		II
 Sub-endothelial immune deposits	 Mesangial proliferation	<50%	III
	 Endocapillary proliferation		 Extracapillary proliferation
 Sub-epithelial deposits			V
 Glomerular sclerosis		≥90%	VI

This figure depicts a simplified version of the “International Society of Nephrology/Renal Pathology Society (ISN/RPS) 2003 classification of lupus nephritis” (Weening, D’Agati et al., 2004).

Additional criteria have been set to quantitate the degree of activity and chronic damage. Besides glomerular lesions, tubular involvement can also develop in patients with SLE and contribute to renal impairment. Furthermore, vascular lesions secondary to ischaemia or primary vessel inflammation can also occur (Bajema, Wilhelmus et al., 2018, Strufaldi, Menezes Neves et al., 2021).

Neuropsychiatric manifestations of SLE (NPSLE) constitute some of the most challenging aspects of the disease. In fact, the spectrum of NPSLE encompasses a variety of acute and chronic conditions affecting either the central, peripheral or autonomic nervous system through micro- or macrovascular inflammatory and/or ischaemic mechanisms, humoral and cell-mediated autoimmunity and alterations in neuronal connectivity (Bonacchi, Rocca et al., 2020, Govoni, Bortoluzzi et al., 2016, Preziosa, Rocca et al., 2019, Ramirez, Canti et al., 2019a, Ramirez, Lanzani et al., 2015a, Unterman, Nolte et al., 2011). Stroke, epilepsy and psychosis are among the most frequent manifestations of SLE at a central neurological level. Headache and mood disorders are also frequent but less specific, due to their high prevalence in the general population (Ainiala, Loukkola et al., 2001, Hanly, 2014). Peripheral neuropathy is also not uncommon in patients with SLE and is therefore listed among the items of the systemic lupus erythematosus international collaborating clinics (SLICC)/American College of Rheumatology (ACR) damage index (SDI) besides the ACR 19-item nomenclature of NPSLE features (ACR Ad Hoc Committee on Neuropsychiatric Lupus Nomenclature, 1999). Attribution of a neuropsychiatric event to SLE is a challenging task due to the lack of univocal tests for the diagnosis and the absence of specific imaging features (Govoni et al., 2016, Jeong, Her et al., 2015, Sarbu, Alobeidi et al., 2015, Sarbu, Toledano et al., 2017, Sibbitt, Brooks et al., 2010). Nonetheless, attribution algorithms based on temporal criteria and on the presence/absence of favouring and confounding factors have recently been developed and validated (Bortoluzzi, Fanouriakis et al., 2017, Bortoluzzi, Scire et al., 2015).

Virtually all internal organs can be involved in the pathogenic processes of SLE. Cardiopulmonary manifestations are more often limited to inflammation of the serosal layers (pleuritis and pericarditis). Nonetheless, autoimmune myocarditis, parenchymal and interstitial lung involvement are also part of the spectrum of SLE and might have a significant impact on morbidity and mortality (Pego-Reigosa, Medeiros et al., 2009, Tanwani, Tselios et al., 2018). Aseptic endocarditis, generally in association with anti-phospholipid antibodies (aPL) might also be more frequent than expected in patients with SLE (Vivero, Gonzalez-Echavarri et al., 2016).

Liver involvement is virtually indistinguishable from isolated autoimmune hepatitis. Pancreatic involvement is uncommon in SLE but may occur either as an acute sterile

inflammatory event, chronically in the context of overlapping Sjögren's syndrome or as the side effect of drugs. Gastrointestinal manifestations are also infrequent (possibly also due to underdiagnosis) and ill-defined and might encompass serosal inflammation (sterile peritonitis), visceral vasculitis or, less frequently, primary enteritis. The course of gastrointestinal involvement might be poorly related to that of the disease in general (Li, Xu et al., 2017, Maruyama, Nagashima et al., 2018).

Altered haematopoiesis is a distinctive feature of SLE and can involve either red blood cells, leukocytes and platelets through different mechanisms. Micro/normocytic inflammatory anaemia is very frequent in SLE and often overlaps with iron deficiency or imbalanced iron metabolism. Coombs-positive haemolytic anaemia is more specific of SLE and often coexists with immune-mediated thrombocytopenia. This clinical cluster, usually referred to as Fisher-Evans' syndrome can also precede the onset of SLE by several years. Leukopenia is another hallmark feature of SLE and other interferon-driven conditions and can be due to either enhanced leukocyte migration into target tissues or to impaired bone marrow responses. Lymphopenia is more often observed although low neutrophil counts can also be found in up to one third of patients. Both conditions are usually benign and show no direct correlation with increased infection rates. Therefore, they do often not require specific treatments (Carli, Tani et al., 2015).

Dysfunctional humoral adaptive response is crucial in the pathogenesis of SLE. Accordingly, a multitude of autoantibodies can be detected in patients with this disease and variably contribute to the clinical phenotype. The following section will briefly present most significant antibodies for clinical practice. Additional pathophysiological information will be provided from page 39. Antinuclear antibodies (ANA) are almost invariably detected in the setting of SLE although are also commonly seen in patients with other connective tissue diseases, patients with thyroid immune-mediated disorders and healthy subjects. Anti-double stranded DNA (ADNA) antibodies are more specifically associated with SLE and can be detectable in up to 98% of patients (Conti, Ceccarelli et al., 2015). Anti-nucleosome and anti-histone antibodies overlap with or extend the diagnostic spectrum of ADNA but are not routinely employed in clinical practice (Ghiggeri, D'Alessandro et al., 2019). Anti-Smith (aSm) antibodies are specific but significantly less prevalent. Additional frequent anti-extractable nuclear antigens antibodies include aSSA and aSSB antibodies (see above) and anti-ribonucleoprotein

(aRNP) antibodies. Antiphospholipid antibodies (aPL) identify a standalone serological-pathophysiological subset within SLE and can in fact develop (with or without clinical correlates) also in patients with other rheumatic disorders or in otherwise healthy subjects. Anticardiolipin (aCL) and anti-beta 2 glycoprotein I (aB2GPI) antibody assays along with lupus anticoagulant test constitute the most robust and widely accepted tests for aPL detection, while antibodies against additional targets are progressively being discovered and validated for clinical use (Chighizola, Raschi et al., 2015, Gaspar, Cohen et al., 2020). Up to 40% of patients with SLE are aPL carriers, while up to 15% also show clinical signs of thrombosis/ischaemia and/or pregnancy morbidity consistent with anti-phospholipid syndrome (APS) (Cervera, Serrano et al., 2015, Ramirez, Efthymiou et al., 2019c).

Immunodeficiency

General considerations

Infectious agents constitute the archetype stimulus accounting for the evolution of the immune system. Accordingly, pathogen-related triggering of self-sustained inflammatory/autoimmune phenomena have repeatedly been described in a multitude of clinical and preclinical settings (Cui, Zhou et al., 2021, Jacobs, Giovannoni et al., 2020, Jasemi, Erre et al., 2021, Kain, Exner et al., 2008, Lloyd, Tamhankar et al., 2021). Re-activation of endogenous retroviral elements might also contribute to inflammatory disease onset or flaring (Khadjinova, Wang et al., 2021, Wang, Hefton et al., 2021). Nonetheless, the actual clinical and pathological relevance of infectious and inflammatory events taken singularly remains elusive. While an association between immunodeficiency and autoimmune manifestations is well established in congenital disorders of the immune response (Azizi, Ghanavatinejad et al., 2016, International Union of Immunological Societies Expert Committee on Primary, Notarangelo et al., 2009), less is known about the pathophysiological role of infections in patients with multi factorial immune-mediated diseases such as SLE (Sawada, Fujimori et al., 2019).

Patients with SLE have a more than two-fold increased risk of infections such as pneumonia, herpes zoster and tuberculosis and a three-fold increased risk of severe infections compared to the general population (Pego-Reigosa, Nicholson et al., 2021). Accordingly, infections constitute a leading cause of hospitalisation and mortality in patients with SLE (Goldblatt, Chambers et al., 2009, Navarro-Zarza, Alvarez-Hernandez

et al., 2010). Regarding the site of infection, the respiratory and urinary tracts are more frequently involved, although skin and soft tissue infections are also highly prevalent (Danza & Ruiz-Irastorza, 2013). Patients with more severe disease in terms of extension (number of involved tissues and organs) and activity, and/or with a higher burden of immunosuppression bear a higher risk of infection (Bosch, Guilabert et al., 2006, Duffy, Duffy et al., 1991, Rua-Figueroa, Lopez-Longo et al., 2017, Ruiz-Irastorza, Olivares et al., 2009, Zonana-Nacach, Camargo-Coronel et al., 2001). Notably, however, effective immunomodulation with the use of antimalarials has a protective effect towards infections (Ruiz-Irastorza et al., 2009). More specifically, antimalarials neutralise the increased infection risk attributable to (moderate to low dose) corticosteroids according to epidemiological evidence (Herrinton, Liu et al., 2016). Annual influenza infection is a major trigger of SLE flares, in contrast to anti-influenza vaccination (Chang, Chang et al., 2016, Joo, Kim et al., 2021, Touma, Gladman et al., 2013). In addition, new-onset infection or reactivation of multiple pathogens have also been associated to SLE activity.

Herpesviruses

Vulnerability to the reactivation of herpesviruses, especially Epstein-Barr virus (EBV) and varicella-zoster virus (VZV) is a clinical/pathophysiological hallmark of SLE (Chakravarty, Michaud et al., 2013). Cytomegalovirus (CMV) infection also has a disproportionately high prevalence among patients with SLE, although the role of CMV reactivation in triggering lupus flares appears less relevant compared to EBV (Draborg, Rasmussen et al., 2018, Rider, Ollier et al., 1997). Multiple pathogenic factors might account to herpesvirus infection/reactivation susceptibility in patients with SLE. Dysfunctional interferon responses might be particularly detrimental for the control of viral infections (see also below regarding the current coronavirus pandemic)(Gupta, Nakabo et al., 2021a). Consistently, non-selective inhibition of interferon alpha (IFN α) prompts an increase in herpes zoster rates in patients with SLE (Khamashta, Merrill et al., 2016, Tummala, Abreu et al., 2021). In addition, exhaustion of T-cell responses due to persistent low-grade viral replication during chronic infection has been hypothesised as a key factor in dysregulated anti-herpetic responses, independent of treatment status (Draborg, Jacobsen et al., 2014).

Similar to other autoimmune disorders such as multiple sclerosis (Jacobs et al., 2020), more consistent evidence exists about a potential role of EBV in the pathogenesis of SLE. This consideration is coherent with the high prevalence of EBV infection in the general population. Specifically, seroprevalence of previous EBV infection in Italy exceeds 70-90% (Leogrande & Jirillo, 1993, Pordeus, Barzilai et al., 2008, Shapira, Poratkatz et al., 2012). Patients with SLE have normal or almost normal humoral immune responses to EBV, but fail to develop efficient cytotoxic T-cell responses and show higher number of viral copies in the circulating blood independent of treatment (Kang, Quan et al., 2004, Moon, Park et al., 2004, Tsokos, Magrath et al., 1983). Anti-EBV T cell responses have been shown to correlate inversely with disease activity (Draborg et al., 2014). Less is known about the potential features of CD4+ T-cell responses, which might behave independently on disease activity (Kang et al., 2004).

COVID-19 and anti-SARS-CoV-2 vaccines

During the last two years, a novel systemic infectious disease has spread pandemically across the World causing immeasurable costs in terms of human lives, acute and chronic morbidity, social relations, political and economic stability. This disease has been named COVID-19 after its causative agent, severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), which was isolated in late 2019. Briefly, COVID-19 is characterised by prominent involvement of the upper and lower respiratory tract and can be complicated by severe systemic inflammatory manifestations, thrombotic/ischaemic events as well as neurological and endocrine sequelae. Morbidity and mortality due to multi-organ failure are unfortunately frequent in the absence of pre-emptive immunisation or adequate life support (Ciceri, Beretta et al., 2020, Guan, Ni et al., 2020, Rovere Querini, De Lorenzo et al., 2020).

As a result of COVID-19 becoming an unavoidable priority, the whole scientific community has “forcibly” been converted to study the multifaceted aspects of the disease, of its sequelae and of therapeutic and prophylactic strategies aiming at its containment. By doing so, scientists also seized an occasion to reconsider and update consolidated knowledge in General/Internal Medicine and other subspecialties, taking advantage of readily available data on wide cohorts of patients. Along with this line, COVID-19 pandemic also became an unprecedented occasion to study the interaction of immune-

mediated diseases such as SLE and infection and the potential impact of vaccination practices in patients with immune dysfunction. Initial hypotheses suggested that patients with autoimmune diseases and specifically with SLE might indeed have multiple factors conferring theoretical protection from the most severe forms of COVID-19. In fact, while advanced age and male sex are known risk factors for COVID-19-related morbidity and mortality, SLE incidence is higher among young women. Furthermore, defective interferon response is a hallmark of coronavirus infections and has a prominent role in the pathophysiology of COVID-19, while higher levels of systemic interferon levels are detected in patients with SLE (BastardRosen et al., 2020, Garcia-Romo, Caielli et al., 2011).

Indeed, patients with SLE and other systemic immune-mediated disorders have a significant, though modest, increase in their individual risk of infection and complicated COVID-19 course (Ramirez, Gerosa et al., 2020, Ramirez, Moroni et al., 2020, Scire, Carrara et al., 2020, Strangfeld, Schafer et al., 2021). From a pathogenic point of view, these data are consistent with the contention that interferon responses in SLE are more properly dysregulated rather than simply inflated (Banchereau et al., 2016, Gupta et al., 2021a, Gupta, Nakabo et al., 2021b, Sawalha, Zhao et al., 2020). Accordingly, anti-interferon antibodies are detectable both in patients with SLE and with dysfunctional response to COVID-19 (Bastard et al., 2020, Gupta et al., 2021a, Gupta et al., 2021b). Clinically, this evidence is mirrored by the association between active disease and severe COVID-19, independent on treatments (Strangfeld et al., 2021). While there is no clear evidence of an association between activity in specific organ/tissue domains and COVID-19, patients with comorbid asthma might be particularly at risk, consistent with a model of generalised immune dysfunction as a hallmark of severe SLE (Ramirez, Argolini et al., 2021). Furthermore, while the protective effects of young age are likely lost in long-surviving patients with SLE, disease-related alterations in tissue susceptibility to SARS-CoV-2 entry might favour complicated COVID-19 courses (Sawalha et al., 2020).

Vaccination against SARS-CoV-2 has now consistently been introduced into clinical practice, with dramatic changes in infection and death rates at a population level. mRNA-based vaccines showed the best efficacy and safety performances towards COVID-19, at least in part due to their excellent immunogenicity profile and ability to stimulate a robust innate response (Pardi, Hogan et al., 2018, Polack, Thomas et al.,

2020). This feature, however, constituted a potential matter of challenge for patients with immune-mediated diseases, including SLE (Ramirez, Asperti et al., 2021). In fact, both nucleic acids and their liposomal covers might trigger Toll-like receptor (TLR)-related pathways and downstream inflammatory responses, mimicking disease-related pathogenic events (Pardi et al., 2018). Although, episodic, mostly self-limited cases of vaccine-associated flares have been reported (Barbhaiya, Levine et al., 2021), anti-SARS-CoV-2 mRNA vaccines have generally been tolerated by patients with autoimmune diseases, including SLE. Yet, adverse events were more frequent among patients with coexistent allergy history (Nittner-Marszalska, Rosiek-Biegus et al., 2021, Ramirez, Della-Torre et al., 2021), suggesting that impaired tolerance to innocent antigens might associate with hypersensitivity and autoimmune manifestations.

Allergic manifestations

Associations among autoimmune and allergic manifestations in SLE are far less defined than those linking infections to disease flares, possibly due to the contention that immunosuppression could prevent allergen sensitisation and hypersensitivity reaction occurrence. This concept, however, is not supported by clinical evidence even in settings with need for more profound immunosuppression than SLE, such as organ transplant recipients (Dehlink, Gruber et al., 2006, Guo, Fang et al., 2019). In addition, extensive methodological discrepancies exist among different studies. Three small-sized studies from the United Kingdom, Japan and Poland, suggest that allergy prevalence in SLE might be comparable or even lower to that of the general reference population, at least in terms of atopy and “classical” IgE-mediated mechanisms (Morton, Palmer et al., 1998, Sekigawa, Yoshiike et al., 2002, Wozniacka, Sysa-Jedrzejowska et al., 2003). This evidence is in contrast with other small studies (Diumenjo, Lisanti et al., 1985, Shahar & Lorber, 1997). Two larger population studies from Taiwan suggest that accrual of atopic manifestations additively increases the risk of SLE over time (Hsiao, Tsai et al., 2014, Shen, Tu et al., 2014). More consistent evidence links drug allergy and SLE (Parks, Biagini et al., 2010, Petri & Allbritton, 1992, Sequeira, Cesic et al., 1993, Wozniacka et al., 2003), although the hypothesis of a stronger allergy risk in SLE than in other rheumatic disorders is still controversial (Aceves-Avila & Benites-Godinez, 2008, Pope, Jerome et al., 2003). Antibiotic allergy has been suggested to account for the majority of

drug allergy manifestations in patients with SLE, despite the frequent use of drugs with potential allergenicity such as non-steroidal antiinflammatory drugs (Petri & Allbritton, 1992, Pope et al., 2003). In this specific settings, sulphonamides have emerged as preferential culprit drugs (Petri & Allbritton, 1992, Pope et al., 2003). Besides hypersensitivity reactions, patients with SLE are also at increased risk of developing immediate-type hypersensitivity-like reactions such as urticaria and angioedema (Ferriani, Silva et al., 2015, Kolkhir, Pogorelov et al., 2016, Luo, Fan et al., 2019).

Diagnostics and treatment

Diagnostics

The diagnosis of SLE is currently based on a combination of clinical signs and laboratory features. For purposes of classification and inclusion in clinical and translational studies, multiple sets of criteria have been developed over time. The most widely used classification criteria are the revised 1997 ACR criteria and the 2012 SLICC criteria (Hochberg, 1997, Petri, Orbai et al., 2012). More recently, a joint effort by the EULAR and the ACR has led to the development of a novel classification algorithm with improved sensitivity and specificity compared to the previous criteria (Aringer, Costenbader et al., 2019). Dedicated algorithms have also been developed for the classification of NPSLE, in the absence of established and univocal laboratory or imaging tools for a definite diagnosis (ACR Ad Hoc Committee on Neuropsychiatric Lupus Nomenclature, 1999, Bortoluzzi et al., 2017).

Multiple tools have also been developed to measure damage accrual and disease activity in SLE. Accumulation of disability due to tissue and organ dysfunction following irreversible disease-related injury or drug-related toxicity is usually measured with the SDI (Gladman, Goldsmith et al., 2000). The SDI tool is an additive scoring system based on 46 items developed on a limited number of paradigmatic cases by a panel of experts and eventually validated in clinical practice. Increasing SDI scores are in fact correlated with patient prognosis in terms of both overall survival and quality of life (Hanly, 1997, Nossent, 1998, Rahman, Gladman et al., 2001, Stoll, Seifert et al., 1996).

There is much less consensus on the reliability of tools assessing disease activity, especially for purposes of evaluation of the effect of treatments. The SLE disease activity index (SLEDAI) is one of the simplest and most widely used scoring systems to quantitate

disease activity in SLE at a given timepoint. It has been developed through an iterative procedure of selection and eventual weighting of relevant features and takes into account both serological activity (low complement, positive aDNA) and clinical features (Bombardier, Gladman et al., 1992). With time, it has undergone multiple revisions and adaptations to respond to a more extended panel of clinical and research questions. Currently, the Safety of Estrogens in Lupus Erythematosus National Assessment SLEDAI (SELENA-SLEDAI) and the 30- or 10-day SLEDAI-2000 (SLEDAI-2K) version of the original SLEDAI score are most frequently employed in clinical practice and for research studies (Gladman, 2015, Gladman, Ibanez et al., 2002). The SLEDAI-2KG is an additional variant of the SLEDAI-2K accounting for the ongoing glucocorticoid therapy and possibly showing better performances in intercepting treatment efficacy (Touma, Gladman et al., 2018). Further variants of the score have also been developed to emphasize clinical over serological activity (clinical SLEDAI, cSLEDAI) or to conform to specific geographical settings (for example the Mexican version of the SLEDAI or MEX-SLEDAI) (Castrejon, Tani et al., 2014). A second branch of the SLEDAI “family” of disease activity scores encompasses tools able to integrate and measure disease activity variations over time. This set includes the adjusted mean SLEDAI, the SLEDAI-2K responder index 50 (SRI-50), the SLE flare index, and the more recent SLE disease activity score (SLEDAS) (Ibanez, Urowitz et al., 2003, Jesus, Matos et al., 2019). The European Consensus Lupus Activity Measurement (ECLAM) score is a compact disease activity score similar to the SLEDAI-2K score but with enhanced emphasis on laboratory features such as lymphopenia, complement variations over time, non-haemolytic anaemia and erythrocyte sedimentation rate (Mosca, Bencivelli et al., 2000). The British Isles Lupus Assessment Group (BILAG) score has a radically diverging design as it is based on a composite array of mixed qualitative and quantitative scores addressing disease activity by systems or “domains”. Specifically, the latest version of the score (BILAG-2004) encompasses nine domains (constitutional, mucocutaneous, musculoskeletal, neurological, cardiorespiratory, ophthalmic, gastrointestinal, renal, haematological). Each domain can be assigned a qualitative score from A (severe activity) to D-E (no activity in a previously involved or uninvolved domain, respectively) based on the expected Physician’s intention-to treat. Each qualitative score is generated based on an algorithm taking into account the presence of

one or more active clinical features, which are in turn scored 0 (absent), 1 (improving), 2 (stable), 3 (worsening), 4 (new) according to their variation compared to the previous month. Domain scores can also be converted into quantitative scores with the following criteria: A=12; B=8; C=1; D, E=0 (Isenberg, Rahman et al., 2005, Yee, Cresswell et al., 2010). Simple disease activity scores can be combined with numerical rating scales such as the 0.0-3.0 or the 0-3 Physician Global Assessment (PGA) scale to generate composite scores.

Composite scores are increasingly employed to assess treatment response and surrogate clinical remission (van Vollenhoven, Voskuyl et al., 2017) to compensate for SLE complexity. The SLE responder index (SRI) tool incorporates variations in the BILAG scores (no new A domain and no more than one new B domain), PGA (increase in the score not exceeding 0.3 points) and SELENA-SLEDAI (decrease of at least four points) compared to a reference evaluation (Luijten, Tekstra et al., 2012). Variants of the SRI include different SELENA-SLEDAI thresholds (SRI-6, SRI-8,... as opposed to SRI-4). In a similar way, the BILAG-based composite lupus assessment endpoint (BICLA) tool defines treatment response as improved BILAG scores (all A scores turned to B, C, or D; all B scores turned to C or D) provided that no new BILAG A or no more than one BILAG B appear (see above for the SRI), no worsening in the SLEDAI score and no more than 10% worsening of the PGA score are observed (Wallace, Kalunian et al., 2014). Lupus Low Disease Activity State (LLDAS) is a third composite index surrogating disease remission (Zen, Iaccarino et al., 2018) by integrating SLEDAI-2K, PGA, treatment tolerance and occurrence of new manifestations compared to previous visits (Franklyn, Lau et al., 2016). Evidence from clinical trials and “real-life” studies suggests that LLDAS might be easily and reproducibly employed in multiple settings as a treatment endpoint (Golder, Kandane-Rathnayake et al., 2019, Ramirez, Canti et al., 2019b). Additional scores such as the Lupus Multivariable Outcome Score (LUMOS) are currently under development (Abrahamowicz, Esdaile et al., 2018).

In addition to general disease clinimetrics, other indices are used to assess activity, damage and prognosis for specific manifestations. For example, the Cutaneous Lupus Erythematosus Disease Area and Severity Index (CLASI) is selectively used to quantitate chronic and acute mucocutaneous involvement (Klein, Morganroth et al., 2010), while the Global Antiphospholipid Syndrome Score (GAPSS) and the score developed by Petri

et al. are useful for adapting ischemic risk prediction to the setting of SLE with or without aPL (Petri, Barr et al., 2019, Sciascia, Sanna et al., 2013).

Treatments

Despite significant achievements in understanding SLE pathogenesis, only a limited set of treatments are currently available for patients with this disease. Glucocorticoids remain the mainstay of therapy to induce remission from the majority of active lupus manifestations (Fanouriakis, Kostopoulou et al., 2019, Gordon, Amissah-Arthur et al., 2018). However, a detrimental role of glucocorticoids in terms of damage accrual and risk of infectious, metabolic and cardiovascular complications even at low doses is increasingly recognised. Accordingly, a paradigm shift in the use of these drugs is currently ongoing towards the systematic use of very short-term high dose intravenous pulses followed by oral corticosteroids administered with faster tapering regimens starting from lower peak doses and ending sooner with the lowest effective amount of drug (Fanouriakis et al., 2019, Fanouriakis, Kostopoulou et al., 2020, Kidney Disease: Improving Global Outcomes Glomerular Diseases Work, 2021). There is, however, much more debate on the optimal timing for glucocorticoid discontinuation in patients with lower disease activity (Fanouriakis et al., 2020, Fasano, Coscia et al., 2021, Moroni, Gallelli et al., 2006, Tani, Elefante et al., 2019). Conversely, there is unanimous agreement on the use of hydroxychloroquine in all patients with SLE unless contraindicated by allergy or drug-related toxicity. This indication is supported by the excellent safety profile of this drug and the robust long-term evidence indicating its role in promoting patient survival, minimising the risk of flares after remission (Costedoat-Chalumeau, Dunogue et al., 2014, Dorner, 2010, Fasano, Pierro et al., 2017) and possibly contrast the onset of complications (Hsu, Lin et al., 2017). Similar evidence is progressively emerging for belimumab, an anti-B-cell activating factor (BAFF) monoclonal antibody with immunomodulant activity (Bruce, Urowitz et al., 2016, Furie, Petri et al., 2011, Iaccarino, Bettio et al., 2017, Manzi, Sanchez-Guerrero et al., 2012, Urowitz, Ohsfeldt et al., 2019).

A limited set of immunosuppressants are currently available to boost and maintain remission in patients with SLE. Mycophenolate mofetil (or mycophenolic acid) is largely employed for major SLE manifestations and constitutes the first-choice treatment for LN.

Cyclophosphamide is also highly potent and effective but currently less employed due to its major side effects on bone marrow, cardiac and gonadal function. Methotrexate, azathioprine, cyclosporine and, less frequently, leflunomide, tacrolimus or dapsone are also employed for the treatment of patients with SLE. Rituximab, an anti-CD20 monoclonal antibody targeting B-cells while sparing plasma-cells is also employed for remission induction in patients with severe manifestations, especially in case of refractoriness to other treatments. The use of rituximab is, however, off-label in multiple Countries, including Italy, due to controversial efficacy data. Specifically, multiple clinical trials involving the use of rituximab have failed to meet their efficacy endpoints, in contrast with evidence from “real-world” cohorts (Merrill, Neuwelt et al., 2010, Reddy, Jayne et al., 2013, Rovin, Furie et al., 2012, Terrier, Amoura et al., 2010). It is currently still unclear whether biological reasons, such as intrinsic resistance to rituximab by patients with SLE (Reddy, Cambridge et al., 2015, Reddy, Croca et al., 2013), or flaws in the design of the clinical trials could account for this incoherence.

Indeed, multiple clinical trials aiming to demonstrate the potential usefulness of novel pharmacological agents have failed over time, despite promising pre-clinical evidence. The reasons behind this disappointing series of events is, again, unclear. Failure to identify homogeneous groups of patients sharing similar pathogenic and clinical features within the broad spectrum of SLE pathophysiology might be a potential general explanation. Consistently, more recent trials aiming at addressing the efficacy of novel agents in selected disease phenotypes, as in the case of baricitinib for arthritis in SLE have shown promising results (Wallace, Furie et al., 2018). Other investigators have instead taken advantage of post-hoc analyses on previously failing studies to identify patient subpopulations more likely to respond to a given treatment and re-design treatment endpoints based on the clinical profile of these subjects. This was specifically the case of SRI (see above) in the development of the trials involving the use of belimumab. In fact, patients with serological activity (that is low complement and positive ADNA) were more likely to achieve a treatment response after belimumab when assessed through SRI. The same population is also more likely to achieve a SRI-4 endpoint due to the role of SLEDAI as the major driver of SRI-4 responses, with low complement and ADNA accounting cumulatively for four SLEDAI points (Manzi et al., 2012). More recently, two twin trials assessing the potential efficacy of anifrolumab, an interferon

inhibitor, in SLE have been completed. While the former one did not meet its SRI endpoint, the latter one was successful, being based on a BICLA endpoint, and led to the approval of the drug by the US Food and Drug Administration (FDA) and recommended for approval by the European Medicine Agency (Furie, Morand et al., 2019, Morand, Furie et al., 2020). Additional molecules either targeting B-cell function, T cell costimulation or innate immune pathways including dendritic cell maturation and complement activation are currently under clinical and pre-clinical development.

