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EDITED BY

Vasco C. Romão,

Universidade de Lisboa, Portugal

REVIEWED BY

Kristin Andreassen Fenton, UiT The Arctic University of Norway, Norway Hong Zan, Prellis Biologics, United States

*CORRESPONDENCE
Giovanni Fulvio

⊠ giovanni.fulvio92@gmail.com

RECEIVED 26 March 2025 ACCEPTED 12 August 2025 PUBLISHED 01 September 2025

CITATION

Fulvio G, La Rocca G, Tani C, Mosca M and Baldini C (2025) Sjögren's disease and systemic lupus erythematosus overlap: immunological insights and therapeutic implications.

Front. Lupus 3:1600768. doi: 10.3389/flupu.2025.1600768

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Sjögren's disease and systemic lupus erythematosus overlap: immunological insights and therapeutic implications

Giovanni Fulvio^{1,2*}, Gaetano La Rocca^{1,2}, Chiara Tani¹, Marta Mosca¹ and Chiara Baldini¹

¹Rheumatology Unit, Azienda Ospedaliero Universitaria Pisana and Department of Clinical and Experimental Medicine, University of Pisa, Pisa, Italy, ²Department of Clinical and Translational Science, University of Pisa, Pisa, Italy

Sjögren's disease (SjD) and systemic lupus erythematosus (SLE) are distinct autoimmune disorders and their clinical overlap presents a unique immunological entity with specific challenges. While the clinical manifestations of the SjD-SLE overlap have been extensively characterised, its underlying pathogenetic mechanisms remain less understood. This review underscores the immunological features of the overlap, highlighting the roles of genetic predisposition, interferon pathway activation and B-cell dysregulation. Key genetic factors, particularly those associated with HLA and cytokine signaling, underpin disease susceptibility by promoting aberrant immune responses. The consequent and persistent interferon pathway activation drives chronic inflammation and establishes a feedback loop with autoantibody production. Furthermore, Extrafollicular B-cell responses are central to generating hallmark autoantibodies, such as anti-dsDNA and rheumatoid factor, which are frequent in the overlap. Finally, the continuous activation of interferons and Bcells not only increase disease activity but also contributes to lymphoproliferative complications. Despite progress in elucidating these mechanisms, patients with SjD-SLE overlap remain underrepresented in clinical trials, limiting therapeutic advancements. Emerging strategies, including interferon receptor inhibitors, BAFF-blocking antibodies, and advanced B-cell depletion therapies, may offer promising options to hit the distinct immunological abnormalities of these patients.

KEYWORDS

Sjögren's disease, systemic lupus erythematosus, overlap syndrome, genetic predisposition, interferon pathway, B-cell activation, extrafollicular B-cell response, targeted therapy

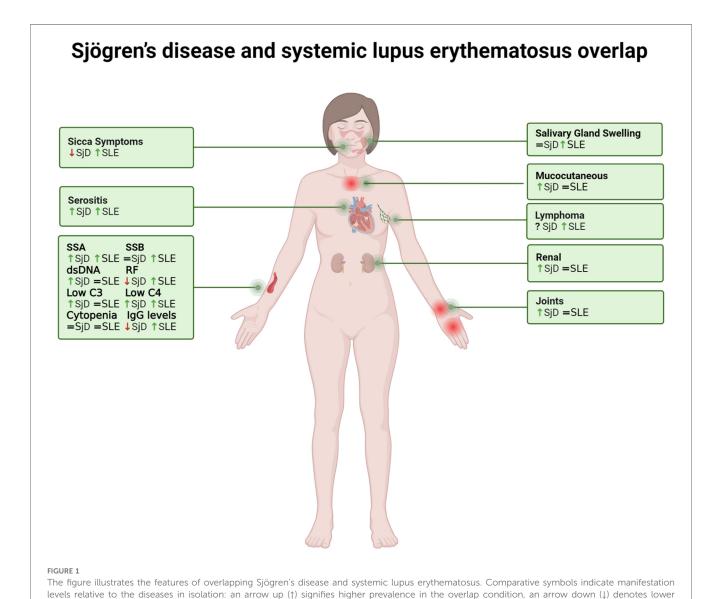
Introduction

Sjögren's Disease (SjD) and Systemic Lupus Erythematosus (SLE) are systemic autoimmune disorders classified among connective tissue diseases. SjD and SLE are indeed distinct diseases; however, their possible coexistence and their pathogenetic similarities have always opened research questions about pathophysiological interplay between the two diseases. SjD is typically characterized by chronic inflammation of the salivary and lachrymal glands, leading to symptoms such as dry mouth and dry eyes (sicca symptoms) (1). Beyond glandular involvement, SjD encompasses a broad spectrum of extra-glandular manifestations including B cell lymphoma (2). SLE, on the

other hand, is distinguished by its heterogeneous clinical presentation, with common involvement of the skin, joints and kidneys. Disease activity