Antigen-specific induction of immune tolerance through repetitive and dose-increasing antigen exposure is an established treatment strategy in patients with IgE-mediated allergy to inhalants or hymenopter venom (Nakagome & Nagata, 2021). Pharmacological strategies aiming to restore immune tolerance towards self antigens has less been developed in the setting of autoimmune disorders, but might be attractive, especially in terms of safety and long-term drug-related toxicities for patients with SLE, who show multiple aspects of impaired immune tolerance towards autoantigens (Robinson & Thomas, 2021). *In vitro* studies showed the potential mechanistic feasibility of histone peptides of inducing Treg cells from PBMC derived from patients with SLE (Zhang, Bertucci et al., 2013). Peptide autoepitopes bound to MHC multimers and embedded in iron oxide nanoparticles caused a selective expansion of antigen-specific regulatory T cells along with reversal of clinical manifestations in murine models of other autoimmune diseases, such as type I diabetes, multiple sclerosis and rheumatoid arthritis (either with wild-type or human transgenic HLA background) (Clemente-Casares, Blanco et al., 2016). Apparently, this approach was superior to alternative strategies based on the induction of tolerogenic antigen presenting cells through nanoparticle delivery of autoepitopes and immunomodulatory signals, which were only able to prevent, but not to treat autoimmunity in murine models (Yeste, Nadeau et al., 2012). Lupuzor, a peptide drug with potential tolerogenic properties identified in mice after screening an array of potential candidates has also been tested in a human setting. Despite promising results in phase II trials, a phase III trial with Lupuzor did not meet its endpoint (Robinson & Thomas, 2021, Wallace, 2019, Zimmer, Scherbarth et al., 2013). As with the previous cases, the reasons for this failure are unclear. Mechanistically, the drug, which derives from the U1-RNP protein, had shown potential evidence of an immunomodulatory role on autophagy and MHC class II expression by B-cells (Robinson & Thomas, 2021).

However, anti-U1-RNP immunity is not SLE-specific and studies on T cell responses against these antigens have shown disappointing results in human settings (Kattah, Newell et al., 2015) (see also below). On the other hand, failure to design appropriate trial endpoints and tools for selecting and monitoring patients for treatment responses based on their individual immune profile might also account for these results.

Aetiopathogenesis

Genetics

Nucleic acids have a central role in the pathogenesis of SLE both as target antigens and as plastic vehicles of genetic information. Extensive evidence from genome-wide association studies suggests that a multitude of polymorphisms affecting the functionality of both innate and adaptive immunity might concur to the protean clinical phenotype of SLE (**Table 1**). Notably, the majority of genetic loci associating with increased SLE susceptibility are located in non-coding regions, indicating a prominent role of dysregulated gene expression control rather than structural abnormalities in key inflammatory proteins as the pivotal mechanism accounting for inflammation in SLE (Bentham, Morris et al., 2015, Chen, Morris et al., 2017). Consistent with a significant modulating role of female sex hormones in enhancing SLE susceptibility, men with SLE show a higher number of autosomal mutations than women with SLE (Hughes, Adler et al., 2012). Patients with early-onset SLE and/or lupus nephritis also show a higher burden of risk polymorphisms for the development of SLE (Chen, Wang et al., 2020).

More recent evidence points to the existence of additional genetic factors associated with selected disease phenotypes. This specific setting of active investigation encompasses genetic loci associating not only with classical inflammatory modulators, but also with tissue/organ-specific structural proteins. Mutations affecting the functionality of these genes might, in fact, affect the ability of targets of inflammation to efficiently adapt to the inflammatory injury and/or prevent irreversible damage (Baqai, Isenberg et al., 2014, Chung, Brown et al., 2014, dos Santos, Bringhentti et al., 2015, Faria, Goncalves et al., 2017, Mohan & Putterman, 2015, Ramirez, 2018, Ramirez et al., 2015a, Ramirez, Lanzani et al., 2015b). Epigenetics also has a relevant role in SLE pathogenesis. Altered histone acetylation and methylation promotes aberrant expression of immunomodulating and enhancing genes besides affecting cell apoptosis and, ultimately,

probability of exposure of key nuclear antigens such as DNA and histones (Hu, Qiu et al., 2008). Altered angiotensin converting enzyme 2 (ACE2) epigenetics has been hypothesised as a potential risk factor for severe COVID-19 in patients with SLE (Sawalha et al., 2020).

Table 1: selected non-HLA genetic loci associated with SLE at genome-wide level of significance

Genetic locus	Functional meaning
<i>Factors involved in innate immune responses</i>	
IRF5	Interferon responses
IRF7	Interferon responses
IRF8	Interferon responses
TLR7	Maturation of antigen-presenting cells
<i>Factors involved in general leukocyte biology</i>	
ITGAM	Cell adhesion
PTPN22	B and T cell activation, interferon responses
STAT4	Interferon responses, lymphocyte activation
TNFAIP3	Reduction of lymphocyte activation through NF-kB inhibition
TYK2	Inflammatory responses downstream IL10 and interferon alpha
<i>Factors involved in B cell and antibody responses</i>	
BLK	B lymphocyte activation
FCGR2A	Antibody-mediated phagocytosis
FCGR2B	Antibody-mediated phagocytosis
IL10	B lymphocyte survival and maturation
<i>Factors involved in T cell responses</i>	
CD40	Co-stimulation
CD152 (CTLA-4)	Co-stimulation
CD80	Co-stimulation
IL12A	Th1 polarisation
TNFSF4 (OX40L)	Co-stimulation

Factors involved in the innate immune response

A first set of SLE-related genes encompasses crucial nodes in the initiation and perpetuation of type I interferon-related pathways. IFN α , in turn, constitutes the key mediator of the hallmark antiviral-like responses characterising SLE and other connective tissue diseases (see below). Interferon regulatory factors (IRF) such as IRF5 and IRF7 are involved in the control of IFN α tone and in the expression of IFN α -related genes (which, in turn, constitute the so-called *IFN-signature*). Polymorphisms in IRF genes and in molecules providing intracellular signalling downstream the IFN α receptor, such as signal transducer and activator of transcription (STAT) 1 and 4, have been linked to increased SLE susceptibility (Niewold, Kelly et al., 2008, Niewold, Kelly et al., 2012, Vaughn, Kottyan et al., 2012). Genetically determined alterations in the expression and functionality of the complement cascade and of innate pattern recognition receptors (PRR) concur with altered IFN α signalling in causing a dysfunctional processing and clearance of exogenous and endogenous antigens, including those deriving from cell death debris and/or reactivation of latently infecting viruses or endogenous retroviral elements (Lee, Lee et al., 2012, Mohan & Putterman, 2015). Among cell-bound PRR, TLRs are crucial to trigger the activation of the innate immune response. Altered TLR7 function affects nucleic acid sensing and has been linked to SLE susceptibility (Ramirez-Ortiz, Prasad et al., 2015). Interestingly, TLR7 along with other SLE-related genes is located on the X chromosome and might escape the X-inactivation programme, potentially contributing to an enhanced susceptibility to SLE among women (Sasidhar, Itoh et al., 2012). Mutations affecting the cytoskeleton have also been associated with SLE and might contribute to a defective clearance of cell death debris by phagocytes (Kim-Howard, Maiti et al., 2010, Maiti, Kim-Howard et al., 2014).

Factors involved in the adaptive immune response

Multiple genetic loci contribute to potential alterations in the adaptive immune response as observed in SLE. Class I and II human leukocyte antigens (HLAs) constitute the key mediator of antigen presentation to T lymphocytes and play an intuitively crucial role in the susceptibility to multiple immune-mediated diseases, including SLE. HLA-DRB1 gene variants have more consistently been associated with SLE susceptibility, in line with a prominent role of CD4⁺ T cell responses in the pathogenesis of SLE (Deng & Tsao,

2010). HLA-DRB1*03:01 and 15:01 have more robustly been associated to the development of SLE, although other variants, such as 07:01, 08:01 and 09:01 might also play a role, possibly with variable significance among distinct ancestries (Arango, Perricone et al., 2017, Bang, Choi et al., 2016, Morris, Taylor et al., 2012, Niu, Zhang et al., 2015, Shimane, Kochi et al., 2013, Teruel & Alarcon-Riquelme, 2016b). Of note, selected HLA-DRB1 variants have also been associated with specific manifestations and complications within the spectrum of SLE rather than to a general predisposing role for the development of the disease (Lundstrom, Gustafsson et al., 2013).

Besides HLA, additional genetically determined factors might contribute to dysfunctional adaptive immune responses. Protein tyrosine phosphatase N22 (PTPN22) is associated with a vast array of functions including B and T cell activation, besides regulation of myeloid-driven IFN α responses. Polymorphisms in PTPN22 have been associated with T cell mediated diseases such as anti-neutrophil cytoplasmic antibody AAV and SLE (Alberici et al., 2014, Bentham et al., 2015, Ivashkiv, 2013). Additional molecules involved in intracellular signalling downstream the B and the T cell receptor have been associated to SLE susceptibility and include the B-lymphocyte kinase (BLK), the leukocyte C-terminal/Yamaguchi sarcoma virus homologue novel tyrosine kinase (LYN) or the C-terminal Src kinase (CSK) (Mohan & Putterman, 2015). Other genetic hotspots for SLE susceptibility involved in the modulation of the adaptive response include T cell costimulatory molecules such as OX40 ligand and CD80 (Mohan & Putterman, 2015, Wang, Zhang et al., 2021). Polymorphisms in immunoglobulin Fc receptors might also prompt dysfunctional humoral adaptive responses including incomplete disposal of cell death debris (Brown, Edberg et al., 2007).

Dysfunction of the innate response

Aberrant deployment of the innate immune response is a hallmark of SLE and might play a more relevant role in the initiation of the pathogenic cascade. Defective clearance of cell death debris, either resulting from apoptosis, necroptosis, pyroptosis or, more significantly, suicidal formation of neutrophil extracellular traps (NETs) constitutes a fundamental mechanism in SLE pathophysiology (Emlen, Niebur et al., 1994, Lood, Blanco et al., 2016, Silva, Garcia et al., 2002). On the one hand, overload of cell remnants might be due to reduced cell survival. Impaired DNA damage response has been

described in SLE and might account for the pathogenic effect of environmental stimuli such as ultraviolet light or endogenous factors such as latent virus or retroviral elements in triggering disease flares (Khadjinova et al., 2021, Sander, Szabo et al., 2005, Souliotis & Sfrikakis, 2015, Trela, Nelson et al., 2016).

NET formation is also a characteristic feature of SLE (Manfredi, Covino et al., 2015, Manfredi, Rovere-Querini et al., 2010). NETs are decondensed chromatin threads of nuclear or mitochondrial origin endowed with a vast array of microbicidal moieties and evolutionarily linked to host defence. Components of NETs include digestive enzymes such as myeloperoxidase, PRR enhancing pathogen opsonisation and pro-coagulant mediators such as tissue factor. Accordingly, exposure of nuclear antigens and pro-thrombotic factors in a pro-inflammatory environment not only promotes the generation of autoimmunity but also may trigger the coagulation cascade (a process termed immunothrombosis in this context) (Engelmann & Massberg, 2013, Mantovani, Cassatella et al., 2011, Villanueva, Yalavarthi et al., 2011).

Upstream factors involved in inducing neutrophils to form NETs are incompletely understood (Manfredi, Ramirez et al., 2018). Platelets constitute key functional partners of neutrophils, besides their haemostatic role. Aberrant interactions between platelets and neutrophils, therefore, constitute a major trigger of neutrophil activation and a promising inciting factor for the development of NETosis (Joseph, Harrison et al., 2001, Maugeri, Cattaneo et al., 2014). Enhanced neutrophil survival possibly in combination with overactive autophagy cell programmes might constitute an additional favouring factor for NETosis and account for the frequent detection of large dense granulocytes in patients with SLE (Maugeri, Campana et al., 2014, Tang, Zhang et al., 2015, Villanueva et al., 2011). Quantitative or qualitative impairment of scavenger mechanisms constitutes a potential additional factor involved in defective elimination of nuclear components and pro-inflammatory mediators resulting from cell death in the setting of SLE. Innate PRR such as pentraxins have a role in opsonising pathogens and self components promoting their clearance and are defectively deployed in SLE. This mechanism might possibly also account for the typical low C-reactive protein levels observed clinically in patients with SLE, despite active inflammation. Low complement levels either due to genetic causes or to extensive antibody responses are also a clinical hallmark of active SLE and might contribute to inefficient humoral innate responses (Chen, Daha et al., 2010, Fischetti &

Tedesco, 2006, Leffler, Martin et al., 2012, Liszewski & Atkinson, 2011, Tsang, Bultink et al., 2017). In addition, inefficient DNA degradation due to genetically determined or acquired DNase deficiency has also been described in SLE and may contribute to facilitated sensitisation to nuclear components (Radic, Herrmann et al., 2011, Shin, Park et al., 2004).

Enhanced antiviral-like IFN α -driven responses constitute the second pillar of innate immune dysfunction in SLE. Strikingly, neutrophil undergoing NETosis are interferogenic as they exert an activating effect on plasmacytoid dendritic cells (Garcia-Romo et al., 2011, Swiecki & Colonna, 2015). IFN α , in turn, promotes myeloid dendritic cell activation facilitating (auto)antigen presentation and downstream adaptive responses. Specifically, IFN α promotes plasmablast expansion and enhances antibody responses, promoting persistence of inflammation (Jego, Palucka et al., 2003, McKenna, Beignon et al., 2005, Swiecki & Colonna, 2015). Interestingly, IFN α -driven responses also contribute to endothelial dysfunction and stimulate endothelial-derived microparticle release, thus contributing to systemic spread of pro-inflammatory signals and promoting tissue infiltration by circulating leukocytes (Dieker, Tel et al., 2016, McCarthy, Moreno-Martinez et al., 2017, Ostergaard, Nielsen et al., 2017, Tyden, Lood et al., 2017). As anticipated, IFN α -targeted diagnostic and therapeutic strategies have been tested in lupus cohorts. Disappointingly, IFN α level tracking demonstrated limited practical value in patient monitoring (Banchereau et al., 2016) and clinical trials with IFN α inhibitors had controversial results (Furie, Khamashta et al., 2017, Khamashta et al., 2016, Morand et al., 2020). Recent research in the setting of anti-SARS-CoV-2 responses provides reconciling evidence: anti-IFN α antibodies might be part of the serological spectrum of SLE and cause improper, rather than simply enhanced, antiviral responses during sterile and non-sterile inflammation (Banchereau et al., 2016, Gupta et al., 2021a, Gupta et al., 2021b, Sawalha et al., 2020). Impaired B regulatory cell differentiation in the absence of low-grade tonic IFN α release constitutes a potential mechanism linking dysregulated IFN α -responses to humoral autoimmunity in SLE (Menon, Blair et al., 2016).

While alterations in platelet-neutrophil, neutrophil-dendritic cell and neutrophil-endothelium axes have an established role in the pathogenesis of SLE, emerging evidence from animal models and human studies suggests the potential contribution of additional cellular innate immune players to the pathogenesis of SLE. In particular, mast cells have

been shown to participate in lupus skin inflammation and might have a role in modulating T cell function through inhibition of T regulatory responses and promotion of antigen presentation by dendritic cells (Kaczmarczyk-Sekula, Dyduch et al., 2015) (Walker, Hatfield et al., 2012). More intriguingly, enhanced activation of the basophil-IgE axis in the setting of Th2-driven responses has recently been claimed as a distinct but significant pathway in the pathogenic network of SLE, besides its conventional role in allergic inflammation (Charles, Hardwick et al., 2010). Data from lupus-prone mice suggest that basophils contribute to B cell responses by releasing pro-B cytokines such as IL4, IL6 and BAFF in the context of secondary lymphoid organs. Evidence of basophil activation in human SLE has also been reported (Dema & Charles, 2014, Dema, Lamri et al., 2017, Henault, Riggs et al., 2016, Pan, Feng et al., 2017, Pellefigues & Charles, 2013).

Dysfunction of the adaptive response

Humoral responses

Autoantibodies play a central role in the pathogenesis of SLE and constitute the mainstay of lupus diagnostic tools besides complement factor measurement. Consistently, transcriptome analyses have shown a robust correlation between plasmablast signature and disease activity (Banchereau et al., 2016). Deposition of antibodies at sites of inflammation with eventual complement activation, leukocyte recruitment and non-resolving inflammation is regarded as the principal cause of direct tissue and organ damage in patients with SLE (Tsokos, 2011). Limited evidence also suggests the potential existence of cell-penetrating antibodies causing non-conventional cell cytotoxicity events and possibly contributing to exacerbated DNA damage responses in SLE (Portales-Perez, Alarcon-Segovia et al., 1998, Zannikou, Bellou et al., 2016). To this regard, some authors also hypothesised a role for these antibodies in shaping the unique susceptibility profile of patients with SLE towards cancer, with frequent solid tumours being relatively less frequent and haematological malignancies more frequent in SLE compared to the general population (Portales-Perez et al., 1998, Zannikou et al., 2016). In addition, autoantibodies may facilitate DNA internalisation by dendritic cells through FC γ IIra, favouring TLR activation and IFN α responses (Bave, Magnusson et al., 2003). Evolutionarily, this mechanism has possibly developed to enhance host response to viruses and might therefore be implicated in the link between infections and lupus flares (Henault et al.,

2016, Joo et al., 2021). Interestingly, anti-DNA class E immunoglobulins are potent inducers of IFN α release by plasmacytoid dendritic cells and might act in synergy with canonical anti-DNA IgG in promoting inflammation. Auto-IgE also correlate with SLE activity possibly supporting a pathophysiological view of SLE as a multilevel dysfunction of the immune system, centred on aberrant nuclear antigen processing but extending to a multitude of inflammatory pathways, including those conventionally associated with anti-parasite or allergic responses (Atta, Santiago et al., 2010, Dema, Pellefigues et al., 2014, Henault et al., 2016). Therapeutic depletion of total IgE showed evidence of possible clinical benefit in patients with SLE (Hasni, Gupta et al., 2019). Besides autoantibody production, B cells can contribute to enhanced autoimmune responses as antigen presenting cells.

Multiple factors might account for dysregulated B cell function in SLE. Female sex hormones enhance B cell responses and increase B cell selection permissibility to autoantigens, possibly accounting for the characteristic demographic profile of SLE (Crispin & Tsokos, 2015). Myeloid (Dema et al., 2017, Scapini, Hu et al., 2010) or T cell-derived B-stimulating soluble factors such as BAFF or a proliferation inducing ligand (APRIL) contribute to B cell activation and rise in correlation with active disease and B-cell depletion failure in patients with SLE (Carter, Isenberg et al., 2013, Salazar-Camarena, Ortiz-Lazareno et al., 2016, Zhao, Li et al., 2010), thus constituting a successful therapeutic target (Stohl, 2014).

T-cell-mediated responses

TCR signalling

T cells are endowed with antigen recognition selectivity at a molecular level, fine-tune the inflammatory response with extreme inter- and intra-individual variability and likely have a non-redundant role in the protean clinical/pathophysiological complexity of SLE. Nonetheless, T cell-mediated responses have less been investigated compared to B cell and antibody-related mechanisms (Rother & van der Vlag, 2015). As anticipated, TCR-MHC engagement constitutes the molecular correlate of specific antigen recognition by T cells and occurs thanks to the contribution of a vast array of ancillary mediators both at the level of the cell surface and intracellular space. In particular, functional TCR signalling requires interactions with the lineage-specific CD3 complex, which, in turn, is

physiologically composed of four protein subunits (gamma, delta, epsilon and zeta). Secondary to genetic or epigenetic factors (Chowdhury, Tsokos et al., 2005), patients with SLE are characterised by low levels of CD3 ζ (Pang, Setoyama et al., 2002), which is structurally and functionally substituted by the common gamma subunit of the immunoglobulin Fc receptor (FcR γ). This latter cell surface protein, in turn, promotes stronger downstream inflammatory signals, consistent with its physiological selective expression on activated effector T cells, besides taking part in the formation of the high-affinity IgE receptor (Katsuyama, Tsokos et al., 2018).

T cell subpopulations

Although CD8⁺ T cell counts correlate with disease activity scores (Kubo, Nakayamada et al., 2017) and might play a role in events such as neuronal damage (Contin-Bordes, Lazaro et al., 2011, Liblau, Gonzalez-Dunia et al., 2013) or nephritis (Zabinska, Krajewska et al., 2016), alterations in CD4⁺ subpopulations have been more robustly detected in patients with SLE. In line with the existence of abnormalities in multiple aspects of the immune and adaptive response in SLE, all CD4⁺ subpopulations likely contribute to the initiation and persistence of chronic inflammation and expand or contract dynamically according to the relapsing/remitting nature of the disease. In clinical practice, low lymphocyte and, more specifically, low CD4⁺ counts constitute routine findings in patients with SLE, especially during active disease (Carli et al., 2015). Pathophysiologically, decreased lymphocyte count might represent enhanced migration into target tissues, exaggerated apoptosis rates or the effect of autoimmune phenomena targeting lymphocytes (Abdirama, Tesch et al., 2021, Dolff, Abdulahad et al., 2010, Fayyaz, Igoe et al., 2015, Li, Harada et al., 2007).

Patients with SLE show abnormal patterns of T cell differentiation into memory cells (Fritsch, Shen et al., 2006, Sen, Chunsong et al., 2004), although SLE heterogeneity may prevent appreciation of numerically significant differences with the reference general population when small sample sizes are considered (Maldonado, Mueller et al., 2003). According to some authors, expansion of CD4⁺ effector memory cells is a characteristic feature of patients with active disease (Piantoni, Regola et al., 2018). Other authors reported lower to normal T_{EM} and T_{CM} levels in patients with SLE, suggesting that only the fraction of these T cell subset expressing selected costimulatory molecules might

identify patients with active disease (Zhou, Hu et al., 2018). Expansion of other T cell subpopulations identifying patients subset at increased risk for cardiovascular complications has also been reported (Baragetti, Ramirez et al., 2017). More recently, evidence has been provided suggesting that total CD4⁺ and CD8⁺ T_{SCM} cells are expanded in patients with SLE and able to efficiently repopulate the host Tfh repertoire (Lee, Park et al., 2018). These data corroborate data from other rheumatologic settings (Cianciotti, Ruggiero et al., 2020) and provide potential clues on the mechanisms underlying a) persistence of inflammation and immunological memory towards target autoantigens despite treatments including B cell depletion; b) maintenance of plasticity in terms of antigen recognition and downstream functional differentiation leading to 1) facilitated sensitisation to antigen showing molecular mimicry with the original stimulus; 2) intraindividual variability in terms of clinical phenotypes induced by the same autoreactive pathway (Salem, Subang et al., 2015).

A numerical deficit in Treg cells has been observed by multiple authors in patients with active disease (Lee, Hong et al., 2008, Piantoni et al., 2018, Yang, Chu et al., 2009). In apparent contrast, other authors found higher Treg counts in patients with SLE, with enrichment of Treg-skewed responses in selected patient clusters, independent on disease activity (Kubo et al., 2017). At the opposite extreme of the spectrum, some authors found evidence of increased Treg counts in patients with active disease (Bonelli, Goschl et al., 2014). Methodological discrepancies in gating strategies for T cell classification, disease activity measurement and lack of repeat assays to control for interindividual variability might account for these diverging results (Zhang, Ma et al., 2018). In addition, numerical variations in the proportion of Treg might be uncoupled from their biological functionality (Bonelli, von Dalwigk et al., 2008). Activity-associated B regulatory cell expansion has also been reported (Yang, Yang et al., 2014). Enhanced Th2 and Tfh(2) responses are intuitively linked to dysregulated antibody production as observed in SLE. Higher levels of Tfh have consistently been detected in patients with SLE both in blood and affected tissues (Kubo et al., 2017, Yang et al., 2014). Th2-inbalanced responses have also been described (Funachi, Ikoma et al., 1998). Furthermore, variations in the Th1/Th2 have been suggested to correlate with specific clinical phenotypes, especially in the setting of lupus nephritis (Miyake, Akahoshi et al., 2011). Th17 role in SLE is growingly appreciated. Numerical expansion of Th17 cells has been reported by multiple

authors (Shah, Lee et al., 2010, Yang et al., 2009, Zhong, Jiang et al., 2018) consistent with increased circulating levels of IL17 (Vincent, Northcott et al., 2013, Zhou et al., 2018). Nonetheless, other studies did not replicate these results (Kubo et al., 2017). Animal models of SLE suggest that IL17 dominates the inflammatory landscape in response to critical SLE target antigens (Kattah et al., 2015, Summers, Odobasic et al., 2014). Pharmacological blockade of IL17 responses has shown promising results in recent trials (van Vollenhoven, Hahn et al., 2018).

Antigen-specific T cells

Very limited evidence exists regarding the nature and behaviour of antigen-specific T cells in SLE. The majority of studies employed peptide libraries from known SLE protein target antigens to stimulate patient or mouse lymphocytes and observe T cell proliferation, expression of cell surface markers of activation and/or release of IFN γ and other cytokines. Chromatin-specific responses have more consistently been reported in the literature in human settings (Bruns, Blass et al., 2000, Lu, Kaliyaperumal et al., 1999), followed by indirect evidence of Sm T cell autoreactivity (Talken, Schafermeyer et al., 2001, Zhao, Ren et al., 2019b). More recent studies found that nuclear antigen-reactive T cells can be detected in blood and urine of patients with SLE, correlate with disease activity and associate with renal involvement (Abdirama et al., 2021, Tesch, Abdirama et al., 2020). Interestingly, similar to data from penicilloylated peptide-stimulated cells (Azoury et al., 2018, Nhim et al., 2013), non-negligible T cell responses were found also in healthy individuals, suggesting the existence of qualitative differences in the behaviour of autoreactive or allergen-reactive T cells between subjects with vs without immune-mediated manifestations rather than simple central tolerance factors (Abdirama et al., 2021). Potential associations among anti-Ro, anti-La responses and disease activity have also been suggested, while more controversial results exist for RNP reactivity (Abdirama et al., 2021, Kattah et al., 2015, Monneaux, Hoebeke et al., 2005), also taking into consideration that RNP is not a SLE-specific antigen from a clinical perspective. Contin-Bordes et al. employed direct *ex vivo* T cell visualisation techniques with class I MHC tetramers to identify myelin autoreactive CD8⁺ cells in patient with NPSLE (Contin-Bordes et al., 2011). A pilot study on patients with APS also identified β 2GPI reacting CD4⁺ T cells adding evidence to a model where sensitisation towards this protein

promotes antigen spreading and progressive accrual of additional autoantibodies and enhancement of local inflammatory responses (Benagiano, Borghi et al., 2019, de Moerloose, Fickentscher et al., 2017, Leu, Lee et al., 2019, Salem, Subang et al., 2018, Salem et al., 2015).

AIM OF THE WORK

SLE is a complex autoimmune disease characterised by the combination of multiple defects in the physiological deployment of the immune response. Pathophysiological complexity is mirrored by extreme clinical intra- and inter-individual variability and scarcity of accurate and flexible tools for patient stratification and individualised treatments. Current strategies for monitoring and classifying patients are currently based on a limited number of serological markers which might not entirely reflect SLE clinical manifestations. To this regard, the occurrence of infectious events as disease triggers and of hypersensitivity reactions as complications of SLE has been suggested in the literature but no evidence exists linking the three aspects of immune dysfunction (that is autoimmunity, allergic diathesis and immunodeficiency) in SLE nor providing clues on the potential underlying mechanisms. Multiple key factors in the pathophysiology of SLE, including IFN α and B cell-driven responses, have been tested for their performance as markers of disease activity and therapeutic targets, leading to controversial results. T lymphocyte dynamics have less been studied in SLE, despite their putative role in promoting and maintaining autoimmunity, besides possibly promoting aberrant responses towards innocent environmental stimuli and pathogens. In particular, little is known about the existence and potential clinical and pathophysiological significance of antigen-specific CD4 $^{+}$ T cells in SLE. In an effort to identify novel tools for disease monitoring and potential future mechanisms for molecularly targeted treatments, this study aims to

- a) seek evidence of clinical correlations among autoimmune, allergic and infectious manifestations
- b) test if antigen-specific T cells recognising clinically relevant autoantigens, allergens and/or microbial antigens are specifically detected in the blood of patients with SLE and functionally able to respond when challenged with these antigens;
- c) assess whether differentiation and functional characteristics of autoantigen-specific T cells correlate with SLE clinical phenotype in terms of disease activity.

RESULTS

Clinical evidence

General features

Two-hundred-twenty-two patients with SLE, including 191 women (86%) and 31 men (14%) were cross-sectionally enrolled and prospectively followed up (see also Methods). Their general disease features are reported in **Table 2**. Most patients (135/222, 61%) had been diagnosed with SLE more than 10 years before, while 16 (7%) had less than two years of disease duration. Joint involvement (arthralgia, non-erosive or erosive arthritis), haematological and mucocutaneous manifestations were the most frequent clinical features in patients' history. Anti-double-stranded DNA antibodies were the most frequent serological feature, having been found in 170 (77%) patients. Antiphospholipid antibodies (aPL) were part of the serological profile of 45% of patients. Anti-Smith antibodies (aSm) had been consistently detected in 21% of the patients. Anti-ribonucleoprotein (aRNP), anti-Ro (aSSA) and anti-La (aSSB) antibodies were less prevalent.

At time of enrolment, most patients (135/222, 61%) were in remission according to the lupus low disease activity state (LLDAS) criteria. Accordingly, the median (interquartile range, IQR) SLEDAI-2K score was 4 (2-5). 43% of patients had irreversible dysfunction in one or more tissues or organs as estimated by SDI. One-hundred-twenty-two patients (55%) were taking prednisone at time of enrolment, with a median dose of 5 (4-7) mg/day. Ninety-three patients (42%) were taking one or more immunosuppressants (including cyclophosphamide, mycophenolate mofetil, azathioprine, cyclosporine A, tacrolimus, methotrexate, or leflunomide). One-hundred-eighty-seven patients (85%) were taking hydroxychloroquine. Regarding treatment history, 57 patients (26%) had ever been treated with methotrexate, 97 (44%) with mycophenolate mofetil, 125 (56%) with azathioprine, 39 (18%) with cyclosporine A, 57 (26%) with cyclophosphamide, 15% (7%) with rituximab and 18 (8%) with belimumab.

Table 2: clinical features of patients with SLE

Clinical features	Measurement
Females: n (%)	191 (86)
Age at onset (years): median (IQR)	28 (20-36)
Age at enrolment (years): median (IQR)	44 (34-53)
Disease duration (years): median (IQR)	13 (6-23)
Main clinical manifestations during the disease course: n (%)	
Mucocutaneous manifestations	145 (65)
Malar rash	42 (19)
Photosensitivity	40 (18)
Oral ulcers	28 (13)
Urticaria	11 (5)
Joint disease	168 (76)
Neuropsychiatric involvement	
ACR criteria	42 (19)
SIR criteria	30 (14)
Haematological manifestations	166 (75)
Haemolytic anaemia	30 (14)
Thrombocytopenia	44 (20)
Leukopenia	117 (53)
Lupus nephritis	79 (36)
Serositis	70 (32)
Pleuritis	37 (17)
Pericarditis	37 (17)
Peritonitis	2 (1)
Vasculitis	20 (9)
Constitutional symptoms	
Fever	31 (14)
Lymphadenopathy	28 (13)
Miscellanea	
Eye disease	7 (3)
Myopathy	5 (2)
Autoimmune hepatitis	12 (5)
Lung involvement	5 (2)
Serology	
ADNA	170 (77)
aSm	46 (21)
aSSA	15 (7)
aSSB	13 (6)
aRNP	39 (18)
aPL	99 (45)

Tripartite associations among disease activity, allergy and infections

Retrospective analysis

Epidemiology of allergy

This first part of the study was mainly focused on allergic events. At enrolment, 107 patients (48%) reported a history of allergy (**Table 3**). This prevalence was higher than expected from data obtained in the Italian general population according to the Italian National Institute for Statistics (ISTAT; reported prevalence of allergy = 10.7%; $p < 0.001$ by binomial test) and the European Institute for Statistics (Eurostat; reported prevalence of allergy excluding asthma for Italy = 15.2; $p < 0.001$ by binomial test). Immediate-type hypersensitivity reactions were most frequent (87%) among patients with allergy history. Nine patients had anaphylaxis, yielding an incidence rate of anaphylaxis of $9.1/10^4$ person-years (95% CI = 4.4-16.7), which is in line with the $10.3/10^4$ person-years incidence rate reported by Tejedor-Alonso et al. (Tejedor Alonso, Moro Moro et al., 2012) in the Spanish general population ($p = \text{NS}$ by binomial test) and lower than the $36/10^4$ person-years anaphylaxis incidence rate reported in the Emergency Department setting for the city of Milan, Italy (Pastorello, Rivolta et al., 2001) ($p < 0.001$ by binomial test).

The point prevalence of anaphylaxis at time of enrolment was 4%, which is higher than expected in the Italian general population (Quercia and Incorvaia et al., 2012: 1.6%; $p = 0.010$ by binomial test). Eighty-one patients with SLE reported a history of drug allergy, which accounted for more than 76% of the total allergy spectrum. The prevalence of drug allergy was higher than expected in the general population as per Wong et al. (Wong, Seger et al., 2019) who reported a 13.8% drug-allergy prevalence in the USA population compared to 36% drug allergy among patients with SLE in this study ($p < 0.001$ by binomial test). 56 patients (25%) had allergy history when drug-related hypersensitivity events were excluded. This figure was higher than expected in the Italian general population according to Quercia and Incorvaia (Quercia, Incorvaia et al., 2012), who reported a prevalence of allergy of 16.5% excluding drug-allergy ($p = 0.001$ by binomial test). There was no significant difference in comparison with other European populations (Langen, Schmitz et al., 2013) (**Appendix 1**).

Among drugs, antibiotics (42%) and specifically beta-lactams (32%) were the most frequent culprit agents. Thirty-three patients had respiratory allergy (prevalence 15%) and nine had allergic asthma (prevalence 4%), although none had allergic asthma as the only

allergic manifestation. The prevalence of respiratory allergy but not of allergic asthma was higher than expected in the Italian general population (Quercia et al.: 6%; $p < 0.001$). Hymenopter venom allergy had a similar prevalence in our SLE cohort than in the Italian general population.

Table 3: allergy features in patients with SLE

	N	% of SLE	% of allergic SLE
Any history of allergy	107	48%	100%
Timing			
Immediate-type hypersensitivity	93	42%	87%
Delayed-type hypersensitivity	18	8%	17%
Both manifestations	13	6%	12%
Clinical features			
Skin manifestations	71	32%	66%
Urticaria/angioedema	69	31%	64%
Atopic dermatitis	2	1%	2%
Contact allergic dermatitis	11	5%	10%
Respiratory allergy	33	15%	31%
Allergic rhinitis	27	12%	25%
Allergic asthma	9	4%	8%
Anaphylaxis	9	4%	8%
Culprit agents			
Drugs	81	36%	76%
Antibiotics	45	20%	42%
Beta-lactams	34	15%	32%
NSAIDs	18	8%	17%
Immunosuppressants	6	3%	6%
Hydroxychloroquine	12	5%	11%
Other	50	23%	47%
Inhalants (grass, dustmites, pollens...)	32	14%	30%
Food	10	5%	9%
Hymenopter venom	2	1%	2%

Timing and clinical features of allergic events

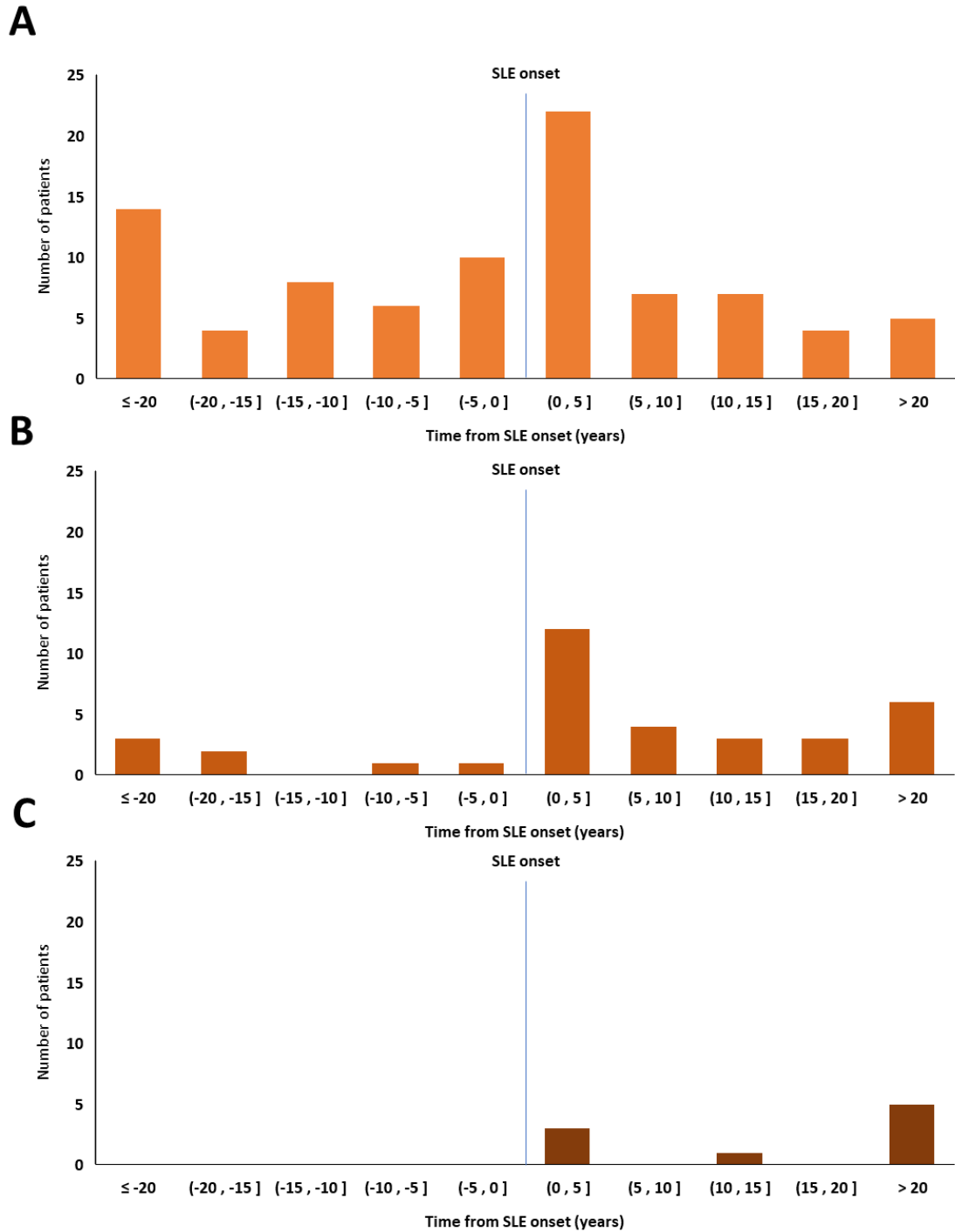
In addition to the 107 patients reporting at least one allergic event, 35 patients reported a second allergic reaction and nine a third allergic event. The median (IQR) time from SLE onset to the onset of the first allergic event was 7.55 (0.91-15.75) years (N=202). Forty-four patients (41% of patients with allergy) had their first allergic manifestation occurring after the onset of SLE. The timing of onset of the first allergic manifestation

tended to cluster around SLE onset, while the second and third manifestations occurred more frequently after disease onset (**Figure 2**). In fact, while the onset of the first allergic manifestation had an incidence rate of 0.17 (95% CI 0.12-0.24) cases per 10 person-years after more than 10 years of disease course or more than 10 years before its onset, the incidence rate of the same event within the 10 years preceding or following SLE onset was 1.52 (1.17-1.93) cases per 10 person-years ($p < 0.001$). Drug-related hypersensitivity events were more frequent in patients with allergy onset after SLE (93%) than in patients with allergy onset before SLE (31%; $\chi^2 = 45.210$; $p < 0.001$). In patients with allergy onset after SLE, a history of allergy was more frequent in patients having ever been treated with cyclosporine A (58% vs 32% in the remainder patients; $\chi^2 = 7.823$; $p = 0.007$) or rituximab (75% vs 33% in the remainder patients; $\chi^2 = 8.428$; $p = 0.009$).

Co-occurrence of infections with allergy was reported for 20/82 (24%) first, 11/33 (33%) second and 3/9 (33%) third allergic events with available data. SLEDAI-2K exceeding four points at time of allergy reaction increased over time as it was reported in 23/82 (28%), 10/33 (30%) and 5/9 (56%) first, second and third episodes, respectively (**Table 4**). Allergy and active SLE manifestations occurred at these time-points despite the fact that 12/107 (11%), 9/35 (26%) and 4/9 (44%) patients with a first, second and third episode respectively were taking a prednisone dose above 5 mg/day.

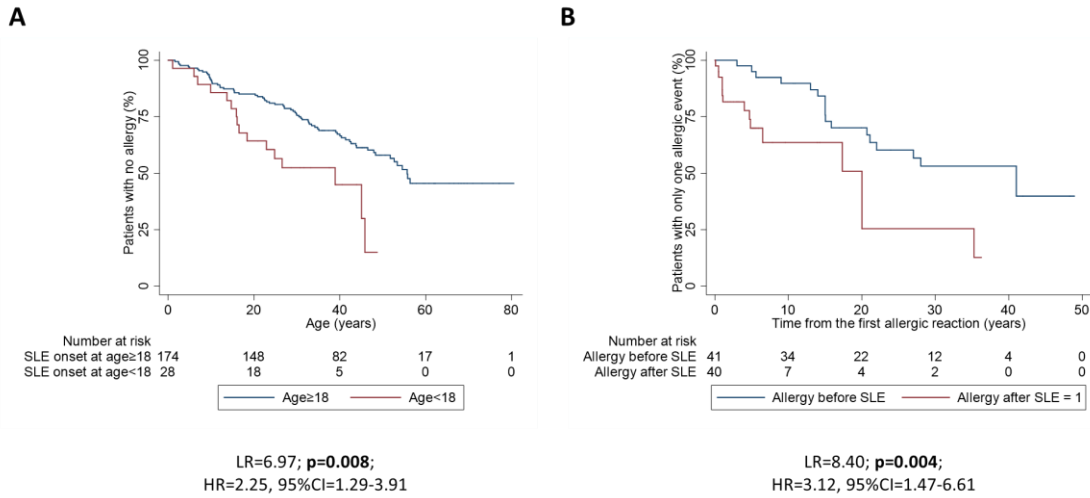
Patients with juvenile SLE (defined as SLE with onset before the age of 18) became allergic more frequently and earlier than patients with SLE onset after 18 years of age (Log rank=6.97; $p = 0.008$; Hazard ratio, HR, =2.25, 95% CI=1.29-3.91). Patients with a first allergic event after the onset of SLE were in turn more likely to become sensitised to a second allergen and to experience a second allergic reaction earlier than patients with allergy onset before SLE (Log rank=8.40; $p = 0.004$; HR=3.12, 95% CI=1.47-6.61; **Figure 3**). There was a statistically non-significant trend towards a higher risk of allergy in women ($p = 0.057$ by Cox's regression analysis) and in patients with vasculitic manifestations ($p = 0.067$ by Cox's regression analysis). Patients with a history of serositis (either pleuritis, pericarditis and/or sterile peritonitis) were slightly less likely to have a history of allergy (Log rank=4.21; $p = 0.040$; HR=0.61, 95% CI=0.38-0.99). There were no other clinical features of SLE showing a differential distribution among patients with or without concomitant allergy. Anti-Smith antibodies showed a possible weak association with allergy (Log rank=4.01; $p = 0.045$; HR=1.64; 95% CI=1.03-2.62).

Figure 2: timing of onset of allergy in relation to SLE onset



Histograms showing the timing of onset of the first (A), second (B) and third (C) allergic event in patient history in relation with SLE onset (blue central line). Each bar represents the number of patients with allergy occurring in a given timeframe before (left of the blue line) or after (right of the blue line) the onset of SLE. The onset of allergy (panel A) was more frequent around or after the onset of SLE. Subsequent allergic events tended to be more frequent after the onset of SLE (panel B and C).

Figure 3: onset of the first and second allergic reactions in patients with SLE



Kaplan-Meier survival curves showing the kinetics of onset of the first (A) and second (B) allergic events in patients with SLE. Patients with early-onset SLE (aged <18 years at disease onset, red line, panel A) had increased chances of becoming allergic compared to patients with later onset. Patients who were diagnosed with allergy after the onset of SLE (red line, panel B) were more likely to experience an additional allergic event during their history.

Damage accrual at time of enrolment did not differ between patients with or without allergy history. There was also no difference in SDI score accrual rate over time between patients with or without at least one allergic reaction. However, patients with a history of two or more allergic events had a higher annual rate of damage accrual (median=0.043 SDI points per year, IQR=0-0.112) compared to patients with only one allergic event (median<0.001 SDI points per year, IQR 0-0.072; p=0.046). There were no significant differences between patients with less vs at least three allergic events.

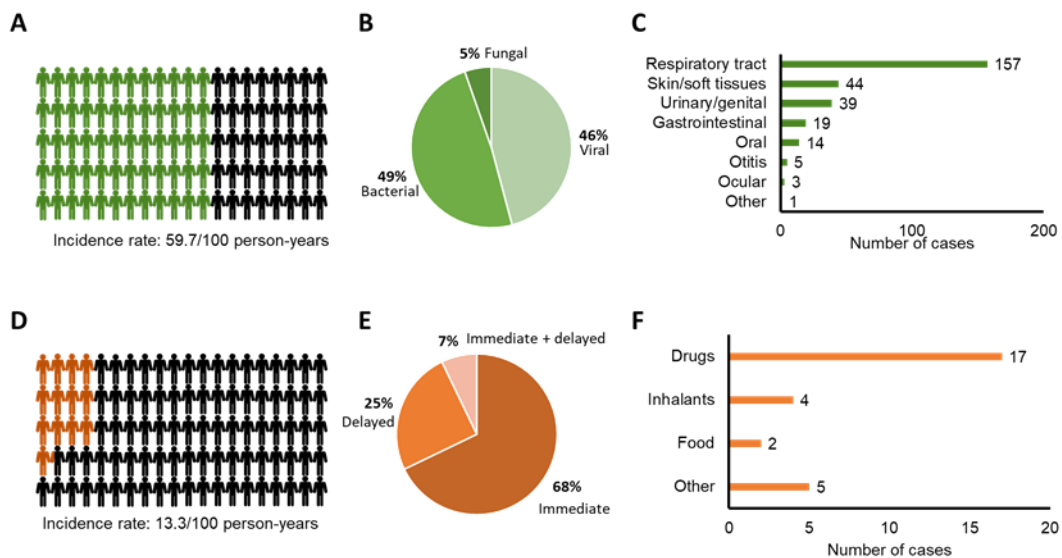
Prospective analysis

One-thousand two-hundred sixty-seven visits (459 cross-sectional visits, 808 follow up visits) were analysed. The median (IQR) interval between each visit was 5.29 (3.45-5.98) months. There were 282 infectious events requiring systemic antimicrobial therapy or absence from work over 472.40 person-years of observation, yielding an incidence rate of 59.7 (95% CI = 53.0-67.0) cases per 100 person-years. The average frequency of recent infection reporting was 18% per patient per visit. The most frequent site of infection was the respiratory tract (55%), followed by skin and mucosal infections (16%) and urinary tract/genital infections (14%). Of 168 infections with definite aetiology, 82 were bacterial

(49%) and nine fungal (5%). There were 77/168 (46%) viral infections including 23 herpesvirus infections (30% of the viral infections, 14% of all infections with definite aetiology (**Figure 4 A-C**).

Twenty-eight allergic reactions (17/28 drug-related events, 3/28 due to beta-lactam drug sensitisation) were recorded over 211.17 person-years, yielding an incidence rate of 13.26 (95% CI = 8.98-18.91) total cases and 8.05 (95% CI = 4.85-12.63) drug-related events per 100 person-years. The average frequency of recent allergy reporting was 3% per patient per visit. Nineteen reactions were of immediate-type only, seven were of delayed-type only and two showed clinical features of both immediate- and delayed-type hypersensitivity (**Figure 4 D-F**). Antibiotics and immunosuppressants (each accounting for 29% of drug-related allergic reactions) along with NSAIDs (12% of drug allergy events) constituted the most frequent culprit drugs.

Figure 4: infections and allergic reactions



Descriptive graphs showing the epidemiological features of infectious (green, panel A-C) and allergic (orange, panel D-F) events in a prospective study involving 222 patients over 1,267 consecutive visits. Panel A and D show the estimate number of infections (A) and allergic reactions (D) occurring in a year for every 100 persons considered. Panel B depicts the distribution of infectious events by aetiology. Panel C reports the site distribution of the recorded infectious events. Panel E shows the proportion of immediate-, delayed- and combined type of allergic reactions over the total of allergic reactions. Panel F depicts the number of allergic events by culprit agent.

In 795/1,267 visits (63%), patients fitted the criteria for LLDAS. The average frequency of SLEDAI-2K exceeding four points was 21% per patient per visit. The

calculated combined probabilities of observing active disease, recent infections and/or recent allergic reactions retrospectively and prospectively are reported in **Table 4**. In order to test the negative hypothesis that hypersensitivity reactions, infections and disease activity occurred as independent events, the expected probability of observing a combination of two or three events together was calculated as the product of the observed frequencies of each event at prospective analysis. These figures were then compared to the actual frequencies of occurrence of two or three combined events with the binomial test of hypotheses. The observed frequencies of combined autoimmune, allergic and/or infectious manifestations were higher than expected by considering each item independently, both at prospective and retrospective observation.

Table 4: observed and expected frequencies of allergic, infectious and autoimmune manifestations in patients with SLE

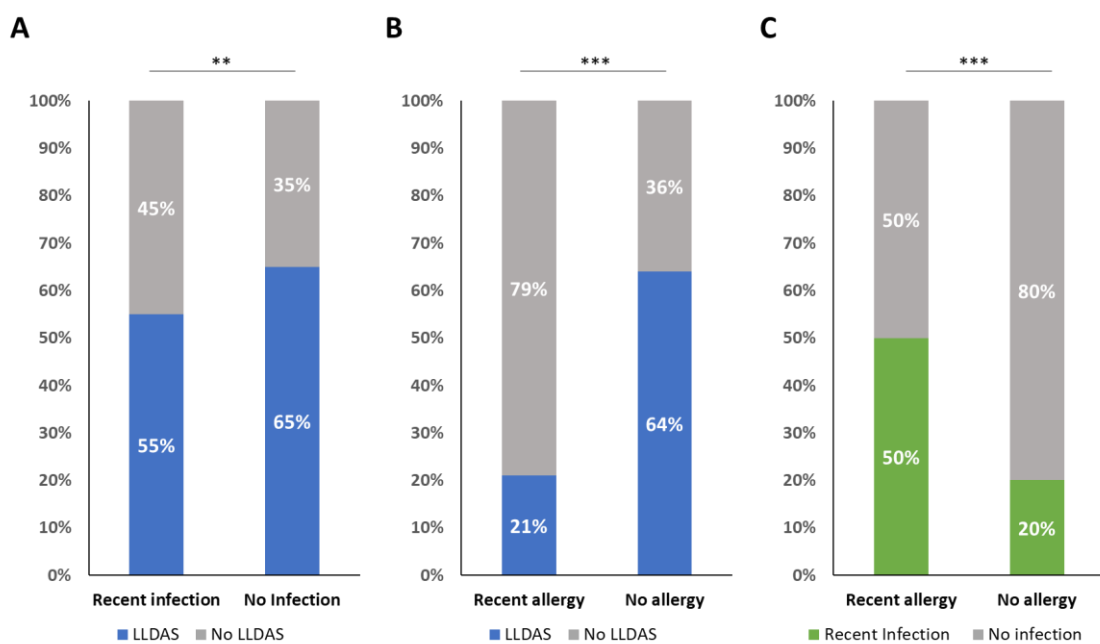
	Observed		Expected
	Retrospective observation	Prospective observation	
SLEDAI-2K>4	ND	21% ^	
Recent infection	ND	18% ^	NA
Recent allergy	ND	3% ^	
SLEDAI-2K>4 + Recent infection	ND	4.12%	3.78% §
SLEDAI-2K>4 + Recent allergy	1 st event: 23/202 (11%)*** 2 nd event: 10/67 (15%)*** 3 rd event: 5/26 (19%)***	1.12% ^*	0.63% §
Recent infection + Recent allergy	1 st event: 20/195 (10%)*** 2 nd event: 11/67 (16%)*** 3 rd event: 3/26 (12%)***	1.01% ^*	0.54% §
SLEDAI-2K>4 + Recent Infection + Recent allergy	1 st event: 7/202 (3%)*** 2 nd event: 4/67 (6%)*** 3 rd event: 2/26(8%)***	0.51% ^***	0.11% §

Abbreviations/symbols. *: p>0.05; **: p<0.010; and ***: p<0.001 by binomial probability test. ^: calculated as the mean rate of each event per single patient per visit; § calculated by multiplying each isolated probability observed prospectively.

Consistently, at prospective analysis, LLDAS was inversely associated with a recent infection ($\chi^2=8.234$; p=0.005; RR=0.67, 95% CI 0.51-0.88) or allergy ($\chi^2=20.912$;

p<0.001; RR=0.16, 95% CI 0.06-0.39). Patients with a recent history of allergy were more likely to also report a history of a recent infection ($\chi^2=15.509$; p<0.001; RR=4.08, 95% CI 1.92-8.67; **Figure 5**). Patients reporting a recent history of allergy were younger (median age 35 (24-46) years) than patients with no recent allergy (median age 43 (34-53); p=0.008) and had higher SLEDAI-2K scores (4 (3.5-11) vs 3 (2-4); p<0.001). Twenty-six out of 28 allergic events (93%) occurred in patients with a known history of allergy.

Figure 5: associations among SLE activity, allergic reactions and infections



Bar charts showing the relative frequencies of recent infections and allergic events among patients in remission vs with active disease according to the achievement of lupus low disease activity state (LLDAS) criteria (panel A, B). Panel C shows the relative frequency of allergic events among patients also reporting vs not reporting a recent infection. Abbreviations/symbols: **: p<0.01; ***: p<0.001.

Genetic studies

Frequency of HLA-DRB1 genotypes among patients and controls and in the general population

HLA-DRB1 genotype data were obtained from 185 patients with SLE, 80 patients with TAK and 86 healthy subjects. Population data from relatively large sample sizes were only available for low-resolution HLA-DRB1 genotyping. At low resolution, HLA-DRB1*03 was more prevalent in patients with SLE and HLA-DRB1*07 in patients with TAK than expected in the Italian general population (**Table 5**).

Table 5: low-resolution HLA-DRB1 allele frequencies

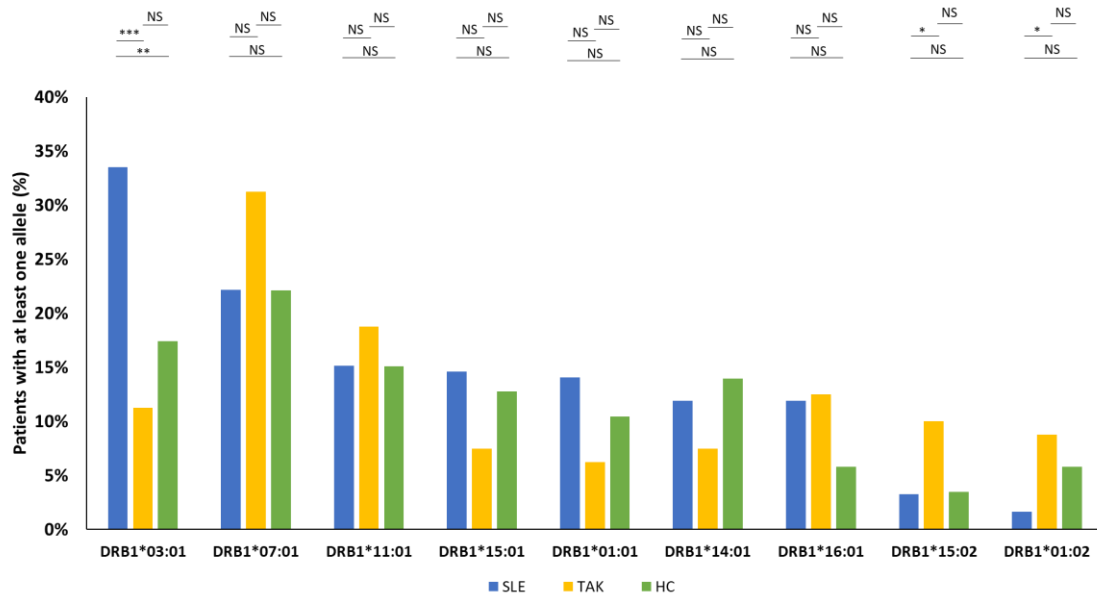
	SLE		TAK		HC		Italian General Population*	
	%	Sample size	%	Sample size	%	Sample size	%	Sample size
DRB1*03	34%	185	11%	80	17%	86	20%	159,311
DRB1*11	29%	185	40%	80	34%	86	48%	159,311
DRB1*07	22%	185	31%	80	22%	86	25%	159,311
DRB1*13	21%	185	24%	80	26%	86	31%	159,311
DRB1*15	18%	185	18%	80	16%	86	26%	159,311
DRB1*01	18%	185	15%	80	19%	86	18%	159,311
DRB1*04	15%	185	20%	80	24%	86	16%	159,311
DRB1*14	13%	185	9%	80	14%	86	10%	4,575
DRB1*16	13%	185	14%	80	7%	86	9%	4,575
DRB1*08	5%	185	5%	80	2%	86	6%	159,311
DRB1*10	3%	185	10%	80	3%	86	3%	159,311

*Data were retrieved from the Allele Frequency Net - <http://www.allelefreqencies.net> - (Gonzalez-Galarza, McCabe et al., 2019), based on data from multiple studies (De Re, Caggiari et al., 2010, Rendine, Borelli et al., 1998).

High-resolution data are shown in **Figure 6** and in **Appendix 2**. Consistent with low-resolution data, HLA-DRB1*03:01 was significantly more frequent in patients with SLE than in HC ($\chi^2=7.455$; $p=0.006$) or in patients with TAK ($\chi^2=14.114$; $p<0.001$). HLA-DRB1*15:01 and 01:01 were also more frequent in patients with SLE than in controls. HLA-DRB1*07:01 and 11:01 were more frequent in patient with SLE and with TAK

compared to HC. HLA-DRB1*15:02 and 01:02 were significantly more frequent in patients with TAK than in SLE ($\chi^2=5.095$; $p=0.035$ and $\chi^2=7.815$; $p=0.010$, respectively).

Figure 6: high-resolution HLA-DRB1 allele frequencies



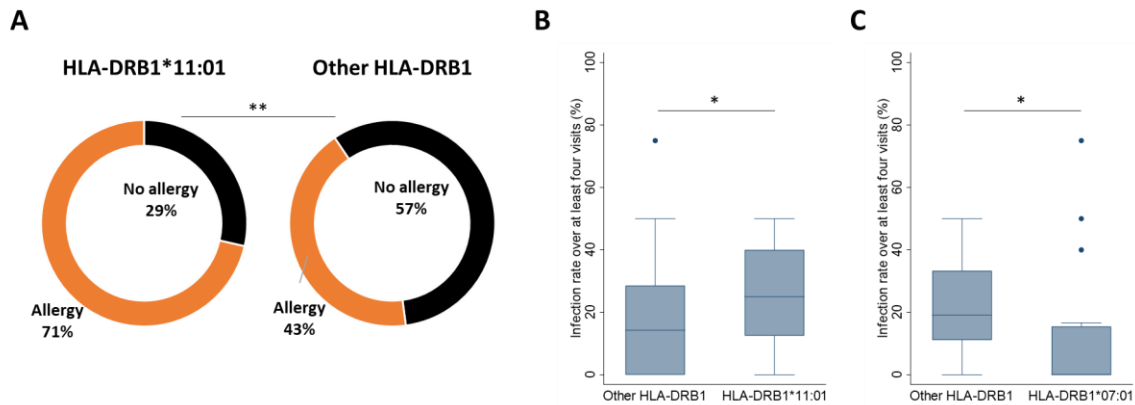
Bar chart showing the frequency of selected HLA-DRB1 genotypes in patients with SLE (blue), patients with TAK (yellow) and HC (green). Abbreviations/symbols: NS: non-significant; *: $p<0.05$; **: $p<0.01$; ***: $p<0.001$.

Genotype-phenotype associations

There was no specific association among autoimmune manifestations of SLE and HLA alleles. Patients with at least one HLA-DRB1*11:01 allele had more frequently a history of allergy (71%) than patients with other HLA-DRB1 variants (43%, $\chi^2=7.886$; $p=0.007$). Among patients with data from at least four follow up visits in the frame of prospective clinical analyses (N=70), those with HLA-DRB1*11:01 reported higher rates of infections (25% of the visits, IQR 12.5-40%) compared to patients with other HLA profiles (14%, IQR 0-29%; $p=0.044$). Patients with at least one copy of the HLA-DRB1*07:01 reported lower rates of infections (<1%, 0-15% vs 19%, 11-33%; $p=0.011$; **Figure 7**). Of 160 genotyped patients who were monitored for SARS-CoV-2 infection, nine (5.6%) had symptomatic COVID-19 in 2020. Their clinical features are reported in **Appendix 3**. None of them carried a HLA-DRB1*07:01 allele ($p=0.206$). The frequency of HLA-DRB1*03:01 and of HLA-DRB1*11:01 alleles did not differ significantly among patients who had (22% both alleles) or did not have COVID-19 (34% and 16%,

respectively). Patients with HLA-DRB1*15:01 were significantly more frequent among COVID-19 cases (4/9, 44%) than among subjects without COVID-19 (19/151, 13%; $p=0.025$).

Figure 7: associations among HLA genotypes, allergic and infectious manifestations



This figure shows the associations among HLA genotypes, allergic manifestations and infectious events in patients with SLE. Patients with SLE who had at least one copy of the HLA-DRB1*11:01 allele had more frequently a history of allergy compared to patients with SLE with a different HLA profile (panel A). When observed prospectively over the course of at least four visits, patients with SLE with at least one HLA-DRB1*11:01 allele showed higher rates of infections (panel B), while patients with HLA-DRB1*07:01 alleles showed lower infection rates (panel C) compared to patients with other genotypes. Abbreviations/symbols: NS: non-significant; *: $p<0.05$; **: $p<0.01$; ***: $p<0.001$.

Peptide epitopes

Based on the results above, on literature review and on the use of an HLA binding prediction software (see Methods) a list of potential candidate autoantigens was generated and eventually shortened to a narrower list of potential peptide epitopes of interest (**Appendix 4 and 5**). The final list of peptides is reported in **Table 6**. Regarding autoantigens of interest, histone H3 and H4-derived peptides were preferred over peptides derived from Smith antigen, β 2GPI, U1-RNP or other histone proteins due to the high prevalence of anti-nuclear immunity in the study population, existing evidence of CD4+ T-cell immunogenicity of at least one epitope in the literature (Lu et al., 1999) and high likelihood of binding to the study HLA-DRB1 molecules according to the Immune Epitope Database (IEDB) and the binding parameters requested by the MHC-tetramer manufacturer. A penicilloylated albumin peptide was selected as a marker of allergenicity due to the high-prevalence of beta-lactam allergy in the study population and the role of

penicilloylated albumin as the major antigenic determinant in beta-lactam hypersensitivity (Li, Yeung et al., 2020, Mirakian, Leech et al., 2015). Evidence of efficient binding to both HLA-DRB1 molecules and of CD4+ T cell immunogenicity further supported the choice of the penicilloylated albumin sequence reported in **Table 6** (Azoury et al., 2018). EBV latent-cycle sequences (EBNA1 and EBNA2) were selected as markers of the response to infectious agents, due to the high prevalence of EBV infection in the general population (Leogrande & Jirillo, 1993, Pordeus et al., 2008), a more relevant role of EBV over other pathogens in the pathogenesis of SLE (see also the Introduction) and to evidence of CD4+ T cell response and HLA binding to epitopes from the selected antigens (Draborg et al., 2014, Draborg, Jorgensen et al., 2012, Draborg et al., 2018, Draborg, Sandhu et al., 2016, Long, Chagoury et al., 2013, Meckiff, Ladell et al., 2019).

Table 6: synthetic peptide sequences employed for T-cell studies

Peptide #	Antigen	HLA restriction	Peptide sequence (aminoacid number)	Reference
1	Penicilloylated albumin	DRB1*03:01 DRB1*11:01	PELLFFAK*RYKAAFT	(Azoury et al., 2018)
2	Histone H3	DRB1*11:01	LPFQRLMREIAQD (66-78)	ND
3	Histone H4	DRB1*03:01	GLIYEETRGVLKVFL (49-63)	(Lu et al., 1999)
4	EBNA1	DRB1*11:01	HIFAEVLKDAIKDL (569-582)	ND
5	EBNA 2	DRB1*03:01	PAQPPPGVINDQQLHHLPSG (301-320)	(Long et al., 2013, Meckiff et al., 2019)

*: denotes penicilloylation of the lysine residue. Abbreviations. ND: no data

T cell phenotype

General features

Thirty-two patients with SLE, 11 patients with TAK and 10 HC (one of whom tested for both HLA-DRB1*03:01 and HLA-DRB1*11:01-related epitopes) with compatible HLA-DRB1 had sufficient cell material and were comparable in terms of sex distribution and age to be included in T-cell studies. Demographics are reported in **Table 7** and **Appendix 6**. Additional details on SLE-specific features, including laboratory test results at time of blood sampling and clinimetrics, are reported in **Table 8**. Five patients with SLE were tested during remission and active disease, as an exploratory analysis on longitudinal variations of T cell parameters over time. All these five patients were taking

mycophenolate mofetil to maintain the remission phase, whereas they were on azathioprine (n=3) or no immunosuppression (n=2) during the active phase. The median (IQR) prednisone dose in this subset of patients was 5 (5-5) mg/day during the active phase and 5 (0-5) mg/day during the remission phase.

Table 7: subjects included in T-cell studies

	SLE (N=32)	TAK (N=11)	HC (N=10*)
Females: N (%)	28 (88)	10 (91)	9 (90)
Age (y): median (IQR)	41 (34-51)	44 (36-47)	41 (34-51)
HLA-DRB1*03:01: N(%)	15 (47)	4 (36)	6 (60)
HLA-DRB1*11:01: N(%)	19 (59)	7 (64)	5 (50)
Disease duration (y): median (IQR)	17 (9-23)	10 (7-15)	NA
Prednisone dose (mg/day): median (IQR)	1 (0-4)	5 (3-5)	0

* One of the ten HC had both HLA-DRB1 alleles of interest and was therefore tested for T responses to both HLA-DRB1*03:01- and HLA-DRB1*11:01-bound peptides.

Table 8: SLE-specific clinical features of patients included in T-cell studies

Parameter	Value	
Disease activity indices		
LLDAS: N(%)	23 (72)	
SLEDAI-2K: median (IQR)	2 (2-4)	
Total BILAG score: median (IQR)	1 (0-9)	
PGA: median (IQR)	1 (0-1)	
Patient NRS: median (IQR)	7 (7-8)	
Chronic damage (SDI): median (IQR)	1 (0-2)	
Laboratory features		
	Value	Reference range
Haemoglobin (g/dl): median (IQR)	13 (12-15)	F: 12-16 M: 14-18
Platelets x 10 ³ /microlitre: median (IQR)	255 (215-324)	130-400
WBC (cells/microlitre): median(IQR)	5,900 (4,480-7,425)	4,800-10,800
Neutrophils (%): median(IQR)	60 (54-66)	40-75
Lymphocytes (%): median(IQR)	29 (23-33)	20-50
Monocytes (%): median(IQR)	8 (7-9)	2-15
Eosinophils (%): median(IQR)	2 (1-3)	1-6
Basophils (%): median(IQR)	1 (0-1)	0-2
ESR (mm/h): median(IQR)	11 (6-32)	1-20
CRP (g/l): median(IQR)	1 (0-4)	<6
Serum creatinine (mg/dl): median(IQR)	0.8 (0.7-1.0)	0.5-1.1
Complement C3 (mg/l): median(IQR)	0.95 (0.76-1.07)	0.90-1.80
Complement C4 (mg/l): median(IQR)	0.19 (0.13-0.21)	0.10-0.40

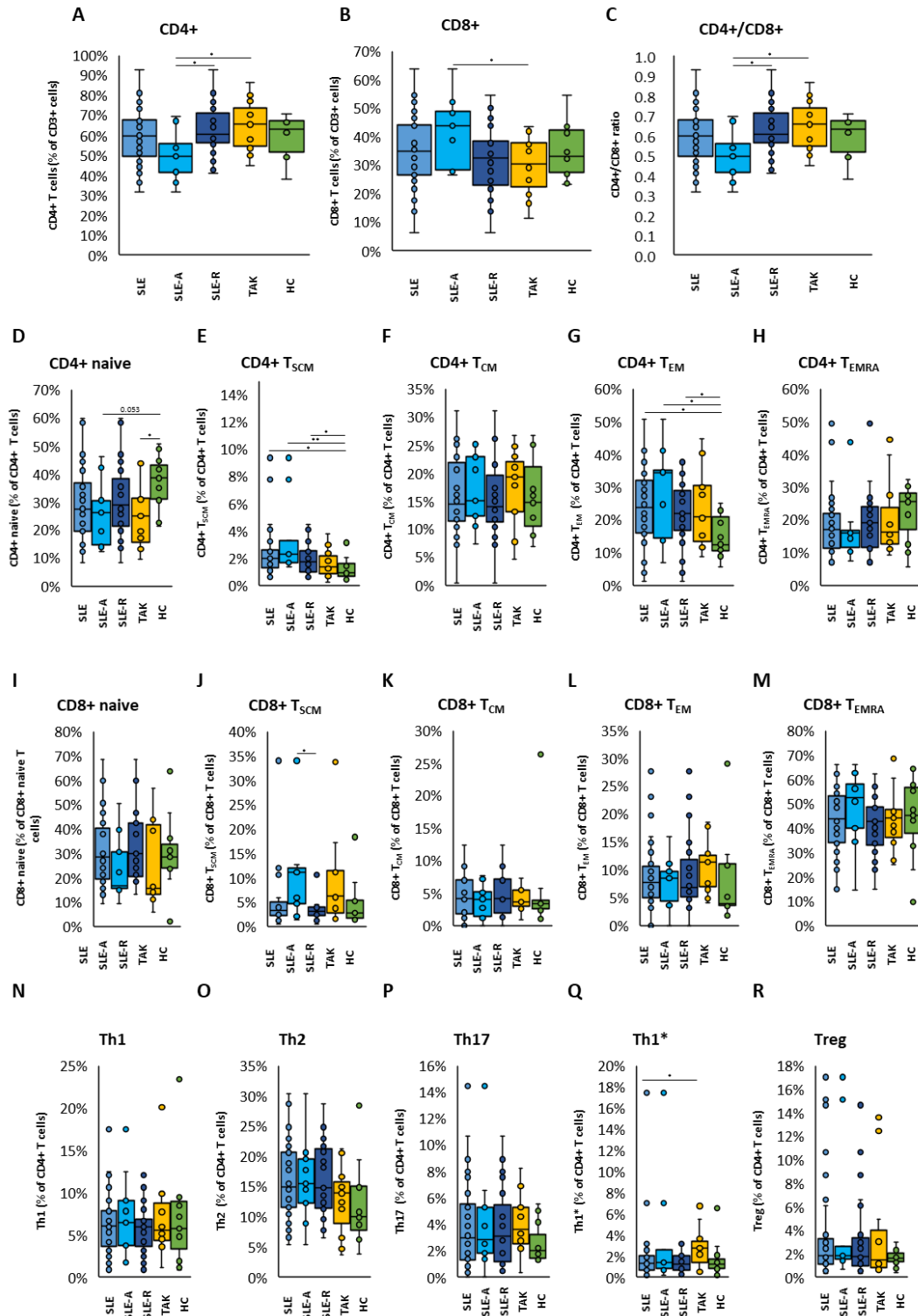
Positive aDNA: N (%)	18 (56)	Negative
aDNA titre: N(%)		
borderline	2 (11)	Negative
low	4 (22)	Negative
moderate	8 (44)	Negative
high	2 (11)	Negative
very high	2 (11)	Negative
<hr/>		
Treatment features: N (%)	Current	Ever
Immunosuppressants	18 (56)	30 (81)
Cyclophosphamide	0 (0)	8 (25)
MMF	12 (38)	15 (47)
MTX	3 (9)	10 (31)
AZA	2 (6)	14 (44)
Cyclosporine A	0	5 (16)
RTX	1 (3)	4 (13)
Immunomodulants	28 (88)	31 (97)
HCQ	28 (88)	31 (97)
BEL	1 (3)	2 (6)

At basic flow cytometry analysis, there was no significant difference among patients with SLE and controls in terms of circulating CD4+ or CD8+ T lymphocytes. Patients with active SLE (LLDAS=0) had lower CD4+ counts (49% of total CD3+, IQR=42-56%) compared to patients with SLE in remission (61%, IQR=56-73%; p=0.020) and to patients with TAK (65%, IQR=53-67%; p=0.038). Patients with active SLE had higher CD8+ counts (44% of total CD3+, IQR=28-49%) than patients with TAK 30%, IQR=20-39%; p=0.044). Accordingly, patients with active SLE had lower CD4/CD8 ratios than patients with SLE in remission and patients with TAK.

Patients with SLE had significantly more circulating T_{SCM} (2.00%, IQR=1.25-2.62%) compared to HC (0.91%, IQR=0.67-1.77%; p=0.012). Circulating CD4+ T_{EM} were increased in patients with SLE (24%, IQR=16-33%) as compared to HC (13%, IQR=10-23%; p=0.014). T_{SCM} and T_{EM} populations were expanded in patients with active SLE (2.30%, IQR=1.70-3.27% and 34%, IQR 14-35%; p=0.007 and p=0.030, respectively). Conversely, naïve CD4+ cells were more represented among HC (38%, IQR=31-45%) than among patients with TAK (25%, IQR=14-32%; p=0.024) and active SLE (26%, IQR=15-31%; p=0.053). The difference between the proportion of CD8+ T_{SCM} among patients with active (11%, IQR=5-12%) vs non active SLE (3%, IQR=2-4%; p=0.014) was also statistically significant.

In terms of T cell polarisation, there was no statistically significant difference among patients with SLE with or without active disease and HC, although Th2 cells were more represented within the CD4+ repertoire in patients with SLE than in controls. Among patients with SLE, patients on immunosuppressants had lower Th1 (4.23% CD4+ cells, IQR=2.21-6.44%) and Th2 cells (12.30% CD4+ cells, IQR=9.61-15.13%) than patients without immunosuppressants (7.20% Th1/CD4+ cells, IQR=5.31-10.61%, $p=0.028$; 20.13% Th2/CD4+ cells, IQR=17.74-22.90%, $p=0.002$). Th1* cells were more expanded in patients with TAK (2.73%, IQR=0.65-3.61%) compared to patients with SLE (1.27%, IQR=0.67-2.06%, $p=0.048$; **Figure 8**).

Figure 8: T-cell memory and polarisation phenotype in patients and controls



Boxplots showing the differential distribution of T cells in patients with SLE (blue) with active disease (bright blue, SLE-A) or in remission (dark blue, SLE-R), patients with Takayasu’s arteritis (TAK, yellow) and healthy controls (HC, green), as assessed by flow cytometry. Panel A-B depict the frequency of CD4+ and CD8+ T lymphocytes, whereas the ratio between CD4+ and CD8+ cells is shown in panel C. Panel D-H show the frequency of CD4+ T cells according

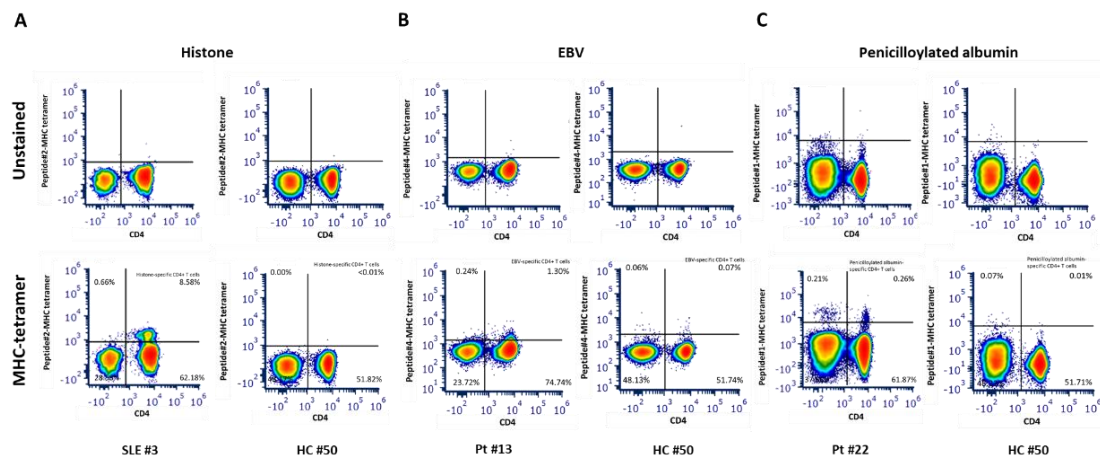
to their memory/differentiation phenotype. Panel I-M show the frequency of CD8+ T cells according to their memory/differentiation phenotype. Panel N-R show the frequency of CD4+ T cells according to their polarisation.

Abbreviations. T_{SCM}: stem-cell memory T cells, T_{CM}: central memory T cells, T_{EM}: effector memory T cells, T_{EMRA}: terminally differentiated T cells. *: p<0.05; **:p<0.01. For further details on the gating strategy see **Table 14** and **Table 15**.

Antigen-specific T-cell phenotype

Antigen-specific CD4+ events were detected at low frequencies in patients and controls (**Figure 9**).

Figure 9: antigen-specific T cells



Representative density plots elaborated on flow cytometry data and showing the frequency of histone- (A), EBV- (B), and penicilloylated albumin-specific (C) CD4+ T cells in three patients with SLE (left) and one HC (right). The upper plots show the control signal obtained without tetramer staining.

Histone-specific responses in patients and controls

Histone-specific CD4+ T cells above the diagnostic threshold for positive ADNA in patients' history (**Appendix 7**) were more frequent in patients with SLE (23/32, 72%) than in HC (0/(10+1); p<0.001) and TAK (3/11, 27%; p<0.014). Two of the three patients with TAK with histone-specific CD4+ T cells (patient #36 and patient #39) had positive ANA in their clinical history.

Quantitatively, the fraction of absolute total histone-specific CD4+ T cells over CD3+ cells was higher in SLE (4.03‰, IQR=3.54-4.26‰) than in HC (0.09‰, IQR=0-0.25; p<0.001) and TAK (0.51‰, 0-2.13‰; p=0.008). The corresponding fractions of CD4+

cells were 6.37‰ (6.23-8.84) in SLE, 0.14‰ (0-0.41) in HC (p<0.001 vs SLE) and 0.76‰ (0-2.46) in TAK (p=0.003 vs SLE).

When compared to HC, patients with SLE showed a harmonic expansion of histone-specific CD4+ T cells at different stages of differentiation and with distinct polarisations. Specifically, histone-specific CD4+ naïve, T_{SCM}, T_{CM} and T_{EM} cells and histone-specific Th2, Th17 and Treg (along with similar trends for Th1 and Th1*) cells were all expanded in patients with SLE compared to HC. The same findings were obtained by either considering the fraction of each subpopulation over the total CD3+ or CD4+ cells. Within the histone-positive compartment, T_{CM} were particularly expanded in patients with SLE. Similar findings were obtained in comparison with patients with TAK, who showed lower levels of circulating histone-specific CD4+ naïve, T_{CM} and T_{EM} cells and lower histone-specific Th2, Th17, Th1 and Treg cells compared to patients with SLE (**Table 9**).

Table 9: histone-specific CD4+ T cell subpopulations in patients and controls

Antigen-specific CD4+ T cells	Median (IQR) n/10 ⁵ CD3+ cells			Median (IQR) n/10 ⁵ of CD4+ cells			Median (IQR) % of Tetramer+ cells		
	SLE	TAK	HC	SLE	TAK	HC	SLE	TAK	HC
By memory phenotype									
Naïve	8.8 (0.8-102.88) ^{§§^}	0 (0-1.52)	0 (0-1.99)	15.68 (1.81-143.33) ^{§§^}	0 (0-1.76)	0 (0-3.23)	28 (10-44)	0 (0-19)	13 (0-33)
T _{SCM}	3.38 (0-44.92) ^{§§}	0 (0-1.03)	0 (0-0)	4.7 (0-69.71) ^{§§}	0 (0-1.48)	0 (0-0)	6 (0-15)	2 (0-15)	0 (0-4)
T _{CM}	15.01 (3.27-66.96) ^{§§§^}	1.01 (0-5.57) [§]	0 (0-0.62)	25.23 (5.54-110.68) ^{§§§^}	1.51 (0-7.27)	0 (0-1.02)	22 (12-35) [§]	27 (15-40)	0 (0-9)
T _{EM}	8.33 (2.1-24.84) ^{§§§^}	0 (0-0.88)	0 (0-0.49)	13.33 (4.36-37.92) ^{§§§^}	0 (0-1.29)	0 (0-0.73)	10 (5-29)	5 (0-13)	0 (0-9)
T _{EMRA}	1.98 (0-12.51)	0 (0-0.51)	0 (0-0.94)	3.09 (0-23.37)	0 (0-0.76)	0 (0-1.53)	3 (0-12)	0 (0-13)	9 (0-23)
By polarisation phenotype									
Th1	0 (0-9.51)	0 (0-0)	0 (0-0)	0 (0-12.29)	0 (0-0)	0 (0-0)	0 (0-5)	0 (0-1)	0 (0-1)
Th2	8.28 (1.17-26.1) ^{§§§^}	0 (0-0.92)	0 (0-1.21)	11.87 (2.3-36.51) ^{§§§^}	0 (0-1.06)	0 (0-2.02)	13 (3-32)	0 (0-19)	1 (0-22)
Th17	0 (0-3.39) ^{§^}	0 (0-0)	0 (0-0)	0 (0-5.47) ^{§^}	0 (0-0)	0 (0-0)	0 (0-5)	0 (0-0)	0 (0-0)
Th1*	0 (0-2.59) [^]	0 (0-0)	0 (0-0)	0 (0-4.78) [^]	0 (0-0)	0 (0-0)	0 (0-2)	0 (0-0)	0 (0-0)
Treg	1.91 (0-43.39) [^]	0 (0-0.46)	0 (0-0.3)	2.76 (0-54.46) ^{§^}	0 (0-0.53)	0 (0-0.5)	8 (0-24)	0 (0-5)	4 (0-27)

^:p<0.05, ^^:p<0.01 vs TAK; §: p<0.05, §§: p<0.01, §§§: p<0.001 vs HC

EBV-specific responses in patients and controls

Eight out of ten subjects with established positive EBV status had detectable EBV-specific CD4+ T cell events. With EBV-specific CD4+ T cell count threshold set on the median count in this subset, EBV-specific CD4+ T cell-positive subjects tended also to be more frequent in patients with SLE (18/32, 56%) than in HC (3/(10+1), 27%; p=0.162) and TAK (4/11, 36%, p=0.310).

Patients with SLE had a higher proportion of EBV-specific absolute total CD4+ T cell counts over total CD3+ cells (6.38‰, IQR=0.44-20.24‰) and CD4+ cells (12.25‰, IQR=0.78-28.27) than HC (1.01‰ of CD3+ cells, IQR=0.00-2.86‰; p=0.039; and 1.61‰ of CD4+ cells, IQR=0.00-5.85‰; p=0.041).

The fraction of EBV-specific CD4+ T_{SCM} cells over CD3+ cell count was higher in patients with SLE than in HC, whereas EBV-specific Th1* cells were relatively more frequent in SLE than in TAK. There were no substantial differences among TAK and HC (Table 10).

Table 10: EBV-specific CD4+ T cell subpopulations in patients and controls

Antigen-specific CD4+ T cells	Median (IQR) n/10 ⁵ CD3+ cells			Median (IQR) n/10 ⁵ of CD4+ cells			Median (IQR) % of Tetramer+ cells		
	SLE	TAK	HC	SLE	TAK	HC	SLE	TAK	HC
By memory phenotype									
Naïve	31.73 (0-124.53)	0 (0-40.01)	3.9 (0-23.18)	63.26 (0-200.97)	0 (0-60.67)	5.87 (0-52.04)	38 (10-58)	32 (0-48)	36 (28-49)
T _{SCM}	14.41 (0-32.56) [§]	1.01 (0-17.32)	0.98 (0-3.43)	24.29 (0-54.07)	1.51 (0-29.08)	1.47 (0-6.84)	11 (3-27)	11 (2-19)	6 (3-9)
T _{CM}	4.19 (0-56.31)	0 (0-12.57)	2.93 (0-12.47)	8.09 (0-97.65)	0 (0-16.94)	4.4 (0-29.47)	11 (1-23)	7 (0-18)	15 (12-21)
TEM	4.07 (0-41.52)	1.01 (0-34.4)	2.28 (0-9.95)	9.02 (0-74.79)	1.51 (0-58.63)	3.3 (0-21.27)	7 (0-13)	13 (7-28)	14 (8-20)
T _{EMRA}	9.05 (0-27.98)	1.01 (0-10.84)	2.93 (0-12.83)	15.34 (0-43.43)	1.51 (0-19.16)	4.4 (0-22.01)	6 (2-20)	10 (7-18)	19 (13-27)
By polarisation phenotype									
Th1	0 (0-0)	0 (0-0.46)	0 (0-3.73)	0 (0-0)	0 (0-0.53)	0 (0-5.85)	0 (0-0)	0 (0-1)	0 (0-2)
Th2	0 (0-2.53)	0 (0-0.92)	0 (0-4.69)	0 (0-3.86)	0 (0-1.06)	0 (0-8.18)	0 (0-4)	0 (0-3)	0 (0-2)
Th17	0 (0-2.11)	0 (0-0.3)	0 (0-3.37)	0 (0-3.3)	0 (0-0.49)	0 (0-6.03)	0 (0-1)	0 (0-0)	0 (0-1)
Th1*	0 (0-4.59) [^]	0 (0-0)	0 (0-12.24)	0 (0-6.75) [^]	0 (0-0)	0 (0-19.36)	0 (0-7)	0 (0-0)	0 (0-7)
Treg	3.81 (0-27.66)	0 (0-4.62)	0 (0-87.7)	5.09 (0-43.65)	0 (0-5.28)	0 (0-135.45)	9 (0-52)	0 (0-9)	0 (0-41)

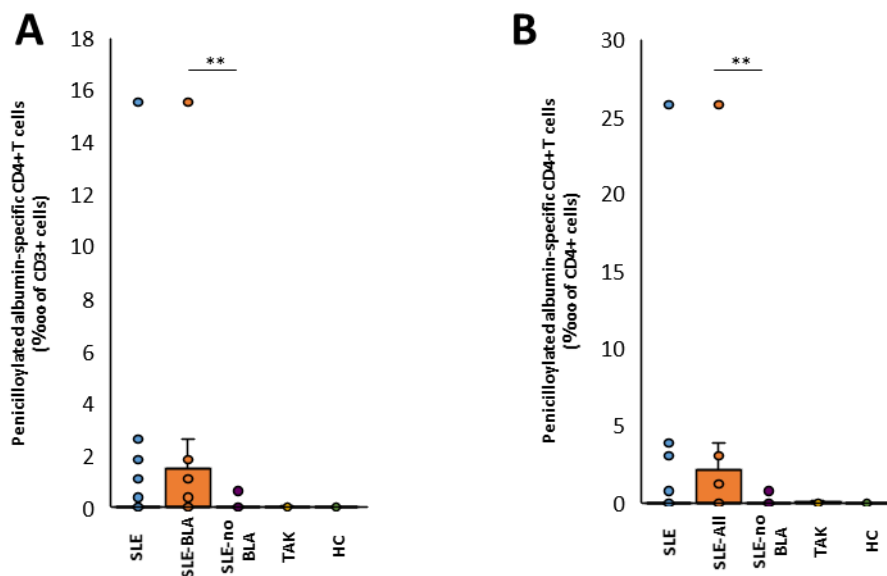
[^]:p<0.05, ^{^^}:p<0.01 vs TAK; [§]: p<0.05, ^{§§}: p<0.01, ^{§§§}: p<0.001 vs HC

Penicilloylated albumin-specific responses in patients and controls

Penicilloylated albumin-specific CD4+ T cells above the diagnostic threshold for beta-lactam allergy (Appendix 7) were absent in patients with TAK and HC and detected in 5/11 (45%) patients with SLE with beta-lactam allergy and 1/21 (5%) patients with SLE without beta-lactam allergy ($\chi^2=7.846$; p=0.011). This latter patient (patient #29) had, however, a history of allergy to tetracyclines, which might have constituted a confounder (Hamilton & Guarascio, 2019). Patients with SLE and beta-lactam allergy had higher levels of absolute total anti-penicilloylated albumin-specific CD4+ T cells over the total count of CD3+ and CD4+ cells than patients with SLE and no beta-lactam allergy (p=0.005 for both variables; Figure 10). Patients with SLE and beta-lactam allergy had

lower EBV-specific CD4+ T_{EM} cells with reference to total CD4+ cells (0‰, IQR=0-1.19‰) than patients without allergy history (2.04‰, IQR=0-8.66 ‰; p=0.038). No other significant differences were found in terms of histone or EBV-specific CD4+ T cells between these groups. Penicilloylated albumin-specific CD4+ T cells were expanded at various stages of differentiations and with prominent expansion of the extreme (naïve and T_{EMRA}) subpopulations. In terms of polarisation, Th2 and Treg cells recognising penicilloylated peptides were more significantly expanded in patients with SLE and beta-lactam allergy (Table 11).

Figure 10: total penicilloylated albumin-specific T cells



This figure shows the proportion of antigen-specific CD4+ T cells recognising penicilloylated-albumin peptides over the total CD3+ (A) and CD4+ counts (B) in patients with SLE, TAK and HC. Abbreviations. SLE-BLA: SLE and beta-lactam allergy; SLE no-BLA: SLE without beta-lactam allergy. **:p<0.01.

Table 11: penicilloylated albumin-specific CD4+ T cells in patients with SLE

Antigen-specific CD4+ T cells	Median (IQR) n/10 ⁵ CD3+ cells		Median (IQR) n/10 ⁵ of CD4+ cells		Median (IQR) % of Tetramer+ cells	
	SLE - allergy to beta-lactams	SLE - no allergy to beta-lactams	SLE - allergy to beta-lactams	SLE - no allergy to beta-lactams	SLE - allergy to beta-lactams	SLE - no allergy to beta-lactams
By memory phenotype						
Naive	0 (0-18.2) ^{^^}	0 (0-0)	0 (0-24.94) ^{^^}	0 (0-0)	50 (33-71)	35 (35-35)
T _{SCM}	0 (0-0.48) [^]	0 (0-0)	0 (0-0.63) [^]	0 (0-0)	1 (0-5)	0 (0-0)
T _{CM}	0 (0-1.44) [^]	0 (0-0)	0 (0-1.89) [^]	0 (0-0)	2 (0-3)	0 (0-0)
T _{EM}	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
T _{EMRA}	0 (0-24.67) ^{^^}	0 (0-0)	0 (0-39.62) ^{^^}	0 (0-0)	29 (22-45)	65 (65-65)
By polarisation phenotype						
Th1	0 (0-0) [^]	0 (0-0)	0 (0-0) [^]	0 (0-0)	0 (0-6)	0 (0-0)
Th2	0 (0-1.29) ^{^^}	0 (0-0)	0 (0-1.52) ^{^^}	0 (0-0)	8 (6-13)	0 (0-0)
Th17	0 (0-0.41) [^]	0 (0-0)	0 (0-0.51) [^]	0 (0-0)	5 (0-6)	0 (0-0)
Th1*	0 (0-1.64)	0 (0-0)	0 (0-2.02)	0 (0-0)	25 (0-27)	100 (100-100)
Treg	0 (0-5.53) ^{^^}	0 (0-0)	0 (0-7.6) ^{^^}	0 (0-0)	28 (17-69)	0 (0-0)

[^]:p<0.05, ^{^^}:p<0.01.

Comparison of antigen-specific T cell profiles in patients with SLE

In patients with SLE, the fraction of histone-specific CD4+ T cells over total CD3+ and CD4+ cells was correlated to the respective fractions of EBV-specific CD4+ T cells ($\rho=0.464$; $p=0.008$ and $\rho=0.412$; $p=0.019$, respectively). Patients with beta-lactam allergy also showed a positive correlation among the fraction of penicillin-specific CD4+ T cells over the whole CD3+ and CD4+ population and the fraction of EBV-specific CD4+ T cells over the total CD4+ count ($\rho=0.612$; $p=0.026$ for both variables). This correlation was possibly more evident in patients with beta-lactam allergy and active disease ($\rho>0.999$; $p=0.001$; $n=4$). In patients with SLE the fraction of total histone-specific CD4+ T cells over CD3+ and CD4+ cells were also correlated to platelet count at time of clinical evaluation ($\rho=0.388$; $p=0.028$ and $\rho=0.360$; $p=0.043$, respectively). There was no correlation among ADNA titres at time of sampling and total histone-specific T cells. ADNA titres at time of sampling also showed no correlation with the majority of histone-specific CD4+ T cell subpopulation counts and were only slightly inversely correlated with the proportion of histone-specific Th1* cells over total CD3+ and CD4+ cells ($\rho=-0.382$; $p=0.034$ and $\rho=-0.387$; $p=0.031$, respectively).

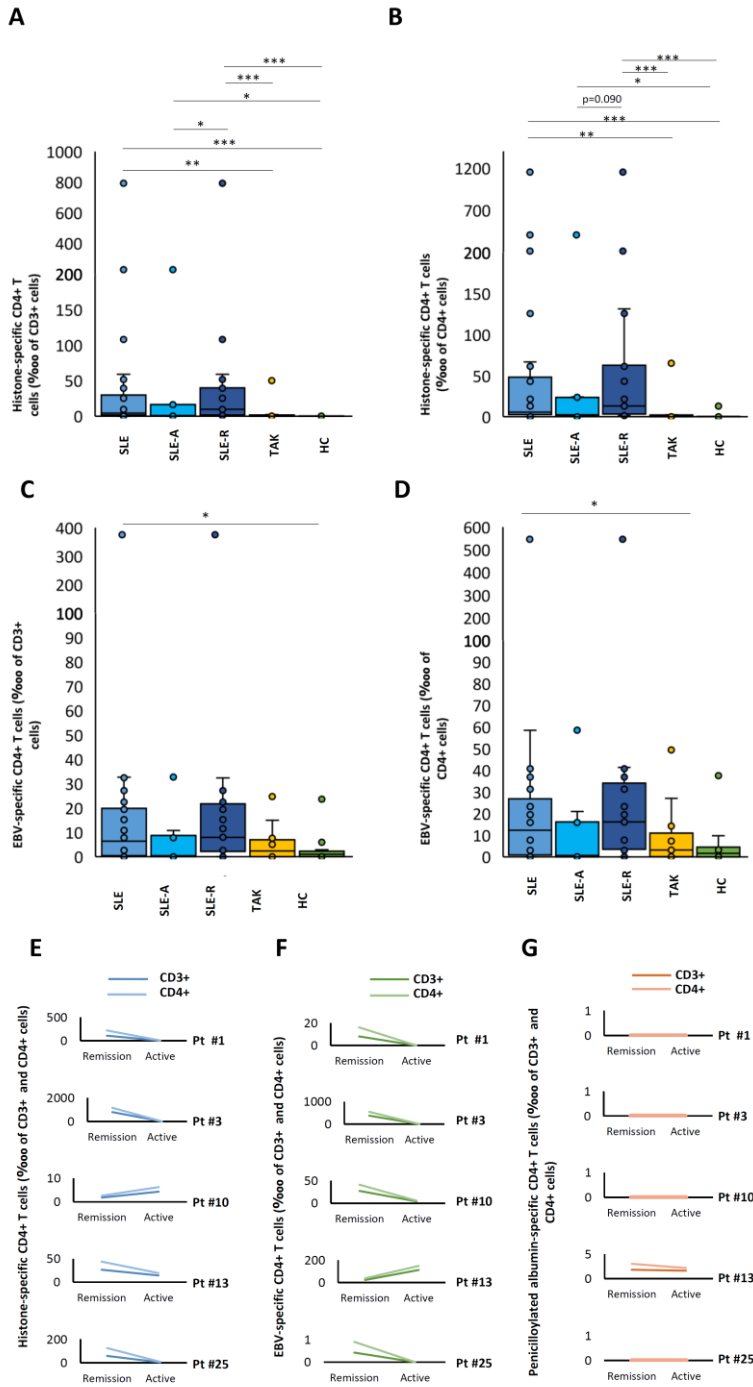
Impact of SLE activity on antigen-specific T cells

There were no substantial differences in total antigen-specific T cells and in antigen-specific T cell subpopulations when patients with SLE were stratified by disease manifestations. In terms of disease activity, patients with active disease had lower total histone-specific CD4⁺ T cell counts (0.76‰ of CD3⁺ cells, IQR=0.43-16.22‰ and 2.43‰ of CD4⁺ T cells, IQR=0.97-23.59‰) than patients fitting the criteria for LLDAS (9.52‰ of CD3⁺ cells, IQR=1.75-39.87‰; p=0.047; and 13.01‰ of CD4⁺ T cells, IQR=3.13-63.74‰; p=0.089). Consistently, patients tested in both conditions had higher total histone-specific CD4⁺ T cell counts when in remission than during active disease (median Δ = -55‰ of CD3⁺ and median Δ =-117‰ of CD4⁺ during active disease; p=0.089). Total EBV-specific T cells tended to decrease during disease activity. Patient #13 who was allergic to beta-lactams and was tested during remission and activity, showed a decrease in total penicilloylated albumin-specific CD4⁺ T cells during disease activity (**Figure 11**).

When the comparison among patients with active disease and remission was extended to antigen-specific subpopulations, histone-specific and EBV-specific CD4⁺ T cell subpopulations were found generally decreased with regard to total CD3⁺, CD4⁺ and tetramer⁺ cells. Histone-specific and EBV-specific CD4⁺ T_{EM} cells were more prominently reduced in patients with active disease. A descending trend of histone-specific CD4⁺ T_{EM} cells was also observed in patients tested during remission and active disease (median Δ = -11‰ of CD3⁺ and median Δ =-22‰ of CD4⁺ during active disease; p=0.080), who also showed a relative increase in histone-specific T_{CM} (median Δ =13% of tetramer⁺ cells; p=0.043) and a decrease in EBV-specific CD4⁺ T_{SCM} (median Δ =-25% of tetramer⁺ cells; p=0.043). Histone-specific Th2 and Treg (and less strongly Th1 and Th1*) cells were all significantly reduced in patients with active disease. An activity-related reduction in histone-specific Th2 cells (median Δ = -7‰ of CD3⁺ and median Δ =-14‰ of CD4⁺ compared to remission; p=0.043), along with similar trends in the other Th subpopulations, were consistently observed in patients with SLE tested under different disease activity states. Furthermore, histone specific CD4⁺ Treg cells were inversely correlated with SLEDAI-2K (ρ =-0.437; p=0.012) and showed a possible hyperbolic decrease with increasing SLEDAI-2K values (**Appendix 8**). EBV-specific CD4⁺ T cell reduction was more prominent in Th17, Th1* and Treg subpopulations

(Table 12). In patients tested twice, ADNA titres did not change significantly from remission to active disease and were not correlated to changes in histone-specific T cell subpopulations.

Figure 11: total antigen-specific T cells by disease activity



This figure shows variations of total antigen-specific CD4+ T cells with disease activity in patients with SLE and provides comparative information from control groups. Boxplots A-D report the frequency of histone-specific (panel A-B) and EBV-specific (panel C-D) CD4+ T cells over the total CD3+ and CD4+ counts in patients with SLE, TAK and HC. Panel E-G show the variations in the proportion of histone specific (E, blue), EBV-specific (F, green) and penicilloylated albumin-specific (G, orange) CD4+ T cells in five patients with SLE with repeat samples during remission and active disease. Abbreviations. SLE-A: active SLE; SLE-R: SLE in remission. *: $p < 0.05$; **: $p < 0.01$; ***: $p < 0.001$.

Table 12 antigen-specific CD4+ T cell subpopulations in patients with SLE by disease activity

Antigen-specific CD4+ T cells	Median (IQR) n/10 ⁵ CD3+ cells		Median (IQR) n/10 ⁵ of CD4+ cells		Median (IQR) % of Tetramer+ cells	
	SLE - active	SLE- remission	SLE - active	SLE- remission	SLE - active	SLE- remission
Histone-specific CD4+ T cells						
By memory phenotype						
Naïve	0 (0-50.87)	13.27 (3.51-146.34)	0 (0-73.09)	22.38 (6.12-219.51)	25 (0-36)	31 (12-49)
T _{SCM}	0 (0-11.56)	3.95 (0-51.05)	0 (0-16.61)	6.07 (0-86.26)	7 (0-13)	4 (0-15)
T _{CM}	1.45 (0-46.25)	19.74 (8.8-77.18)	2.94 (0-66.44)	28.49 (13.2-128.29)	23 (4-28)	20 (13-38)
T _{EM}	2.18 (0-7.25) [^]	11.44 (4.04-35.24)	6.02 (0-14.71)	21.16 (6.08-69.64)	33 (9-38)	9 (5-22)
T _{EMRA}	0 (0-4.35)	3.07 (0-25.83)	0 (0-8.83)	5.07 (0-48.57)	5 (0-20)	3 (0-11)
By polarisation phenotype						
Th1	0 (0-0) ^{^^}	4.72 (0-24.5)	0 (0-0) ^{^^}	5.11 (0-46.39)	0 (0-0)	2 (0-10) [^]
Th2	0 (0-3.33) ^{^^}	10.37 (5.15-69.39)	0 (0-6.27) ^{^^}	14.15 (9.71-129.84)	13 (0-18)	13 (6-34)
Th17	0 (0-0.83)	0.94 (0-4.77)	0 (0-1.57)	1.02 (0-7.54)	0 (0-4)	0 (0-4)
Th1*	0 (0-0) ^{^^}	1.71 (0-9)	0 (0-0) ^{^^}	2.75 (0-11.2) ^{^^}	0 (0-0)	0 (0-4) [^]
Treg	0 (0-0) ^{^^^}	9.49 (1.2-110.27)	0 (0-0) ^{^^^}	13.74 (1.86-178.97) ^{^^^}	0 (0-0)	13 (4-43) ^{^^}
EBV-specific CD4+ T cells						
By memory phenotype						
Naïve	0 (0-108.15)	35.5 (0-146.82)	0 (0-174.4)	71.74 (0-207.57)	33 (6-52)	38 (20-60)
T _{SCM}	0 (0-21.63)	18.52 (4.7-34.36)	0 (0-32.25)	36.53 (7.27-56.26)	19 (3-27)	11 (3-25)
T _{CM}	0 (0-10.82)	8.81 (0-69.86)	0 (0-16.12)	15.06 (0-106.74)	10 (1-21)	11 (1-23)
T _{EM}	0 (0-0) [^]	9.8 (0.64-47.71)	0 (0-0) [^]	14.89 (0.76-78.35)	0 (0-7)	8 (2-15)
T _{EMRA}	0 (0-13.06)	9.65 (0.49-28.56)	0 (0-26.48)	16.28 (0.81-43.6)	7 (1-23)	6 (3-18)
By polarisation phenotype						
Th1	0 (0-0)	0 (0-0.85)	0 (0-0)	0 (0-1.6)	0 (0-0)	0 (0-5)
Th2	0 (0-0)	0 (0-3.31)	0 (0-0)	0 (0-5.79)	0 (0-1)	0 (0-6)
Th17	0 (0-0) [^]	0 (0-2.55)	0 (0-0) [^]	0 (0-4.61)	0 (0-0)	0 (0-4)
Th1*	0 (0-0) [^]	2.59 (0-6.75)	0 (0-0) [^]	5.5 (0-10.77)	0 (0-0)	4 (0-12)
Treg	0 (0-0) ^{^^}	8.49 (0.86-37.69)	0 (0-0) ^{^^}	9.6 (1.17-59.66)	0 (0-0)	24 (5-71)

[^]:p<0.05, ^{^^}:p<0.01, ^{^^^}:p<0.001.

Associations among antigen-specific T cells and treatments in patients with SLE

In patients with SLE, there was no significant correlation among immunosuppressant or prednisone dose and antigen-specific T cell counts. Patients taking at least one immunosuppressant (n=18/32, **Table 8**) had higher naïve histone-specific CD4+ T cells (3.51‰ CD3+, IQR=0.31-26.46‰; 5.01‰ CD4+, IQR=0.72-32.61‰) than patients without immunosuppressants (0.33‰ CD3+, IQR=0-0.88‰, p=0.044; 0.50‰ CD4+, IQR=0.72-1.34‰, p=0.034). Histone-specific T_{EMRA} were also higher in patients on immunosuppressants (0.73‰ CD3+, IQR=0-6.66‰; 0.17‰ CD4+, IQR=0-8.89‰) than in patients on immunomodulant treatment only (0‰ CD3+, IQR=0-0.36‰, p=0.023; 0‰ CD4+, IQR=0-0.63‰, p=0.025). Within the histone-specific compartment, Th2 cells were more represented in patients without immunosuppressants

(33.64%, IQR=12.66-40.00%) than in patients on immunosuppressants (9.29%, IQR=0.95-14.81%; p=0.010). There were no significant variations in EBV-specific and penicilloylated albumin-specific T cell counts with taking at least immunosuppressant.

Regarding specific treatments, (**Table 8**), there was no significant difference in antigen-specific T cell counts when patients were stratified for current or past history of treatment with azathioprine, cyclosporine A, cyclophosphamide, rituximab and belimumab. Patients having ever been treated with methotrexate had higher total EBV-specific T cell counts over the total CD3+ T cell count (19.45‰, IQR=7.83-32.38‰) than the remainder patients (2.17‰, IQR=0-8.70‰, p=0.031). Patients with a history of methotrexate treatment also had higher EBV-specific T_{EMRA} cells (2.76‰ CD4+, IQR=0.97-5.41‰) than patients having received different treatments (0.05‰ CD4+, IQR=0-1.26‰; p=0.038).

Patients with a current (n=12, 9/12 in remission) and/or past history (n=15) of treatment with mycophenolate mofetil had higher levels of total histone-specific CD4+ T cells over CD3+ count (22.16‰, IQR=5.63-56.29‰ and 12.00‰, IQR=3.52-39.11‰, respectively) than patients having never received mycophenolate mofetil (1.91‰, IQR=0.99-14.76‰, p=0.037 and 1.74‰, IQR= 0.72-13.29, p=0.034, respectively). Patients having been treated with mycophenolate mofetil during their disease history also had a higher fraction of histone-specific CD4+ T cells over the total CD4+ T cell count (16.15‰, IQR=5.30-53.79‰) than the remainder patients (3.37‰, IQR=1.64-21-98‰, p=0.045). A current and/or past history of mycophenolate mofetil also associated with higher histone-specific CD4+ T_{EM}: 3.34‰ CD4+, IQR=1.12-16.69‰ in patients on mycophenolate at time of sampling vs 0.66‰, IQR=0.11-2.14‰ in patients treated with other drugs (p=0.015); 2.23‰ CD4+, IQR=0.76-6.31‰ in patients having ever been treated with mycophenolate mofetil vs 0.60‰, IQR=0-2.12‰ in the remainder patients with SLE (p=0.037). The fraction of histone-specific T_{EMRA} cells over the total CD4+ count was also higher in patients with current (4.86‰, IQR=0.25-11.43‰) and/or past (1.37‰, IQR=0.05-7.49‰) history of mycophenolate mofetil treatment than in patients with SLE having been receiving other treatments (0.05‰, IQR=0-0.68‰, p=0.005 and 0‰, IQR=0-0.63‰, p=0.013, respectively). Patients having been treated at least once with mycophenolate mofetil showed higher histone-specific naïve T cells

(2.94‰ CD4+, IQR=1.66-14.39‰) than patients with SLE treated with other therapeutic regimens (0.50‰ CD4+, IQR=0-1.34, p=0.048).

T cell activation assays

PBMC from 20 of the 53 subjects included in previous direct *ex vivo* immunophenotype studies (15 patients with SLE, including five with active disease and five HC; see Methods) were stimulated for 24h with peptide #1-5 as listed in **Table 6** according to their respective HLA-DRB1 profile. Unstimulated PBMC and PBMC stimulated with phytohaemagglutinin (PHA) served as controls. T cell activation was assessed by measuring the expression of CD69, OX40, CD40L, CD137 and HLA-DR on CD4+ and CD8+ T cells by flow cytometry. Double-positive CD69+OX40+ CD4+ subpopulations were used to validate classification of subjects into responders and non-responders to each stimulus. This approach was combined with measurement of 12 Th-related cytokines by flow cytometry using a cytokine bead array. Unstimulated PBMC from patients with active SLE showed significant signs of spontaneous cell activation and had higher IL6 levels (50.5 pg/ml, IQR=31.8-111.8) compared to patients with SLE in remission (6.8 pg/ml, IQR=3.4-13.5; p=0.002) and HC (13.5 pg/ml, 3.4-50.5; p=0.118). No significant differences were found in terms of CD8+ responses.

There were 7/13 activation marker responders to histone peptides among patients with SLE and 0/5 among controls ($\chi^2=5.115$; p=0.044), while cytokine responses were detected in 6/13 patients with SLE and 1/5 HC. Consistently, patients with SLE had a median 1.01 (0.99-1.53)-fold increase in CD69 expression on CD4+ T cells after stimulation with histone peptides, while HC showed a relative decrease in CD69 expression (0.76-fold change, IQR=0.70-0.85 compared to no stimulation; p=0.022). Activation responses (either by surface marker expression and/or cytokine release) to histones tended to correlate with the detection of circulating histone-specific T cells by MHC-tetramer staining ($\chi^2=5.445$; p=0.054). Furthermore, histone-responders by activation marker assays were more frequent among patients with beta-lactam allergy (5/6) than in patients without beta-lactam allergy (2/7; p=0.103). Activation marker expression following EBV-related peptides was observed in 3/9 patients with SLE and 1/5 HC. All these four subjects had at least one HLA-DRB1*11:01 allele (p=0.221). Cytokine responses were observed in 5/9 patients and 2/5 HC. All these subjects had

either a clinical history of EBV infection and/or evidence of EBV-specific T cells at immunophenotype analyses. Activation marker responses after penicilloylated albumin peptide stimulation were 6/8 among patients (with 7/8 having a history of beta-lactam allergy) and 2/5 among HC (**Table 13**).

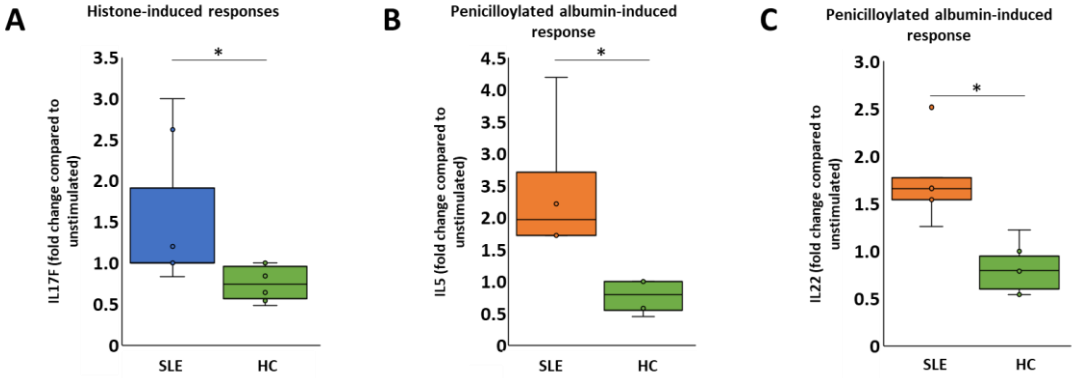
Patients with SLE and HC had diverging quantitative cytokine response profiles to peptide stimuli. Histone-induced IL17F levels were higher in patients with SLE than in HC. There was also a trend toward higher IL5, IL9 and IFN γ responses after histone peptide stimulation in patients than in controls (**Figure 12**). There were no significant differences in EBV-induced responses when HC were compared to patients with SLE. However, patients with active SLE had lower IFN γ , TNF α and IL22 EBV peptide-induced responses ($p=0.044$ for all three variables), when compared to HC. Subjects with HLA-DRB1*03:01 showed enhanced IL4 responses to EBV peptides compared to subjects with at least one HLA-DRB1*11:01 allele ($p=0.033$). Patients with SLE had enhanced IL5 and IL22 responses to penicilloylated albumin peptides compared to HC (**Figure 12**) and showed a trend towards higher penicillin-induced increases in IL17F secretion ($p=0.088$).

Table 13: reactogenicity of study epitopes

Subject ID	HLA-DRB1	Diagnosis	Histone-specific responses				Beta-lactam-specific responses				EBV-specific responses			
			Positive ADNA	Histone-specific T cells	Activation induced molecules	Cytokine response	Allergy to beta-lactams	Penicilloylated albumin-specific T cells	Activation induced molecules	Cytokine response	History of EBV infection	EBV-specific T cells	Activation induced molecules	Cytokine response
#1	03:01	SLE	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes	Yes	No	Yes
#2	11:01	SLE	Yes	Yes	No	No	No	No	NT	NT	Yes	Yes	No	No
#3	11:01	SLE	No	Yes	No	Yes	No	No	NT	NT	Yes	Yes	Yes	Yes
#4	11:01	SLE	Yes	Yes	Yes	No	No	No	NT	NT	Yes	No	Yes	No
#5	03:01	SLE	Yes	Yes	NT	NT	No	No	No	Yes	Yes	Yes	No	Yes
#9	11:01	SLE	Yes	Yes	NT	NT	Yes	Yes	No	Yes	ND	Yes	No	Yes
#11	11:01	SLE	Yes	Yes	Yes	Yes	No	No	NT	NT	ND	Yes	Yes	No
#12	03:01	SLE	No	Yes	Yes	No	Yes	No	Yes	NT	ND	No	No	No
#13	11:01	SLE	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	ND	Yes	Yes	Yes
#17	03:01	SLE	Yes	Yes	No	No	No	No	NT	NT	ND	No	NT	NT
#22	03:01	SLE	No	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	NT	NT
#25	03:01	SLE	Yes	Yes	No	Yes	No	No	NT	NT	ND	No	NT	NT
#28	03:01	SLE	Yes	No	No	No	No	No	NT	NT	ND	No	NT	NT
#30	03:01	SLE	No	No	Yes	Yes	Yes	Yes	Yes	Yes	ND	Yes	NT	NT
#32	03:01	SLE	Yes	Yes	Yes	No	Yes	Yes	Yes	Yes	ND	No	NT	NT
#47	11:01	HC	No	No	No	Yes	No	No	No	Yes	ND	Yes	No	Yes
#48	03:01	HC	No	No	No	No	No	No	No	No	Yes	No	No	Yes
#49	11:01	HC	No	No	No	No	No	No	Yes	No	ND	No	No	No
#50	03:01 and 11:01	HC	No	No	No	No	No	No	Yes	No	ND	Yes	Yes	No
#53	03:01	HC	No	No	No	No	No	No	No	No	ND	No	No	Yes

Comparison of reactivity data obtained with different methods for each antigen-of-interest and clinical phenotype. Activation-induced molecule responses were defined as the presence of higher levels of CD4+ CD69+ OX40+ after stimulation than in each respective negative control. Cytokine responses were defined as evidence of increased levels of at least one inflammatory cytokine after stimulation in comparison to each respective negative control. Abbreviations: HC: healthy control; ND: no data; NT: not tested; SLE: systemic lupus erythematosus.

Figure 12: cytokine responses in patients and controls



Boxplots showing variations in cytokine secretion compared to unstimulated conditions after exposure of PBMC from patients with SLE (blue and orange) and HC (green) to histone-derived peptides (panel A) and penicilloylated albumin peptides (panel B and C). Symbols: *: $p < 0.05$.

DISCUSSION

Summary and significance of the acquired evidence

This study employed a translational design involving a combination of clinical, genetic and cellular biology data to characterise the multifaceted aspects of immune dysfunction in patients with SLE. The main findings obtained from clinical and experimental data are:

- a) patients with SLE are at increased risk of allergic events compared to the general population;
- b) allergic events co-occur with inflammatory flares and infections, suggesting that maladaptive responses to pathogens trigger or enhance tolerance loss towards self or environmental antigens;
- c) dis-immune events including infections tend to cluster with specific HLA subtypes, which might be more permissive to aberrantly present innocent stimuli under inflammatory conditions and promote loss of tolerance towards them;
- d) CD4⁺ T_{SCM} cells are expanded in patients with SLE, especially in the context of active disease;
- e) antigen-specific CD4⁺ T cells recognising histone peptides and the penicillin major antigenic determinant correlate with a clinical history of positive ADNA and beta-lactam allergy, respectively;
- f) patients with SLE bear increased levels of histone-, penicilloylated albumin-, EBV-specific CD4⁺ T cells compared to healthy and inflammatory disease controls of comparable demographics;
- g) in patients with SLE, quantitative variations in these three T cell subtypes are correlated, mirroring what is observed clinically;
- h) antigen-specific CD4⁺ T cell counts, especially in the T_{EM} compartment and in Th2 and Treg subsets tend to decrease during active SLE, likely reflecting their migration into target tissues;
- i) consistent with immunophenotype data in unstimulated cells, immunogenic peptides from histones, EBNA and albumin bound to a penicilloyl group elicit T cell activation and cytokine release;
- j) patients with SLE show more consistent responses to histone peptides than HC, although only a fraction of the expected ADNA/anti-histone positive cell

population mount significant cytokine and T cell activation responses, in line with previous studies (Lu et al., 1999); HC showed a decrease in cell activation following epitope exposure, possibly as the expression of tolerogenic responses;

- k) penicilloylated-albumin triggers significant T cell responses in allergic patients with SLE, although also a non-negligible fraction of non-allergic HC shows detectable in vitro T cell reactivity, consistent with the hypothesis of natural penicillin reactogenicity in the general population (Azoury et al., 2018);
- l) in response to histone and penicilloylated-albumin peptide, patients with SLE show a peculiar secretory profile, characterised by a mixture of pro-inflammatory and pro-allergic cytokines including IL5 and IL17; patients with active disease also have impaired cytokine release after EBV-derived peptide stimulation.

Interpretation of clinical findings

Clinical evidence from a well-characterised cohort of patients with long-term follow up reveals that autoimmune, allergic and infectious events tend to co-occur. This study also shows that the onset of an allergic diathesis tends to cluster with the onset of SLE and to be temporally related to an infectious event, consistent with previous reports (Cooper, Dooley et al., 2002, Strom, Reidenberg et al., 1994). The prevalence of allergy was higher in patients with SLE than in the reference population (Quercia et al., 2012), in agreement with previous reports (Hsiao et al., 2014, Sequeira et al., 1993). Furthermore, patients with early-onset SLE, who are generally characterised by a more severe rheumatologic profile (Ambrose et al., 2016), had increased chances of becoming allergic during their lifetime, suggesting that this subset of patients might present a deeper dysfunction of immune regulation, leading to accelerated sensitisation to self and environmental antigens. Allergy onset after SLE was associated with accelerated development of additional hypersensitivity reactions, which further supports a view of SLE deflecting allergy disease trajectories by promoting loss of tolerance to multiple antigens and/or, conversely, of allergen polysensitisation as a risk factor for SLE (Hsiao et al., 2014). Treatment with cyclosporine A or rituximab was associated with a higher allergy prevalence, consistent with the use of these drugs as second/third-line treatments in more

severe subjects (Fanouriakis et al., 2019, Gordon et al., 2018). Finally, accumulating allergic sensitisation events correlated with SLE damage accrual, suggesting that mechanism driving autoimmunity and hypersensitivity to environmental stimuli are deeply interwoven and/or part of a shared defect of immune regulation in patients with SLE.

Pharmacological agents were the most frequent culprit triggers of allergic events in patients with SLE, consistent with the notion of drug allergy as a peculiar feature of SLE phenotype (Parks et al., 2010, Petri & Allbritton, 1992, Sequeira et al., 1993, Wozniacka et al., 2003). Among drugs, antibiotics were most frequently represented, supporting a model in which infectious events leading to antibiotic prescription associate with drug sensitisation and, eventually, allergy, besides facilitating disease flares. Sulphonamide sensitisation has been reported as the major cause of drug allergy in patients with SLE (Petri & Allbritton, 1992). This study showed a significantly higher prevalence of beta-lactam allergy among patients with drug and antibiotic allergy. These data can easily be reconciled, since prevalence of individual culprit drug sensitisations is strongly correlated with prescription attitudes in a given clinical setting, with sulphonamides being progressively less employed in recent years (Strom, Schinnar et al., 2003). Consistent with this principle, NSAIDs and immunosuppressants were relatively more frequent as culprit drugs at prospective (post-SLE onset) than retrospective analyses.

Genetic evidence

Genetic characterisation of the HLA-DRB1 repertoire confirmed the strong association between HLA-DRB1*03:01 and SLE and showed a high prevalence of HLA-DRB1*15:01 in patients with SLE, consistent with the literature (Chung et al., 2014, Deng & Tsao, 2010, Diaz-Gallo et al., 2021, Morris et al., 2012, Teruel & Alarcon-Riquelme, 2016a). HLA-DRB1*11:01 was also highly represented among patients with SLE. Although previous data failed to show a clear association with SLE diagnosis, this finding is still consistent with evidence of association with other connective tissue diseases (Mammen, Gaudet et al., 2012, O'Hanlon, Carrick et al., 2006) and with the observations of (Miyagawa, Shinohara et al., 1997) in which an increased prevalence of HLA-DRB1*07:01, 15:02 was also detected among patients with TAK. Despite this latter condition being usually regarded as a class I MHC-related disease (Carmona et al., 2017),

associations with these two alleles and TAK have been reported by other authors (Dong et al., 1992, Lv et al., 2015). HLA genotypes not only constitute a potential risk factor for SLE, but also might correlate with discrete phenotypes, including the likelihood of experiencing hypersensitivity reactions and infectious events. To this latter regard, my results support a potential protective role of HLA-DRB1*07:01 towards multiple infectious threats (Amanzadeh, Amirzargar et al., 2012, Novelli, Andreani et al., 2020, Starshinova, Dovgalyuk et al., 2018, Wu, Wang et al., 2004) and suggest a potential role of HLA-DRB1*15:01 in modulating COVID-19 risk (Novelli et al., 2020), besides its known association with SLE and with enhanced herpesvirus responses (Kachuri, Francis et al., 2020, Teruel & Alarcon-Riquelme, 2016b).

Correlation of genotype information with clinical data also showed that HLA-DRB1*11:01 is associated with enhanced risk of allergy in patients with SLE, consistent with existing evidence in the literature from non-SLE populations (Bharadwaj, Illing et al., 2012, Park, Ahn et al., 2012, Quiralte, Sanchez-Garcia et al., 1999, Zhao, Zhao et al., 2019a). In this study cohort, HLA-DRB1*11:01 was associated with higher infection rates, further supporting a potential role for this specific HLA subtypes in shaping multiple aspects of immune dysfunction in patients with SLE. In line with this view, HLA-DRB1*11:01 was also associated with distinct cytokine responses after PBMC exposure to EBV-derived peptides.

General and antigen-specific T cell responses

Memory and functional characterisation of the T cell repertoire showed expansion of total T_{SCM} and T_{EM} cells in patients with SLE, consistent with data from SLE and other inflammatory disorders (Cianciotti et al., 2020, Lee et al., 2018, Piantoni et al., 2018). Abnormalities in primary differentiation and secondary activation of memory cells might account for relapse of autoimmune manifestations, spread of sensitisation towards cross-reactive antigens as well as persistent failure in infection control (Agmon-Levin et al., 2012, Fritsch et al., 2006). Total Th subpopulations number did not differ significantly among patients and controls (despite a trend towards higher Th2 counts in patients with SLE), in line with the literature and consistent with the limited role of relatively non-specific markers in adapting to SLE clinical/pathophysiological heterogeneity (Kubo et al., 2017).

Ex vivo visualisation of histone-, penicilloylated albumin- and EBV-specific CD4+ T cells through MHC multimers showed that all three biomarkers had a good diagnostic consistency with the clinical phenotype. Low levels of positive autoreactive and allergen-reactive cells were detected in a minority of non-SLE subjects and non-allergic subjects, respectively. Relatively higher rates of potential false-positive results were detected with T cell activation assays, in line with previous observations with penicilloylated albumin peptides and autoantigens (Abdirama et al., 2021, Azoury et al., 2018, Nhim et al., 2013). These data further support the hypothesis of (low-frequency) natural autoreactive and allergen-sensitive T cells being part of the physiological T cell repertoire of healthy individuals and point to the need for combined information on their functional behaviour to characterise their pathogenicity.

Histone-specific T cell responses

Histone-specific T cells were significantly more abundant in patients with SLE and correlated with a positive ADNA profile. Furthermore, histone-specific CD4+ T cell levels were affected by disease activity with more significant decreases in the T_{EM}, Th2 and Treg compartments, suggesting defective anti-inflammatory responses leading to facilitated peripheralization of effector cells into target tissues (Abdirama et al., 2021, Dolff et al., 2010, Yang et al., 2009). Notably, no significant correlation was found among histone-specific T cells and ADNA titres at time of sampling. Although the interpretation of these results is partially biased by the inclusion of patients' laboratory data from heterogeneous sources, reflecting the complexity of "real-life" clinical practice, these findings might suggest that fluctuations of ADNA titres might be uncoupled from variations in histone-specific T cell counts. Therefore, these two markers might have distinct, possibly complementary roles in monitoring disease activity, also in light of the insufficient ability of ADNA to thoroughly track active SLE manifestations (Conti et al., 2015, Isenberg, Manson et al., 2007). Further studies with homogeneous ADNA quantitation are, however, required to definitely confirm this hypothesis.

There was no clear correlation between histone-specific T cell counts and prednisone dose. Immunosuppression also had relatively little impact on histone-specific T cell counts and, most significantly, did not associate with depletion of these cells, possibly further strengthening the diagnostic utility of antigen-specific T cells as biomarkers and

supporting their pathogenic role in disease maintenance. Mycophenolate mofetil was the most frequent immunosuppressant in the study SLE cohort and its use associated with significantly higher levels of histone-specific CD4⁺ T cells, possibly with a more enhanced effect on naïve, T_{EM} and T_{EMRA} cells. These data suggest that mycophenolate mofetil might possibly exert more prominent anti-inflammatory rather than cytotoxic effects in patients with SLE, preventing flare-specific migration of pathogenic antigen-specific T cells into target tissues without dampening their development and proliferation (Allison & Eugui, 2005). Along with this line, molecularly-targeted treatments based on patient antigen-specific T cell profiles might complement current therapeutic strategies.

Consistent with clinical evidence of reciprocal relations between active SLE, infectious stimuli and allergic events, exploratory analysis on the reciprocal relations among trends of antigen-specific T cells showed that histone-specific T cell counts were correlated with EBV-specific T cell counts. EBV-specific cells in turn, could also be correlated with penicilloylated albumin-reactive cells, especially under active disease conditions. Consistently, T cell activation assays with histone peptides and penicillin allergy major antigenic determinant prompted complex cytokine responses encompassing a mixture of canonical pro-inflammatory and pro-allergic mediators including IL17 and IL5.

EBV-specific T cell responses

Similar to histone-specific T cells, EBV-specific T cells were also quantitatively expanded in patients with SLE compared to TAK and HC (despite comparable frequencies of EBV-positive subjects among the three groups) and decreased during active disease with a possible prominent role of T_{EM} and Treg cells. Consistent with the reciprocal correlation among the three types of immune dysfunction, patients with allergy to beta-lactams also showed reduced EBV-specific T_{EM}. In contrast to histone-specific CD4⁺ T cells, a significant activity-dependent decrease in EBV-specific CD4⁺ T_{SCM} cells (which were generally more represented in patients with SLE than in controls) was observed in concomitance with alterations of the Th17 subpopulations. Reduced EBV-specific CD4⁺ T_{SCM} cell counts might indicate progression of cell differentiation into effector cells in the setting of EBV reactivation with concomitant inflammatory activity (James, Kaufman et al., 1997). More intriguingly, EBV-specific CD4⁺ T_{SCM} drop in

concomitance with active disease might suggest the occurrence of mis-differentiation events favoured by molecular mimicry among EBV and self components (such as the Smith antigen) contributing to antigen spreading and pathological autoreactivity (James et al., 1997, Monneaux & Muller, 2002). Further evidence, including cross-stimulation of sorted antigen-specific T cells with incongruous stimuli, is however needed to validate this hypothesis. Expansion of EBV-specific CD4⁺ T cells in SLE has been reported by some authors (Kang et al., 2004), but unconfirmed by others (Draborg et al., 2014) using indirect detection techniques. Indeed, T cell activation assays in this study showed defective cytokine responses in patients with active disease, in line with previous reports (Berner, Tary-Lehmann et al., 2005, Draborg et al., 2014, Draborg et al., 2016).

Penicilloylated albumin-specific T cell responses

Penicilloylated albumin-specific Th2 cells were particularly expanded in patients with SLE and beta-lactam allergy, consistent with the higher prevalence of canonical, IgE-mediated, immediate-type rather than delayed-type hypersensitivity reactions linked to beta-lactam allergy in the general population (Mirakian et al., 2015). Treg and T_{EMRA} subpopulations were also prominently expanded among patients with beta-lactam allergy, possibly suggesting that while allergic sensitisation might be favoured by excessively permissive presentation of innocuous antigens during infectious/inflammatory flares, persisting allergen-induced inflammation is relatively more efficiently regulated after withdrawal of the inciting stimulus. Nonetheless, expanded naïve CD4⁺ T cells within the penicilloylated albumin-specific population suggest that these patients might be part of a subgroup of predisposed individual with intrinsic tendency to become sensitised to this type of drugs, as previously suggested (Azoury et al., 2018, Nhim et al., 2013).

General considerations

Taken together, these data might fit with a pathogenic model where disease flares are boosted or triggered by aberrant antimicrobial responses possibly delaying pathogen clearance and promoting sensitisation to bystander exogenous moieties such as drugs. The exact pathophysiological mechanisms accounting for misdirected T cell function towards self and environmental stimuli are, however, still unclear and will require additional research. A recent study addressed potential causes of T cell dysfunction in a

mouse model characterised by the development of autoantibodies against histones and allergy-like production of class E immunoglobulins. The authors found that lack of neuritin secretion by T follicular regulatory cells was associated with multidirectional immune dysregulation (Gonzalez-Figueroa, Roco et al., 2021). This molecule constitutes an attractive candidate to account for coexistent deregulation of T cell responses towards multiple antigens in patients with SLE. Anergy-related effective maintenance of regulatory T cell populations towards self antigens, preventing T_{EM} differentiation and eventual migration into target tissues can also have a role in this setting (Kalekar, Schmiel et al., 2016, Morikawa, Ohkura et al., 2014). Consistently, data from the present study show that autoantigen-specific T cells can be detected at very low levels even in HC, but are numerically expanded and functionally uncontrolled in patients with SLE, where histone-specific Treg functions are hyperbolically correlated with SLEDAI-2K.

Strengths and limitations

This study constitutes the first attempt to apply a translational approach based on robust clinical grounds and integrated with genetic and T cell function data to test the existence of evidence supporting a generalised dysfunction of the immune response towards pathogens, autoantigens and environmental antigens in SLE. Clinical evidence was acquired both retrospectively and prospectively on a relatively large cohort of well-characterised patients with SLE, which had the advantage of both cross-validating clues acquired from patients' history with subsequent clinical events and obtaining a comprehensive view of the interaction of infections, allergic events and autoimmune manifestations over time.

Clinical data

Epidemiological data from patients with SLE were compared with evidence in the general population from the literature and public databases, which might constitute a limitation given the methodological discrepancies among different studies. Data from public sources could not be used as reliable comparators to test differences in individual trajectories of allergic sensitisation accrual over time. General population data might also not entirely be appropriate to compare with SLE demographics and do not take into account the confounding effect of SLE treatments towards the risk of allergic sensitisation

and infection susceptibility. Identifying proper controls for allergic and infectious manifestations is, however, not straightforward, as these events are 1) point-like rather than chronic (in addition, allergic reactions are also relatively infrequent in a subject's individual history); 2) non-homogeneous; 3) unpredictable by means of clinical or genetic factors in the general and/or healthy population to the best of current knowledge; 4) not part of mass screening or follow up programmes. Therefore, very large, long-term population-based studies targeted on allergic and infectious events would be required to thoroughly validate the epidemiological results of the present study. Patients with SLE might also show disproportionately high drug allergy rates due to the frequent need to use drugs to combat inflammatory or, more frequently, infectious complications. Along with this line, healthy subjects *stricto sensu* might not have constituted a proper comparator to dissect the peculiar features of allergy in SLE, as they should virtually never have been exposed to inciting stimuli (that is drugs). On the other hand, having considered relatively healthy subjects with scanty clinical history as a potential comparator group would have disclosed additional dilemmas on the extent of pathological issues that can be tolerated for purposes of classification (Marchesini, Marchignoli et al., 2017). Finally, restricting the analysis to a single control disease or a limited set of potential control diseases might have introduced additional biases in terms of comparability of too different treatment regimens or, in the opposite way, too similar therapeutic strategies reflecting too similar pathogenic backgrounds. Taking all these considerations together, the use of public data from the general population, including healthy and unhealthy subjects might be intended as a potential compromise approach to explore potentially unique features of allergy in SLE in a feasible and minimally biased way. Indeed, non-selected control groups have been employed to assess allergy features both in cohort and population studies focused on SLE and rheumatic disorders (Hsiao et al., 2014, Kronzer, Crowson et al., 2019).

Delayed diagnosis is unfortunately still an incompletely resolved issue in the management of patients with SLE and might have further promoted enhanced exposure to a multitude of inappropriate drugs in the early phase of the disease (Oglesby, Korves et al., 2014). Conversely, as anticipated above, a lower prevalence of drug allergy might be expected in healthy subjects and patients with other disorders due to the overall reduced frequency of drug use. This in turn can be attributed to the fact that infectious and allergic events are expected to occur independently and without additional

relationships with autoimmune/inflammatory events in these individuals. By contrast, the co-occurrence of autoimmune, infectious and allergic events in this study was higher than expected from a random combination of independent events, suggesting that immune dysfunction mechanisms due to active disease directly affect allergy risk rather than simply augmenting the number of observed events by expanding the number of potential observations (that is situations in which patients had to use drugs).

Experimental data

T cell analyses were designed to address HLA-DRB1-restricted responses to selected peptide epitopes from autoantigens, allergens and antigens from infectious agents. In this context, patients with SLE were compared with healthy subjects and patients with TAK of comparable age and sex. The choice of TAK as a comparator group is not common in the literature because of the rarity of this disease. Nonetheless, TAK constitutes an ideal model for a T cell-dependent disease (Brack et al., 1997, Weyand et al., 1994) preferentially affecting young women and causing systemic inflammation as in SLE, while lacking SLE/connective tissue disease-specific mechanisms of immune dysfunction such as IFN α dysregulation and anti-nuclear immunity and being therefore unlikely to cause overlap syndromes with SLE. Epitope-bound MHC tetramers were used for selectively detect autoantigen-, allergen- and pathogen-specific CD4 T cells in the peripheral blood of patients with SLE and controls and characterise their function. Using class II MHC tetramers to track CD4+ T cells in autoimmune conditions has been attempted by a minority of authors due to technical and cost challenges (Cianciotti et al., 2020, James et al., 2014). In fact, in contrast to class I MHC, class II MHC is highly polymorphic in the general population, prompting to the need for high-resolution HLA genotyping of a large number of subjects as in the case of this study. Furthermore, in contrast to CD8+ responses (especially towards viral targets), autoreactive CD4+ responses are generally reduced in size and characterised by lower-affinity TCR expression, leading to low intensity MHC tetramer signalling and the need for countermeasures such as protein kinase inhibitors to prevent TCR internalisation (Dolton, Tungatt et al., 2015, Massilamany, Upadhyaya et al., 2011). By using MHC tetramers for *ex vivo* visualization of antigen-specific CD4+ cells, this study provides the first direct evidence of a) autoreactive T cells selectively recognising chromatin-related antigens in

SLE; b) antigen-specific T cells able to recognise penicillin allergy major antigenic determinant in subjects with beta-lactam allergy, possibly overcoming the drawbacks of classical *in vitro* studies, where cultured and stimulated T cells might not reflect the actual *in vivo* phenotype (James et al., 2014).

These data were strengthened by the frequent detection of EBV-reactive cells in patients and controls, confirming previous evidence and consistent with the high rates of EBV infection in the general population. Adding on existing literature on T cell responses against autoantigens, the use of MHC-multimer direct T cell tracking disclosed unprecedented clues on the prevailing differentiation stage, polarisation and dynamics over time of antigen-specific T cells against multiple targets in the circulating blood of patients with SLE. Furthermore, this study provides the first evidence of potential reciprocal correlations among T cells recognising autoantigens, allergens and pathogens, possibly providing a pathophysiological correlate for clinical observations. Finally, genetic analysis on a relatively large sample of patients and controls corroborated clinical observations and previous evidence in the literature, besides showing novel potential associations with specific clinical aspects of SLE. However, interpreting these data requires careful considerations of multiple limitations, which in turn are mainly explainable with the exploratory nature of this research. The design of this study excluded non-peptide and non-HLA-DRB1 restricted epitopes from analysis. This is particularly relevant for DNA-targeted immunity which was assumed to be surrogated by anti-histone immunity (Schett, Smole et al., 2002). In contrast to indirect antigen-specific assays employing peptide libraries (Abdirama et al., 2021, Tesch et al., 2020, Zhao et al., 2019b), this study focused on a relatively limited set of peptides. Less frequent but potentially specific antigens such as the Smith antigen were excluded (Zhao et al., 2019b), preventing a comprehensive view of the broad autoantigen repertoire characterising SLE. In a similar way, the choice of penicilloylated albumin is insufficient to address the whole spectrum of beta-lactam allergy, as many subjects can become sensitised to side chains of beta-lactam drugs, rather than to the penicilloyl group. Besides, allergic responses to non-drug-related antigens and other less frequent allergens could not be addressed by this study. Choosing EBNA1 and 2 as the reference pathogen-related antigens also implies some limitations. In fact, despite having consistently been implicated in SLE flares, EBV causes a chronic infection with potential reactivations instead of being responsible for

acute events. Therefore, data regarding EBV-specific T cell dynamics can likely only partially surrogate the effects of pathogen-related perturbations to the immune response in patients with SLE, pointing to the need for further evidence on other microbial agents such as influenzaviruses. Furthermore, opting for a limited choice of EBV-related peptides prevented a comprehensive analysis of individual variations in the profile of anti-EBV responses and subsequent pathways of SLE flare induction. The absence of complete EBV serological data from the study subjects constitutes an additional limitation to the interpretation of EBV-specific T cell responses. Finally, although attention was paid to select blood samples from patients with as low immunosuppression as possible, treatment profiles were not homogeneous among patients, adding potential confounders to the evaluation of antigen-specific T cell dynamics. Nonetheless, as differences among patients taking and not taking immunosuppressant were minimal, data from this study might suggest that antigen-specific T cell tracking in SLE can robustly be translated into the complexity of routine clinical practice.

T cell activation assays after incubation with peptides employed for MHC-peptide multimer studies provided further evidence supporting the biological relevance of T cell responses targeting these antigens in the pathogenesis of SLE. In contrast to direct antigen-specific T cell tracking analyses, low-grade responses were more frequent in this set of experiments, which prevents a detailed insight in the kinetics and qualitative features of T cell response to direct stimulation with relevant triggers. To this regard the choice of a single-point 24h-time incubation protocol might have been insufficient to comprehensively address surface marker and cytokine dynamics with peaks at different timepoints. Further research is also required to understand whether distinct peptide doses might elicit different T cell responses.

In addition to previous points, expansion of the patient sample size employed for *in vitro* studies will probably provide more informative data and better conform to SLE extreme clinical and pathophysiological variability. Larger studies are also required to address prospectively the potential significance of antigen-specific T cell dynamics over longer observation timeframes, also in light of patient heterogeneity in terms of quantitative and qualitative responses to specific antigens.

Future perspectives

Identifying circulating antigen-specific CD4+ T cells of potential clinical relevance for autoimmune, allergic and infectious manifestations opens multiple potential perspectives for future research and applications. In terms of diagnostics, antigen-specific T cells might become part of the tools employed to profile patients with SLE at diagnosis and monitoring the disease course over time. To this regard expansion of the HLA-multimer and peptide panel (for example to include the SLE-specific HLA-DRB1*15:01, which was unfortunately too infrequent in the subject sample included in this study to be used for *in vitro* studies) in the setting of future research would increase the feasibility of translating antigen-specific T cell tracking in the rheumatologic clinical practice (Abdirama et al., 2021, Tesch et al., 2020). These approaches might also synergise with patient stratification algorithms based on HLA- and antibody profiling and identify subsets of subjects with higher expected success rates following specific treatments (Diaz-Gallo et al., 2021).

The use of tolerogenic approaches employing repeated or regulated exposure of target antigens to affected subjects is widely used in routine allergy practice (Nakagome & Nagata, 2021), while less robust evidence has so far been acquired for autoimmune disorders. MHC multimers loaded with relevant peptide autoepitopes and embedded in iron oxide nanoparticles might widen the therapeutic armamentarium for multiple diseases such as type I diabetes and rheumatoid arthritis (Clemente-Casares et al., 2016). In the setting of SLE, treatment with autopeptide-bound MHC multimers might also synergise with enhanced immunomodulatory approaches based on lipid nanoparticle delivery of antimalarials (Diao, Tao et al., 2019, Serra & Santamaria, 2020, Stevens, Crist et al., 2020). In turn, the use of flow-cytometry assays based on the use of MHC multimers might identify patients with the ideal profile to receive immunomodulating antigen-specific treatments.

Chimeric antigen receptor T (CAR-T) cell therapy is a rapidly emerging potent tool for the treatment of otherwise intractable haematological malignancies. Engineered CAR-T cells exploits T cell selectivity and amplitude of functions to accurately and persistently suppress selected target cells or remodulate inflammatory responses to a given epitope. The efficacy of CAR-T cell therapies in animal models of autoimmunity constitutes an attractive perspective for patients with autoimmune diseases such as SLE (Beheshti,

Shamsasenjan et al., 2022, Jin, Han et al., 2021, Mougiakakos, Kronke et al., 2021). However, besides high costs, extensive interindividual variability among subjects in terms of autoantigen sensitisation profiles constitutes a major limitation for the application of this innovative approach in patients with autoimmune diseases such as SLE, in contrast with clonal disorders, where a fixed target antigen can be relatively more easily identified. Direct *ex vivo* visualization and characterisation of antigen-specific T cells has long been proposed as a tool to optimise vaccine and allergen immunotherapy design based on patient characteristics and expected T cell reactivity (Archila, DeLong et al., 2014, Munz, Bickham et al., 2000). Routine use of MHC-tetramer based approaches for an extended panel of key epitopes for the pathophysiology of SLE might enable patient profiling for effective and tailored CAR-T cell treatments.

Conclusions

Patients with SLE are susceptible to autoimmune, allergic and infectious events, which tend to co-occur, suggesting a shared pathophysiological mechanism accounting for multidirectional immune dysfunction. To this regard, this study provides the first direct evidence in SLE of HLA-restricted antigen-specific CD4⁺ T cells recognising epitopes from key autoantigens, allergens and chronic infectious agents and correlating with the clinical phenotype. Data from T cell differentiation and polarisation phenotyping together with functional tests indicate that these cells undergo dynamic variations mirroring fluctuations in disease activity, which might implicate their potential future use to complement existing diagnostic tools and guide and/or integrate current therapeutic weaponry.

MATERIALS AND METHODS

Patients and controls

This translational study is based on a combination of clinical and experimental data. The general design of the study is depicted in **Figure 13**. Upon informed consent under the Autoimmuno-mol research protocol (approved by the Institutional Review Board of IRCCS Ospedale San Raffaele, ref. 2/2013/INT) 190 patients with SLE and 178 control subjects including 94 healthy controls and 84 patients with TAK were enrolled. SLE was defined according to either the revised 1997 ACR criteria or the 2012 SLICC criteria (Hochberg, 1997, Petri et al., 2012). The diagnosis of TAK was established by the 1996 Sharma's criteria (Sharma, Jain et al., 1996). TAK was selected as an inflammatory control group, being a T cell-dependent disease with similar demographic features compared to SLE. Peripheral blood mononuclear cells (PBMC) were collected from these subjects during routine clinical procedures or visits along with clinical data encompassing disease history, disease manifestations, comorbidities, past and current treatments and the results of routine laboratory tests at time of analysis. Patient selection for *in vitro* studies was based on availability of sufficient PBMC samples, minimisation of discrepancies in terms of confounders (age, sex, corticosteroid and immunosuppressant doses, concomitant non-disease-related clinical events such as trauma or cancer etc.) among groups and on the results of HLA genotyping (see below). Patients with active disease underwent blood sample collection before having been started on new treatments. Fifty-three subjects (32 SLE, 11 TAK, 10 HC) were included in T cell analyses. Five patients with SLE in remission were retested with samples obtained during disease activity. One HC bearing both HLA-DRB1 alleles of interest was tested twice, employing both sets of MHC-tetramers and peptide sets.

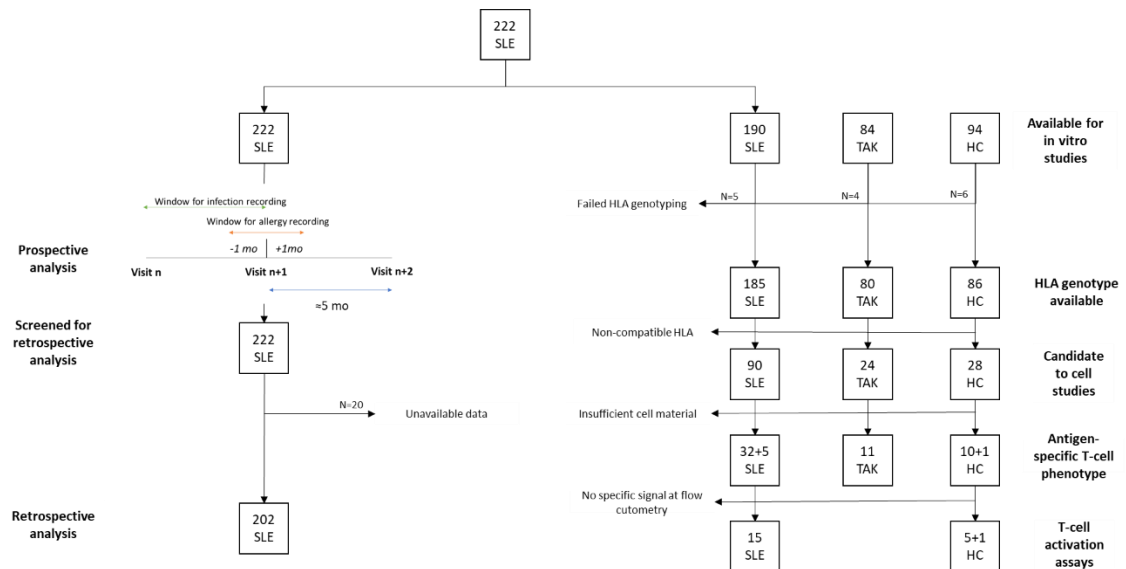
Upon informed consent, a total of 222 patients with SLE including those enrolled in the Autoimmuno-mol protocol were also enrolled in a prospective study focusing on clinical features of patients with multiple immune-mediated diseases (PanImmuno research protocol, approved by the Institutional Review Board of IRCCS Ospedale San Raffaele, ref. 22/INT/2018). Under the frame of this protocol, patients with SLE were cross-sectionally enrolled and prospectively followed up in concomitance with routine clinical evaluations occurring at 3-6-month intervals. Data regarding disease features at time of each visit, the results of laboratory tests employed for clinical assessment

(including complete blood cell count, erythrocyte sedimentation rate and C-reactive protein measurement, renal and liver function tests, complement C3 and C4 levels and ADNA titres), disease activity and disease-related damage, ongoing and new treatments, recent infections and/or allergic reactions were all collected through an in-house software (Clinimatrix®, Italian Society for Authors and Editors, SIAE, registration number 013059-D012254) which I developed based on Microsoft Excel® (Ramirez et al., 2019b, Ramirez, Rocca et al., 2021). Five categories of ADNA were defined (borderline, low, moderate, high, very high) based on the attending Physician's interpretation of the laboratory test results. For ADNA measured by indirect immunofluorescence in a dilution range from 1:20 to over 1:640, the following classes were identified: 1:20 – borderline, 1:40-80 – low, 1:160-320 – moderate, 1:640 high, >1:640 – very high.

Allergic reactions were defined as “hypersensitivity reactions initiated by immunological mechanisms” as per the World Allergy Organization/European Academy of Allergy and Clinical Immunology (WAO/EAACI) consensus definitions (Pawankar, Canonica et al., 2013). Allergic reactions occurring within one month before or after each study visit were considered significant for prospective analysis. Similarly, occurrence of at least one infection requiring systemic antimicrobial therapy or absence from work in the timeframe between each visit was set as the criterion to record infectious events during follow up visits since enrolment. Data regarding COVID-19 infection rates during 2020 were also collected under the same protocol and analysed separately.

In parallel with prospective analyses, data regarding demographics, the course of SLE from disease onset, comorbidities and allergic history were also collected. Regarding allergy history, the same definitions of allergy as per above were applied. For purposes of classification (both in prospective and retrospective studies), only clinical events having at least one of the following characteristics were considered as allergic reactions: a) direct observation of the reaction by a Physician; b) laboratory or clinical evidence of allergic sensitisation through specific IgE testing, basophil activation test, skin prick tests, patch tests or intradermal tests in correlation with a consistent clinical history; c) ability of patients to recall sufficient clinical details being consistent with an allergic reaction as evaluated by an Allergist.

Figure 13: general study flow chart



This picture summarises the general design of the present study, which involved 222 patients with SLE and 178 controls. The left side of the graphs reports the main characteristics of the clinical studies performed within the frame of this work. All patients were followed up prospectively over the course of >1200 outpatient visits occurring approximately every six months for each patient. Infectious events occurring within this timeframe were recorded along with allergic reactions taking place within one month before or after each outpatient visit. Extensive data on disease activity in terms of autoimmune manifestations and on treatments were also collected. Only 202 of the patients enrolled in the prospective study could recall and/or document with clinical charts details about allergic and infectious history before enrolment. On the right side of the chart, the progressive steps leading to the selection of patients suitable for *in vitro* studies is represented. A relatively large number of patients with SLE and controls was screened to define the feasibility of subsequent studies employing major histocompatibility (MHC) tetramers for antigen-specific T-cell detection at flow cytometry. Among these subjects, encompassing healthy controls (HC) and patients with Takayasu’s arteritis (TAK), a subset with sufficient cell aliquots to perform flow cytometry and stimulation assays was identified. A total of 53 subjects (one bearing both HLA-DRB1 alleles-of-interest, tested twice) underwent antigen-specific T-cell phenotyping. Five patients with SLE were tested both during active disease and remission. Among the 53 subjects included in T cell studies, twenty (15 patients with SLE and five HC) were selected for T-cell activation assays based on the results of flow cytometry analyses.

Clinimetrics

In patients with SLE, disease activity was quantitated through a panel of validated measures including the SLE disease activity index 2000 (SLEDAI-2K), the British Isles Lupus Assessment Group (BILAG) 2004 score, and the European Consensus Lupus Activity Measurement (ECLAM) scale (Gladman et al., 2002, Isenberg et al., 2005, Mosca et al., 2000). Lupus low disease activity status (LLDAS) was used a surrogate

index of remission (Franklyn et al., 2016). Physician and patient impression on disease activity were quantitated through a 0.0-3.0 Physician Global Assessment score (PGA) and a 0-10 numerical rating scale respectively. Damage accrual was expressed as SDI (Gladman et al., 2000). Clinimetrics calculation and recording was performed through Clinimatrix®.

Disease activity in patients with Takayasu's arteritis was assessed through the Indian Takayasu disease Activity Score (ITAS-2010)(Misra, Danda et al., 2013). Patients were also categorised by Physician's impression into patients in remission, with smouldering disease, or with active disease.

Population data and bioinformatics

Epidemiological data including prevalence of allergic disorders and EBV infection in the general population were obtained from publicly available databases and by literature search through the National Center for Biotechnology Information and Google Scholar® tools. Specifically, the prevalence of self-reported history of allergy by age-groups in Italy was extracted from Eurostat (<http://ec.europa.eu/eurostat/web/health/data/database>, accessed in September 2019; data referred to 2014) and from the Italian National Institute of Statistics (ISTAT: www.istat.it, accessed in September 2019; data referred to 2017). Additional data were retrieved from a population study (Quercia et al., 2012) and integrated with further analysis on the same database (kind courtesy of Prof. Cristoforo Incorvaia). Data regarding general European demographics were also extracted from Eurostat. A comprehensive summary of these analyses is reported in **Appendix 1**. Expected frequencies of HLA genotypes in the general Italian population were retrieved from the Allele Frequency Net (Gonzalez-Galarza et al., 2019).

Blood and DNA samples

PBMCs were purified from whole blood samples collected into 6 ml EDTA containing tubes (BD Vacutainer®) through gradient separation with Lymphoprep™ and biobanked until use. Live PBMC or residual non-live white blood cells after PBMC extraction were used for DNA extraction. Sample processing and storage were performed by a dedicated staff at a centralised biobank facility (current Centro Risorse Biologiche, CRB) following the internal standard operating procedure IOS SIMT 101.

DNA extraction was performed with silica-membrane spin columns (Cat. #69506) or 96-well plates (Cat. # 69581) from Qiagen® according to the manufacturer's instructions, except for the use of distilled water for the final elution step and for storage. The amount of extracted DNA was checked by mass-spectrophotometry (Nanodrop 1000®, ThermoFisher, Massachusetts, USA).

HLA genotyping

A total of 380 subjects (190 patients with SLE, 190 controls) with available DNA samples were genotyped for their HLA-DRB1 profile. Specifically, high-resolution four-digits HLA typing was performed by sequence-specific oligonucleotide-primed polymerase chain reaction (PCR-SSO), using Histo-spot® DRB1 kits (Cat. No. 726040 and 726098), AstraFormedic, Milan, Italy. These experiments were performed by Dr Benedetta A. Mazzi and collaborators in the Immunogenetics Laboratory, HLA & Chimerism, Department of Immunohematology & Blood Transfusion of IRCCS Ospedale San Raffaele.

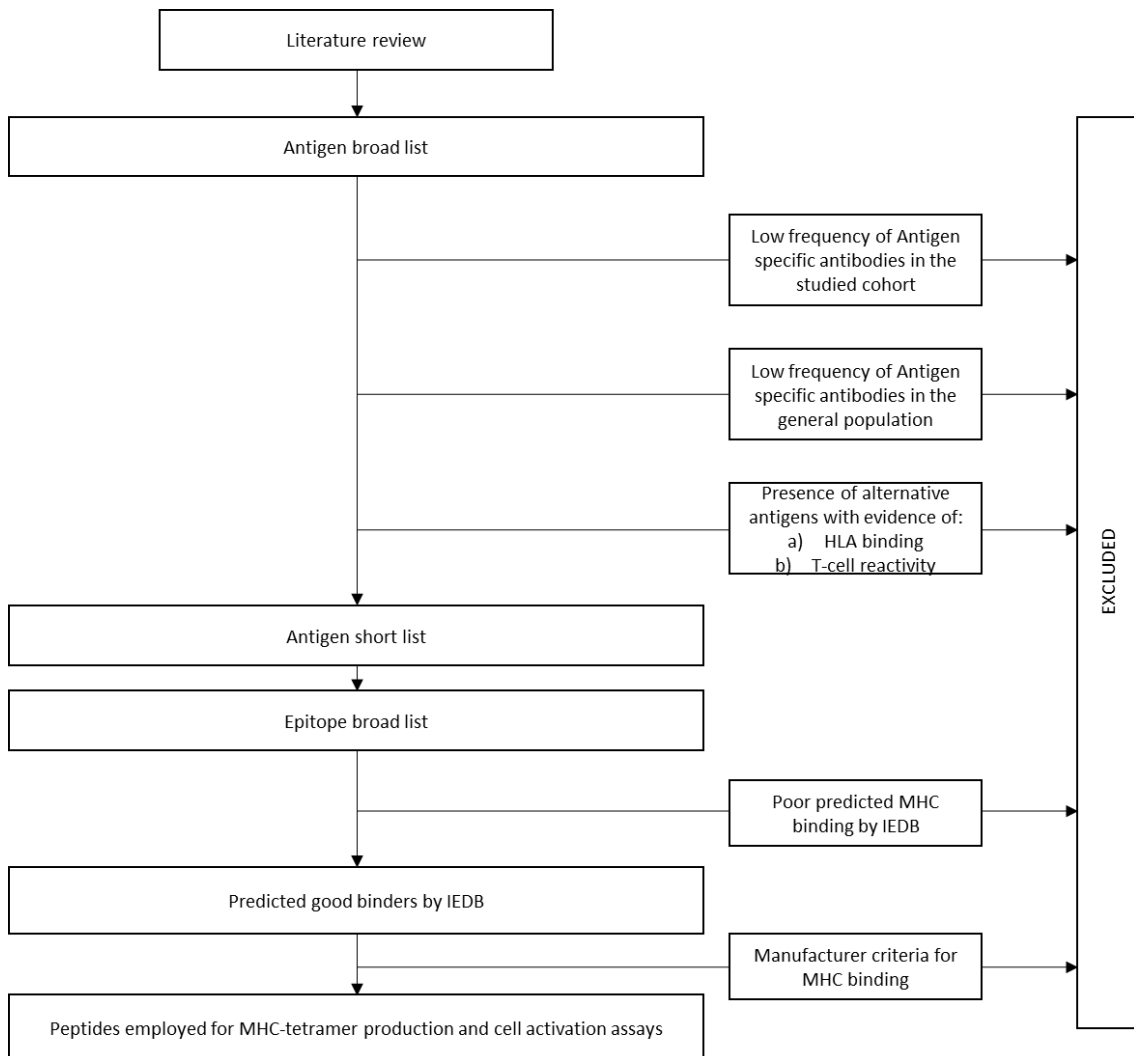
Peptides, antigens and epitopes of interest

***In silico* analyses**

Based on the results of HLA typing (see above and **Appendix 2**) and on literature review, two HLA-DRB1 alleles (HLA-DRB1*03:01 and 11:01) were selected for further studies with the aim of obtaining data from a sufficient number of subjects with a pathogenically meaningful genetic profile. Specifically, expected HLA-DRB1 frequencies in the general population were retrieved from the Allele Frequency Net Database (Gonzalez-Galarza et al., 2019). This information was combined with previous studies reporting on potential associations of selected HLA genotypes with SLE (Arango et al., 2017, Bang et al., 2016, Ceccarelli, Perricone et al., 2015, Cruz, Shao et al., 2016, de Holanda, Klumb et al., 2018, Massa, Mazzoli et al., 2002, Morris, Fernando et al., 2014, Morris et al., 2012, Niu et al., 2015, Teruel & Alarcon-Riquelme, 2016b), infection susceptibility (Amanzadeh et al., 2012, Kawase, Tanaka et al., 2019, Muro, Mondejar-Lopez et al., 2013, Starshinova et al., 2018, Wu et al., 2004), and/or allergy (Azoury et al., 2018, Lara-Marquez, Yunis et al., 1999, Nhim et al., 2013, Padovan et al., 1997, Park et al., 2012, Quiralte et al., 1999).

Potential candidate peptides for MHC binding and cell stimulation were identified starting from a broad list of known autoantigens, allergens and antigens belonging to infectious agents (**Figure 14**). This selection was refined by ruling out candidate antigens whose corresponding antibodies had a low prevalence in the studied cohort or in the reference population. Further shortening of the initial list was performed by selecting antigens endowed with peptides having already shown evidence of a) efficient binding to the HLA-DRB1*03:01 and/or HLA-DRB1*11:01; b) ability to elicit T-cell responses in vitro in patients with SLE or other subjects against antigens with no such evidence in the literature when available. After this preliminary selection, full FASTA sequences of each antigen in the shortlist were retrieved from the U.S. National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/protein>). These sequences were then inputted in the Immune Epitope Database (IEDB) and Analysis Resource (www.iedb.org), developed by the U.S. National Institute of Allergy and Infectious Diseases to identify potential T-cell epitopes restricted for the two MHC of interest. This tool integrates multiple algorithms for peptide-MHC binding prediction and provides a global percentile rank reflecting the likelihood of each sequence to bind a given MHC molecule (Paul, Lindestam Arlehamn et al., 2015). Only peptides showing a percentile rank below 25 were considered. More stringent criteria were applied after further counselling from the MHC tetramer manufacturer (Proimmune®) to include only peptides with a nonamer core fitting specific binding criteria.

Figure 14: flow-chart for selecting peptides for MHC-tetramers and cell activation assays.



This flow chart depicts the steps taken to narrow an initial list of potential candidate antigens and epitopes of possible significance for the study into a shortlist of peptides. Abbreviations: HLA: human leukocyte antigen; IEDB: Immune Epitope Database; MHC: major histocompatibility complex.

Peptide synthesis and reconstitution

The same peptide sequences employed for MHC-tetramer experiments were used for cell stimulation and were purchased as five-mg powders from Biomatik Corporation (Ontario, Canada). The penicilloylated PELLFFAKRYKAAFT human albumin peptide was produced as described by Scornet et al. (Scornet, Delarue-Cochin et al., 2016). One mg of powder was first tested for solubility in DMSO, then mixed to the remaining

amount and aliquoted. Specifically, 5 mg of each peptide were reconstituted in 250 μ l DMSO and stocked at -80°C in aliquots of 10 μ l until use. For cell stimulation, each 10 μ l aliquot was diluted with 20 μ l PBS to reach a final concentration of 6.7 μg peptide / μ l PBS+DMSO. A volume of 1.5 μ l of this solution was added to 500 μ l of cell culture medium (see below), yielding an operative peptide concentration of 20 $\mu\text{g}/\text{ml}$. The total concentration of DMSO in the cell medium was therefore 0.1%, which is below the 0.5% threshold of cytotoxicity conventionally recommended for T cell experiments.

Tetramers

Peptide-bound MHC tetramers of HLA-DRB1*03:01 and HLA-DRB1*11:01 were purchased from ProImmune Ltd (Oxford, United Kingdom). The penicilloylated PELLFFAKRYKAAFT sequence was produced by Biomatik Corporation as described above and incorporated by Proimmune into HLA-DRB1*03:01 and HLA-DRB1*11:01 MHC tetramers. Phycoerythrin (PE)- and allophycocyanin (APC)-bound MHC tetramers were generated for histone and penicilloylated albumin peptides respectively. EBV-derived peptides were provided by Proimmune as 35 $\mu\text{g}/88\mu\text{l}$ HLA-DRB1*03:01 and HLA-DRB1*11:01 MHC-biotin monomers. Tetramerisation of MHC monomers was performed as follows, by adapting the protocol provided by ProImmune for tetramerising PE-bound MHC monomers and that of Lu et al. for fluorescein isothiocyanate (FITC)-bound MHC monomers (Lu, Yoo et al., 2019). FITC-streptavidin to MHC-monomer molar ratio was set to 1:4. Therefore, assuming that MHC monomers had a molecular weight of 58-65 kDa, a starting MHC amount of 0.569 nmol was calculated, which implied the need for 0.14 FITC-streptavidin nmol. A 500 $\mu\text{g}/\text{ml}$ FITC-streptavidin aliquot (Biolegend) was centrifuged at 14,000 g at 4°C for three minutes and then kept on ice protected from light. Ten μg FITC-streptavidin (>0.14 nmol) was then added in five steps separated by 15-minute intervals of incubation to the MHC monomer solution. The resulting 108 μl FITC-MHC-tetramer solution was then further diluted in PBS to 400 μ l total volume. To test whether unbound FITC-streptavidin could prompt non-specific FITC-positive signal on flow cytometry, 1×10^6 PBMC from healthy donors were stained with FITC-streptavidin up to 10-fold the concentration achieved in the FITC-MHC-tetramer solution. Unstained samples and samples stained with an anti-CD3-FITC

antibody (Biolegend) served as control tests. FITC-streptavidin fluorescence intensity was undistinguishable from the negative (unstained) control (**Appendix 9**).

Flow cytometry

Gating strategies

The following fluorochrome-bound antibodies were used for cell staining and phenotyping: anti-CD3-Pacific Blue (Cat #300431), anti-CD4-PE-cyanin7 (Cat #300512), anti-CD8-peridinin-chlorophyll-protein(PerCP)-cyanin 5.5 (Cat #344710), anti-CD45RA APC-cyanin 7 (Cat #304128), anti-CD62L AlexaFluor 700 (Cat #304820), anti-CD95 PE-Dazzle (Cat #305634), anti-CD3 Brilliant Violet 510 (Cat #317332), anti-CD127 PerCP-cyanin 5.5 (Cat #351322), anti-CCR4 PE-Dazzle (Cat #359420), anti-CCR6 Brilliant Violet 421 (Cat #353408), anti-CXCR3 APC-cyanin7 (Cat #353722), anti-CD69 APC-cyanin 7 (Cat #310914), anti-CD40L AlexaFluor 700 (Cat #310846), anti-CD137 PE (Cat #309804), anti-HLA-DR APC (Cat #307610), anti-OX40 FITC (Cat #350006; all from Biolegend) and anti-CD25 allophycocyanin-Alexa Fluor 700 (Beckman Coulter, Cat #A86356). In addition, vital staining was performed with Zombie Aqua™ (Biolegend, Cat #423101). Antibody and tetramer staining concentrations were optimised through preliminary tests with increasing reagent amounts. A stain index (SI) with the following equation was used to rank the resulting mean fluorescence intensities (MFI) according to their difference from negative (unstained) controls: $SI = \frac{MFI_{pos} - MFI_{neg}}{SD_{neg} \times 2}$ (SD=standard deviation; pos: positive sample, neg: negative control). Flow cytometry data were acquired and compensation performed through a Beckman Coulter Navios flow cytometer. Consistency among experiments in terms of fluorescence readings was checked by the use of Spherotech Spero™ rainbow calibration particles. Flow cytometry data were analysed with FCS Express version 7 and eventually exported to Microsoft Excel 2019 for further analysis and merging with clinical data. Absolute tetramer-positive cell counts were calculated as the number of CD4+ tetramer+ events after subtraction of CD4- tetramer+ events. Positive histone-, EBV- and penicilloylated albumin-reactive CD4+ T cell statuses were defined by diagnostic thresholds based on ADNA status, EBV serology or history and beta-lactam allergy history, respectively (see Statistical analyses). Three staining panels were set up.

Panel A: lymphocyte differentiation

In this panel, PBMC from patients and controls were stained with Zombie Aqua™, anti-CD3-Pacific Blue, anti-CD4-PE-cyanin 7, anti-CD8-PerCP-cyanin 5.5, anti-CD45RA APC-cyanin 7, anti-CD62L AlexaFluor 700 and anti-CD95 PE-Dazzle antibodies with or without MHC-PE, MHC-FITC and MHC-APC tetramers. Preliminary tests revealed the presence of a large population of cells with coexistent strong FITC-MHC/PE-MHC fluorescence without dead cell exclusion. Back-gating this cell population on the vital stain histogram confirmed that these cells were all non-living (Staats, Divekar et al., 2019). Therefore, an exclusion gate for “spurious” events was created to eliminate the potential confounding effect of these cells on subsequent gate setting and analysis (**Appendix 10**). T cell subsets were further classified based on the gating strategy reported in **Table 14** (Cieri et al., 2015, Gattinoni et al., 2017, Kubo et al., 2017).

Table 14: gating strategy for lymphocyte differentiation analysis

Lymphocyte subset	Immunophenotype
T-lymphocytes	CD3+
T helper	CD4+
Naïve T helper	CD4+ CD45RA+ CD62L+ CD95-
Stem cell memory (T _{SCM})	CD4+ CD45RA+ CD62L+ CD95+
Central memory (T _{CM})	CD4+ CD45RA- CD62L+
Effector memory (T _{EM})	CD4+ CD45RA- CD62L- CD95+
Terminally differentiated (T _{EMRA})	CD4+ CD45RA+ CD62L-
T cytotoxic	CD8+
Naïve T cytotoxic	CD8+ CD45RA+ CD62L+ CD95-
Stem cell memory (T _{SCM})	CD8+ CD45RA+ CD62L+ CD95+
Central memory (T _{CM})	CD8+ CD45RA- CD62L+
Effector memory (T _{EM})	CD8+ CD45RA- CD62L- CD95+
Terminally differentiated (T _{EMRA})	CD8+ CD45RA+ CD62L-

Panel B: polarisation

In this panel, PBMC from patients and controls were stained with anti-CD3 Brilliant Violet 510, anti-CD127 PerCP-cyanin 5.5, anti-CCR4 PE-Dazzle, anti-CCR6 Brilliant Violet 421, anti-CD25 APC-Alexa Fluor 700 and anti-CXCR3 APC-cyanin 7 antibodies, with or without MHC-PE, MHC-FITC and MHC-APC tetramers. In the absence of vital

stain in this panel, the exclusion gate defined for panel A was applied with the same parameters to panel B. Functional polarisation cell subsets were defined as reported in **Table 15**, based on the literature (Becattini, Latorre et al., 2015, Kubo et al., 2017, Zhong et al., 2018).

Table 15: gating strategy for T cell polarisation analysis

Lymphocyte subset	Immunophenotype
T-lymphocytes	CD3+
T helper	CD4+
Regulatory	CD4+ CD25bright CD127low
T helper 1	CD4+ CXCR3(=CD183)+ CCR6 (=CD196)- CCR4(=CD194)-
T helper 17	CD4+ CXCR3(=CD183)- CCR6 (=CD196)+ CCR4(=CD194)+
T helper 1*	CD4+ CXCR3(=CD183)+ CCR6 (=CD196)+ CCR4(=CD194)+
T helper 2	CD4+ CXCR3(=CD183)- CCR6 (=CD196)- CCR4(=CD194)+

Panel C: T cell activation

This panel encompassed Zombie Aqua™ staining along with anti-CD3-Pacific Blue, anti-CD4-PE-cyanin7, anti-CD8- PerCP-cyanin 5.5, anti-CD69 APC-cyanin 7, anti-CD40L AlexaFluor 700, anti-CD137 PE, anti-HLA-DR APC and anti-OX40 FITC antibodies. A subpanel with staining for CD3, CD4 and CD8 was also set for positive (phytohaemagglutinin, PHA-exposed) controls to determine the background fluorescence for each activation marker. Double-positive CD69+OX40+ CD4+ subpopulations were used to classify subjects into responders and non-responders to each peptide/control stimulus (Pallikkuth, Williams et al., 2021, Xiaoyan, Pirskanen et al., 2006).

Staining protocol for unstimulated T-cell phenotyping

For flow cytometry assays cells were gently thawed and resuspended in 15 ml RPMI medium (ThermoFisher, Gibco, Cat#72400-021) with 1/1000 gentamicin and 10% FBS (culture medium). After centrifugation at room temperature, 1500 rpm for 10 minutes, the supernatant was disposed to avoid DMSO contamination and the cell pellet resuspended in 8 ml culture medium. After overnight incubation at 37°C, 5% CO₂, 1 x 10⁶ cells per tube were placed in four polypropylene tubes per patient corresponding to panel A for differentiation studies, panel B for T polarisation phenotyping with and

without peptide-bound MHC tetramers. After washing with 2 ml washing solution (PBS + 2% bovine serum albumin) per tube, vital staining was performed with Zombie Aqua™ (panel A). After 10-minute incubation at room temperature, dasatinib 10 μ M 1 μ l was added to the cell pellet (in \sim 50 μ l volume). After 15' of additional incubation at 37°C, three (HLA-DRB1*11:01) or five μ l (HLA-DRB1*03:01) tetramers were added to 2/4 tubes. Tetramers were centrifuged at 14,000 rpm at 4°C before use. Incubation with tetramers was performed for 2h at 37°C as per the manufacturer instructions. After incubation, the cells were washed again and two mixtures of fluorochrome-bound antibodies (see above) were added to panel A and panel B tubes respectively. After an additional wash, the cells were resuspended in 300 μ l washing buffer and analysed through a Beckman Coulter Navios flow cytometer.

T-cell activation assays

PBMC from patients with SLE (n=15) and HC (n=5) who had been previously genotyped for HLA-DRB1 and studied for antigen specific T-cell phenotype at resting state were thawed, washed and resuspended in culture medium as described above and placed in a 48-well plate containing approximately 1×10^6 cells in 500 μ l culture medium per well. After one-hour recovery at 37°C, 5% CO₂, 20 μ g/ml of penicilloylated-albumin peptide, histone-derived or EBV-derived peptides were added into separate wells according to subject genotype and antigen-specific T cell phenotypes at previous analyses (Azoury et al., 2018, Kalluri, Grummel et al., 2018, Kattah et al., 2015, Monneaux, Briand et al., 2000, Snir, Backlund et al., 2012). HC were tested for all three types of peptides independent on the result of antigen-specific T cell assays. Unstimulated cells and cells stimulated with 1 μ l/ml phytohaemagglutinin (PHA) served as negative and positive controls for each subject. An incubation time of 24h was set based on the average release kinetics of target cytokines according to the literature (**Appendix 11**) and on the kinetics of expression of surface markers of activation (Testi, Phillips et al., 1989). In addition, longer incubation times were excluded to minimise the risk of tolerance induction (Zhang et al., 2013).

After 24h-incubation, 100 μ l of cell supernatant were collected from each well, purified from cell debris through centrifugation at 1500 rpm per one minute and stocked at -80°C until use. After thawing, cell supernatants were analysed for the expression of

the following T-helper cell-related cytokines through a multiplex bead array (Biolegend Legendplex, Cat. #741028): IL2, IL4, IL5, IL6, IL9, IL10, IL13, IL17A, IL17F, IFN γ , TNF α , IL22. All steps were performed in polypropylene tubes, all filled with 25 μ l Assay buffer provided by the manufacturer. For each experimental session eight tubes were employed for a standard curve, encompassing six serial 1:4 dilutions of a Standard cocktail provided by the manufacturer into Assay buffer, one undiluted standard sample and a blank control. Twenty-five μ l of undiluted supernatants were placed in each sample tube. After intense vortexing, 25 μ l of cytokine binding beads were added to each sample or standard tube. Tubes were incubated with continuous basculation for two hours, protected from light. Eventually, 25 μ l biotinylated antibodies were added to each tube, followed by an additional hour of incubation and mixing. Twenty-five μ l of streptavidin-PE were then added to each tube, followed by 30 minutes of incubation and mixing. Sample and standard tubes were then washed with 200 μ l washing buffer and centrifuged at 1,000 g for 5'. After gentle aspiration of the washing buffer, samples and standard were resuspended in 200 μ l washing buffer. Fluorescence intensities were then measured through a Beckman Coulter Navios flow cytometer and converted into concentrations through a dedicated software provided by Biolegend.

Peptide-, PHA-stimulated and unstimulated cells from patients and controls were transferred into polypropylene tubes and washed with 2 ml washing solution per tube. Vital staining was then performed with Zombie AquaTM. After 10-minute incubation at room temperature and further washing, staining with panel C antibodies was performed. One duplicate per subject of PHA-stimulated cells were stained with anti-CD3, anti-CD4 and anti-CD8 antibodies only as described above. After 10 minutes of incubation at room temperature and further washing the cells were resuspended in 300 μ l washing buffer and analysed through a Beckman Coulter Navios flow cytometer.

Activation marker and cytokine responses after stimulation with peptides and PHA were calculated as the fold change of each analyte compared to the negative (unstimulated control). Patients showing activation marker or cytokine variations exceeding one fold change for an analyte with respect to the negative control were classified as responders to that analyte.

Statistical analyses

Incidence rates of events-of-interest were calculated as the fraction of total events over the sum of the time intervals of observation of each subject. Cut-off values for optimal discrimination of anti-DNA-positive and beta-lactam allergic subjects based on histone-specific and penicilloylated albumin-specific T cell counts respectively were identified through receiver operating characteristics curves (**Appendix 7**). Since incomplete information on EBV status was available, the cut-off for EBV-specific T cells was set on the median value of EBV-specific T cells among subjects with established EBV infection. Frequencies of categorical variables among groups were compared by using the chi-square test with Fisher's exact correction and are expressed as percentages unless otherwise specified. Deviations from expected distributions of events among different analyses or in comparison with the general population were performed with the binomial test of hypotheses. Non-normally distributed continuous variables were compared through the Mann-Whitney's test or the Kruskal-Wallis' test among two or more groups. Variations in quantitative variables within the same subjects observed under different conditions were tested through the Wilcoxon's matched-pairs signed-rank test. Comparisons of normally distributed continuous variables among two or more groups were performed with the Student's t-test or with ANOVA with Bonferroni's correction respectively. Univariate Cox's regression analysis was used to analyse the association of disease phenotypes with time-dependent outcomes.

All analyses were performed with Statacorp STATA® version 15.0, Microsoft Excel® 2019 version or the OpenEpi online suite (<http://www.openepi.com>). Data are expressed as median (interquartile range, IQR) unless otherwise specified.

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APPENDICES

Appendix 1: prevalence of allergy and asthma in the general population according to different data sources

Source	Year	Region	Method	Allergy	Allergy excl. drug allergy	Drug Allergy	Allergy excluding asthma	Asthma
Eurostat	2014	EU	Simplified questionnaire	ND	ND	ND	16.9%	5.9%
Eurostat	2014	Italy	Simplified questionnaire	ND	ND	ND	15.2%	4.9%
Eurostat	2014	Sweden	Simplified questionnaire	ND	ND	ND	22.7%	7.8%
(Quercia et al., 2012)	ISTAT	2017	Italy	Simplified questionnaire	10.7%	ND	ND	ND
	ND	Italy	Specific questionnaire	ND	ND	ND	ND	6.1%
	ND	Italy	Survey on physician-confirmed diagnosis	ND	16.5%*	ND	ND	3.6%
(Wong et al., 2019)	2000-2013	USA	Supervised ICD-9-based analysis	ND	ND	13.8%	ND	ND
(Langen et al., 2013)	2008-2011	Germany	Survey on physician-confirmed diagnosis	ND	30%	ND	ND	8.6%

*Data kindly provided by Prof. Cristoforo Incorvaia in addition to those reported in the original manuscript.

Abbreviations. Eurostat: European Institute of Statistics; ICD: International Classification of Diseases; ISTAT: Istituto Nazionale di Statistica (Italian National Institute for Statistics); ND: no data.

Appendix 2: complete high-resolution HLA-DRB1 genotype frequency in patients, controls, and in the general population

	SLE		TAK		HC		Italian General Population*	
	%	Sample size	%	Sample size	%	Sample size	%	Sample size
DRB1*03:01	33%	185	11%	80	17%	86	19%	975
DRB1*07:01	22%	185	31%	80	22%	86	25%	975
DRB1*11:01	15%	185	19%	80	15%	86	31%	4,575
DRB1*15:01	14%	185	8%	80	13%	86	9%	4,575
DRB1*01:01	14%	185	6%	80	10%	86	14%	4,575
DRB1*14:01	12%	185	8%	80	14%	86	5%	975
DRB1*16:01	12%	185	13%	80	6%	86	10%	975
DRB1*11:04	11%	185	16%	80	14%	86	28%	4,575
DRB1*13:02	10%	185	10%	80	10%	86	9%	4,575
DRB1*13:01	7%	185	10%	80	10%	86	11%	4,575
DRB1*04:01	4%	185	8%	80	7%	86	3%	975
DRB1*08:01	3%	185	4%	80	2%	86	4%	975
DRB1*15:02	3%	185	10%	80	3%	86	2%	4,575
DRB1*04:04	3%	185	1%	80	2%	86	2%	975
DRB1*11:03	3%	185	5%	80	3%	86	3%	975
DRB1*13:03	3%	185	4%	80	1%	86	3%	975
DRB1*04:02	3%	185	4%	80	6%	86	3%	975
DRB1*10:01	2%	185	3%	80	5%	86	4%	975
DRB1*04:03	2%	185	3%	80	6%	86	3%	975
DRB1*01:03	2%	185	0%	80	2%	86	1%	4,575
DRB1*04:05	2%	185	5%	80	2%	86	3%	975
DRB1*08:04	2%	185	1%	80	0%	86	0%	975
DRB1*01:02	2%	185	9%	80	6%	86	4%	4,575
DRB1*14:04	1%	185	1%	80	0%	86	1%	975
DRB1*16:02	1%	185	1%	80	1%	86	1%	975
DRB1*09:01	1%	185	0%	80	1%	86	1%	975
DRB1*13:05	1%	185	0%	80	3%	86	1%	975
DRB1*13:04	1%	185	0%	80	0%	86	0%	975
DRB1*04:07	1%	185	0%	80	1%	86	1%	975
DRB1*12:01	1%	185	4%	80	3%	86	2%	975
DRB1*04:10	1%	185	0%	80	0%	86	0%	975
DRB1*11:02	1%	185	0%	80	1%	86	1%	975
DRB1*08:02	1%	185	0%	80	0%	86	0%	975

*Data were retrieved from the Allele Frequency Net - <http://www.allelefrequencies.net> - (Gonzalez-Galarza et al., 2019), based on data from multiple studies (De Re et al., 2010, Rendine et al., 1998). ND= No data available.

Appendix 3: HLA-DRB1 genotype and clinical features of patients with SLE and COVID-19

#	Age (years)	Sex	Disease duration (years)	HLA-DRB1 genotype	Main SLE features	COVID-19 course
1	56	M	23	*01:01, *16:01	Nephritis, myopericarditis, leukopenia, thrombocytopenia, arthritis, positive ADNA, low complement	Mild respiratory symptoms. Post-COVID-19 myocardial infarction
2	57	F	21	*03:01, *15:01	Serositis, arthritis, Kikuchi-Fujimoto's disease, positive ADNA.	Moderate respiratory, GI and systemic symptoms. Persistent cough.
3	53	F	28	*11:01, *14:01P	Skin manifestations, arthritis, positive ADNA, low complement	Mild respiratory symptoms.
4	41	F	9	*03:01, *13:01	Serositis, arthritis, polyadenomegaly, positive ADNA, low complement	Mild respiratory symptoms and low-grade arthritis flare.
5	37	F	10	*11:01, *15:01	Neuropsychiatric SLE (epilepsy, headache), arthritis, serositis, leukopenia, positive ADNA.	Mild respiratory symptoms.
6	50	F	37	*01:01, *15:01	Nephritis, aseptic peritonitis, arthritis, positive ADNA and aPL, low complement	Mild respiratory symptoms.
7	44	F	24	*13:01, *16:01	Serositis, leukopenia, thrombocytopenia, interstitial lung disease, positive ADNA and aRNP, low complement	Mild respiratory symptoms.
8	28	F	7	*01:01, *15:01	Arthritis, photosensitive rash, positive ADNA and anti-Sm, DVT+pulmonary embolism	Mild respiratory symptoms.
9	27	M	2	*01:03, *13:02	Fever, photosensitive rash, oral ulcers, arthritis, nephritis, myocarditis, positive ADNA and aRNP, low complement	Mild systemic symptoms

Appendix 4: candidate antigens for antigen-specific T cell studies

Candidate antigen	References	Clinical evidence		Experimental evidence			Reasons for exclusion
		Prevalence in SLE cohort	Prevalence in the general population	Peptide sequences available	T-cell immunogenicity	HLA binding	
Autoantigens							
Smith antigen	(Zhao et al., 2019b)	Ab: 21%	NA	Yes	Yes	Yes	Low prevalence in the study cohort
U1-RNP	(Kattah et al., 2015)	Ab: 18%	NA	Yes	Yes	No	Low prevalence in the study cohort. Non SLE-specific antigen. Poor results with patients with SLE
β2-GPI	(Benagiano et al., 2019, de Moerloose et al., 2017, Salem et al., 2018, Salem et al., 2015)	Ab: 19%	NA	Yes	Yes	No	Low prevalence in the study cohort. Limited number of patients reported in the literature, no reported HLA compatibility with the present study.
Peptide surrogate for DNA	(Putterman & Diamond, 1998)	Ab: 77%	NA	Yes	No	No	Too limited evidence from murine studies.
Histone H1	(Bruns et al., 2000, Bruschi, Moroni et al., 2021, Lu et al., 1999)	Ab: 77%*	NA	No	No	No	Non-nucleosome component. Too limited evidence.
Histone H2			NA	Yes	Yes	No	
Histone H3			NA	Yes	Yes	No	NA
Histone H4			NA	Yes	Yes	No	
Allergens							
Jug r2 (walnut)	(Archila et al., 2015, McWilliam, Koplin et al., 2015)	<1%	2%	Yes	Yes	No	Low prevalence in the study cohort and in the general population.
Poa p1, Lol p1, Lol p5a, Poa p5a, Phl p1, Phl p5a (Graminaceae)	(Archila et al., 2014, Olivieri, Verlato et al., 2002) (Macaubas et al., 2006)	5%	12%	Yes	Yes	No	Low prevalence in the study cohort. Heterogeneity of antigens.
Der p1 (dust mites)	(Boonpiyathad, Sokolowska et al., 2019, Olivieri et al., 2002)	5%	15%	Yes	Yes	Yes	Low prevalence in the study cohort. Reference publication after preliminary analysis.
Beta-lactams	(Li et al., 2020)	15%	2%	Yes	Yes	Yes	NA
Antigens from infectious agents							
Influenza A PB1 or Haemagglutinin	(Uchtenhagen, Rims et al., 2016)	ND	ND	Yes	Yes	Yes	Heterogeneity of antigens. Limited evidence of a pathogenic role in SLE.
CMV	(Draborg et al., 2018, Pordeus et al., 2008)	ND	77%	ND	ND	ND	Limited evidence of a pathogenic role in SLE.
EBNA 1 (EBV)	(Munz et al., 2000) (Leogrande & Jirillo, 1993, Long et al., 2013, Meckiff et al., 2019, Pordeus et al., 2008)	ND	83%	No	No	No	NA
EBNA 2 (EBV)		ND	83%	Yes	Yes	Yes	NA

* Assuming a substantial overlap among anti-nucleosome/histone antibodies and anti-DNA antibodies (Bruns et al., 2000). Abbreviations. Ab: antibodies; CMV: Cytomegalovirus; EBV: Epstein-Barr virus

Appendix 5: extended shortlist of peptides for T cell studies

Antigen	HLA restriction	Peptide sequence (aminoacid number)	IEDB adjusted rank	Reference
Autoantigens				
Histone H4	DRB1*03:01	GLIYEETRGVLKVFL (49-63)	17.00	(Lu et al., 1999)
		VVYALKRQGR TLYGFG (87-102)	1.50	ND
Histone H3	DRB1*11:01	LPFQRLMREIAQD (66-78)	1.47	ND
Allergens				
Penicilloylated albumin	DRB1*03:01	PELLFFAK*RYKAAFT	26.00	(Azoury et al., 2018)
	DRB1*11:01		2.00	
Antigens from infectious agents				
EBNA 2	DRB1*03:01	PAQPPPGVINDQQLHHLPSG (301-320)	19.00	(Long et al., 2013, Meckiff et al., 2019)
		PPGVINDQQLHHL P (305-317)	4.37	ND
		TYHLIVDTDSLGNP (13-26)	6.14	ND
	DRB1*11:01	GPLASAMRMLWMANY (125-139)	19.00	ND
		MPTFY LALHGGQTY (1-14)	10.66	ND
EBNA 1	DRB1*03:01	EVLKDAIKDLVMTK (573-586)	9.48	ND
		AEVLKDAIKDLVMTK (572-586)	12.00	ND
	DRB1*11:01	HIFAEVLKDAIKDL (569-582)	22.61	ND

Appendix 6: clinical features of patients included in T-cell studies

Subject ID	Sex, Age (y)	HLA-DRB1	Diagnosis	Disease duration (y)	Disease activity		HCQ	PDN dose (mg/day)	Immunosupp.
					SLEDAI-2K	LLDAS			
#1*	F, 32	3	SLE	12	4	1	Yes	0	MMF
#1b	F, 30	3	SLE	10	10	0	Yes	0	AZA
#2	F, 25	11	SLE	7	2	1	Yes	3.75	MMF
#3*	F, 47	11	SLE	11	0	1	Yes	5	MMF
#3b	F, 45	11	SLE	10	8	0	Yes	5	AZA
#4	F, 25	11	SLE	8	30	0	No	37.5	IVIG
#5	F, 56	3	SLE	28	2	1	Yes	5	MMF
#6	F, 36	11	SLE	15	12	0	Yes	5	MMF
#7	F, 51	3 and 11	SLE	36	1	1	No	5	None
#8	F, 34	3	SLE	16	2	0	Yes	0	None
#9	F, 59	11	SLE	12	4	1	Yes	2.5	None
#10*	F, 35	11	SLE	7	0	1	Yes	5	MMF
#10b	F, 34	11	SLE	6	9	0	Yes	6.25	AZA
#11	M, 53	11	SLE	19	2	1	Yes	0	None
#12	F, 43	3	SLE	17	0	1	Yes	0	MMF
#13*	F, 34	11	SLE	12	4	1	Yes	5	MMF
#13b	F, 33	11	SLE	11	13	0	Yes	5	None
#14	F, 48	3	SLE	8	0	1	Yes	0	None
#15	F, 35	11	SLE	25	2	1	Yes	0	None
#16	F, 38	11	SLE	22	6	0	Yes	0	None
#17	F, 57	3	SLE	22	8	0	Yes	2.5	MMF
#18	F, 61	11	SLE	32	0	1	Yes	0	None
#19	F, 58	11	SLE	34	2	1	Yes	0	None
#20	M, 45	11	SLE	24	0	1	Yes	0	AZA
#21	F, 23	11	SLE	7	2	1	Yes	0	None
#22	F, 38	3	SLE	19	2	1	Yes	0	None
#23	F, 25	11	SLE	9	9	0	Yes	5	MTX
#24	F, 35	3	SLE	22	2	1	No	2.5	None
#25*	F, 26	3	SLE	5	4	1	Yes	0	MMF
#25b	F, 24	3	SLE	4	16	0	Yes	5	None
#26	M, 42	3 and 11	SLE	8	4	0	Yes	2.5	None
#27	F, 52	11	SLE	19	4	1	Yes	2.5	MTX
#28	F, 39	3	SLE	20	8	0	No	0	AZA
#29	F, 51	11	SLE	26	4	1	Yes	1.25	MMF
#30	F, 44	3	SLE	11	2	1	Yes	0	None
#31	M, 31	3	SLE	1	6	0	Yes	0	MMF
#32	F, 64	3	SLE	36	2	1	Yes	2.5	MTX

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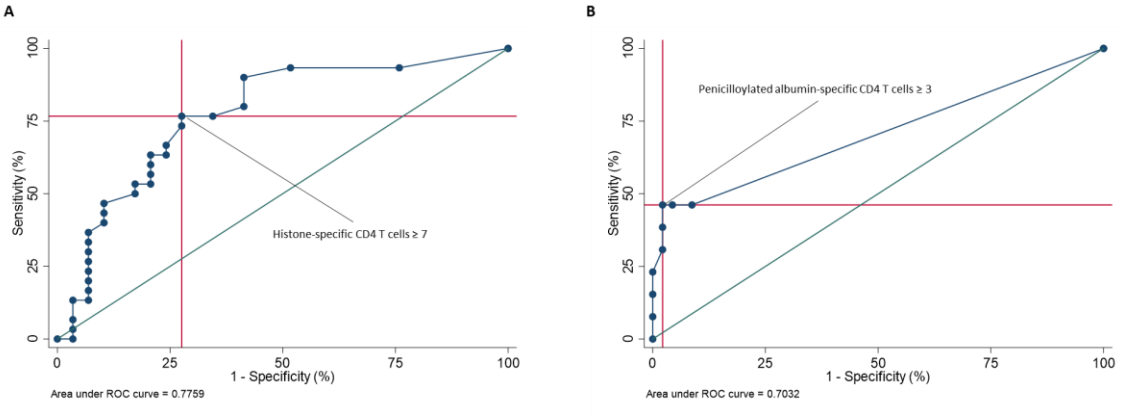
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Subject ID	Sex, Age (y)	HLA-DRB1	Diagnosis	Disease duration (y)	Disease activity		HCQ	PDN dose (mg/day)	Immunosupp.
					ITAS	Clinical impression			
#33	F, 36	11	TAK	12	3	Smouldering	No	5	sirolimus
#34	F, 27	3	TAK	5	0	Remission	No	5	MTX, Infliximab
#35	F, 65	3	TAK	17	1	Active	No	0	MTX
#36	F, 46	11	TAK	28	0	Remission	No	5	MTX, Tocilizumab
#37	F, 39	11	TAK	12	2	Remission	No	10	Abatacept
#38	F, 35	3	TAK	6	0	Remission	No	0	AZA
#39	F, 47	11	TAK	7	0	Smouldering	No	0	MTX
#40	F, 44	3	TAK	9	0	Remission	No	5	AZA, Infliximab
#41	F, 47	11	TAK	17	0	Remission	No	5	None
#42	M, 22	11	TAK	5	1	Smouldering	No	10	MTX, Infliximab
#43	F, 50	11	TAK	10	1	Remission	No	5	MTX, Infliximab
Subject ID	Sex, Age (y)	HLA-DRB1	Diagnosis						
#44	M, 25	11	HC						
#45	F, 33	3	HC						
#46	F, 59	3	HC						
#47	F, 32	11	HC						
#48	F, 42	3	HC						
#49	F, 51	11	HC						
#50	F, 25	3	HC						
#51 [^]	F, 25	3 and 11	HC						
#52	F, 31	11	HC						
#53	F, 48	3	HC						

*: re-tested during active disease. [^]tested twice

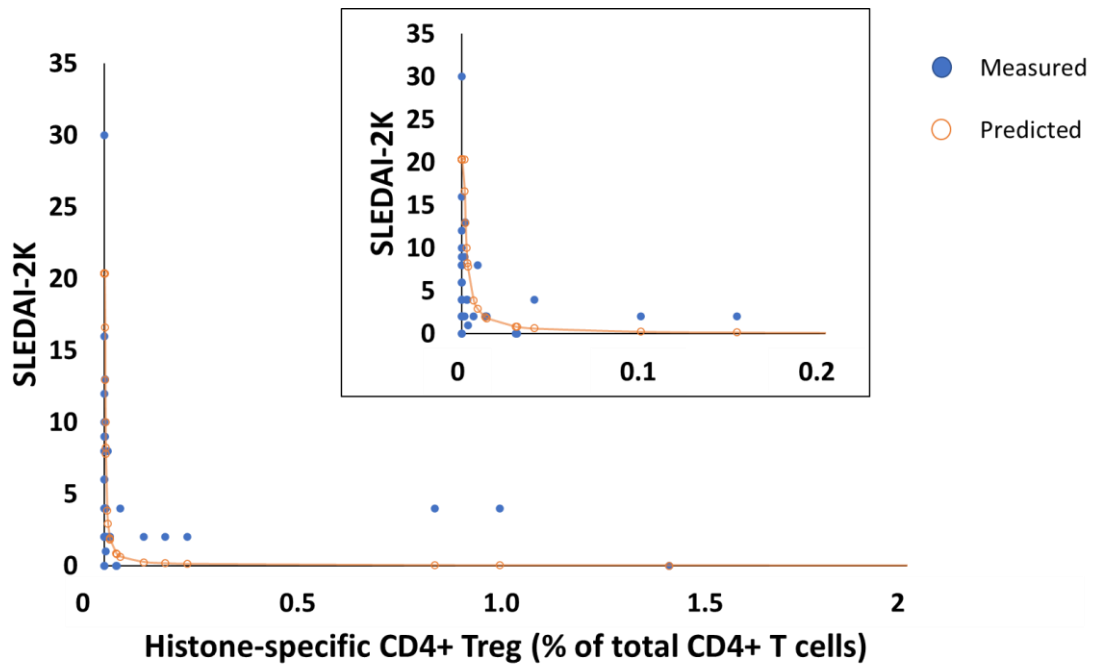
Abbreviations. AZA: azathioprine, HC: healthy control, ITAS: Indian Takayasu Disease Activity Score, IVIG: intravenous immunoglobulins, LLDAS: lupus low disease activity state, MMF: mycophenolate mofetil, MTX: methotrexate, PDN: prednisone, SLE: systemic lupus erythematosus, SLEDAI-2K: SLE disease activity index 2000, TAK: Takayasu's arteritis.

Appendix 7: receiver operating characteristics curves for antigen-specific T cell counts.



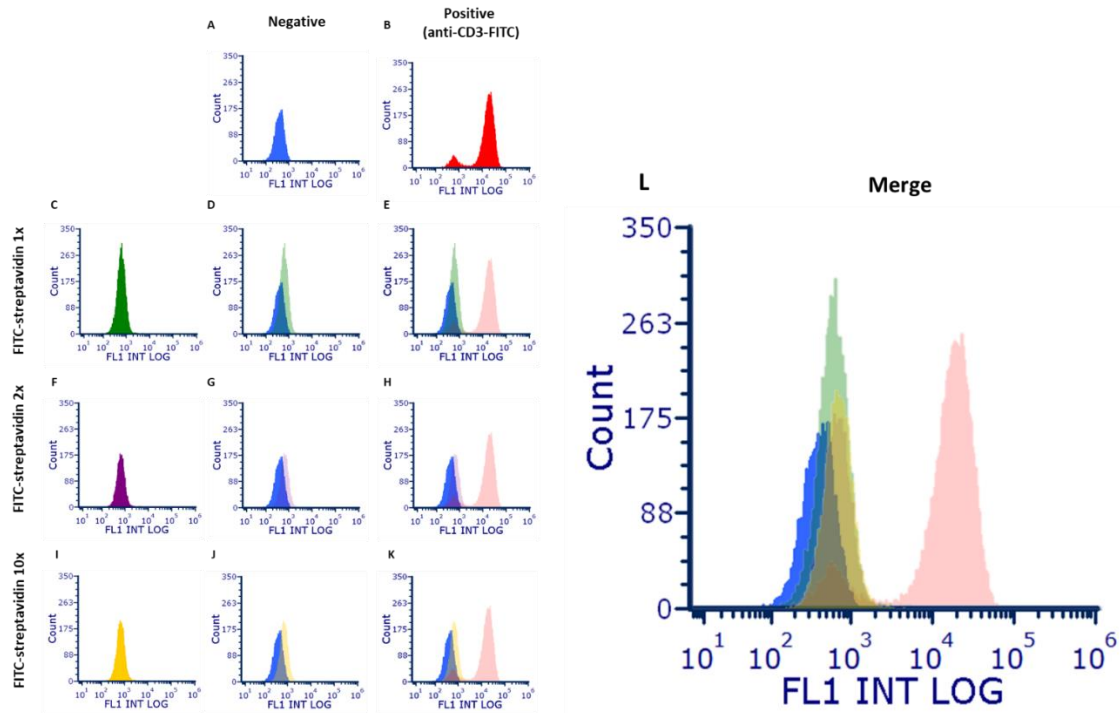
Receiver operating characteristics curves showing the diagnostic performance of total absolute histone-specific (A) and penicilloylated albumin-specific (B) CD4+ T cell counts for identifying subjects with positive antiDNA and allergy to beta-lactams, respectively. The red reference lines highlight sensitivity and 1-specificity values of optimal cut-offs for both continuous variables.

Appendix 8: curve fitting for SLEDAI-2K and histone-specific T-reg CD4+ T cells



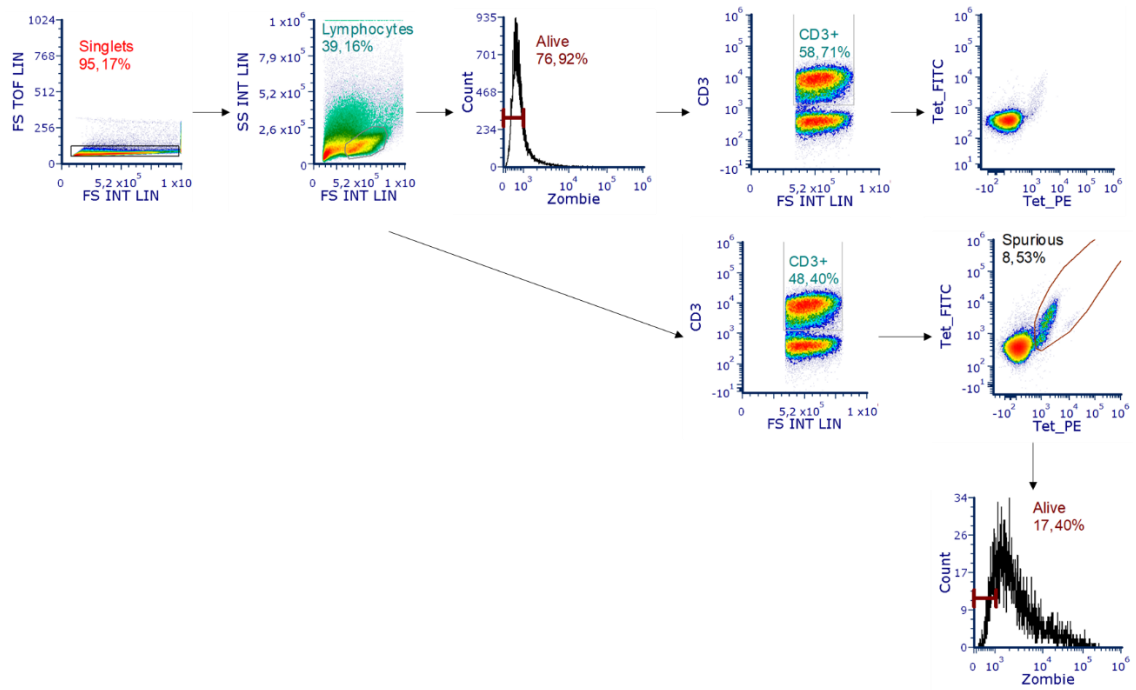
This figure shows the inverse relation between histone-specific CD4+ Treg cells and SLEDAI-2K. Measured SLEDAI-2K / histone specific CD4+ Treg percentages of CD4+ cells are depicted in blue. Orange empty dots and lines show the hyperbolic interpolation curve generated by calculating expected SLEDAI-2K values based on histone-specific CD4+ Treg cell % of total CD4 cells. The internal subpanel shows the curve fit for lower percentages of In particular, the curve had the following equation: $SLEDAI_2K = \frac{0.25}{(1000+HTreg\%CD4)}$. For non-null values the curve had a good fit with real SLEDAI-2K values ($R^2=5.616$; $p<0.001$), whereas it was unable to predict SLEDAI-2K for null histone-specific CD4+ Treg cells.

Appendix 9: FITC-streptavidin staining



Histograms showing the fluorescence intensity of FITC-streptavidin staining on PBMC from a healthy donor in comparison with no staining (Negative, panel A) and control positive staining with an anti-CD3-FITC antibody (Panel B) after gating through singlet events and lymphocyte physical parameters. PBMC were stained with 1x (panel C-E), 2x (panel F-H), 10x (panel I-K) the concentration of FITC-streptavidin employed to generate FITC-MHC tetramers. Panel L shows a merged view of the previous panels. FITC-streptavidin alone did not generate a significant fluorescence compared to the negative (unstained) and positive controls. Data were acquired with a Beckman Coulter Navios Flow Cytometer, elaborated into graphs with FCS Express version 7 and merged with Microsoft PowerPoint 2019.

Appendix 10: exclusion gating for spurious events



This figure depicts the gating strategy employed to exclude spurious FITC/PE co-fluorescent signals from flow cytometry analyses employing MHC-FITC/MHC-PE tetramers. In this representative example PBMC from a healthy subject are shown. Most double positive (“spurious”) cells were dead as confirmed by back-gating.

Appendix 11: kinetics of selected T-helper-related cytokines

Cytokine	Timing of measurement/release (h)	Reference
IL2	0.5-4-14-18-24-30	(Hartmann, Marjanovic et al., 2014, Oh, Chen et al., 2016, Parlesak, Haller et al., 2004)
IL4	6-12-24	(Barata, Ying et al., 1998, de Boer, Fillié et al., 1998, Krouwels, Hol et al., 1998)
IL5	6-12-24	(Barata et al., 1998, Krouwels et al., 1998)
IL6	10-18-24-70	(Hartmann et al., 2014, Parlesak et al., 2004, Stanley & Lacy, 2010)
IL9	12-96	(Liu, Harberts et al., 2014, Louahed, Zhou et al., 2001)
IL10	0.5-24-30	(Oh et al., 2016, Parlesak et al., 2004)
IL13	20-40-48	(de Boer et al., 1998, Ohshima, Yang et al., 1999)
IL17A	4-6-48	(Ferretti, Bonneau et al., 2003, He, Lang et al., 2013, Naji, Smith et al., 2014)
IL17F	4-24-36-72	(Burns, Maroof et al., 2020, Duhén, Geiger et al., 2009, Garcia-Arellano, Hernandez-Palma et al., 2018, Naji et al., 2014, Saini, Ramesh et al., 2013)
IL22	18-36-72	(Duhén et al., 2009, Perriard, Mathias et al., 2015, Zheng, Danilenko et al., 2007)
IFN- γ	0.5-6-24-24-48-70	(Krouwels et al., 1998, Oh et al., 2016, Ohshima et al., 1999, Parlesak et al., 2004, Stanley & Lacy, 2010)
TNF	0.5-10-18	(Hartmann et al., 2014, Oh et al., 2016, Parlesak et al., 2004, Stanley & Lacy, 2010)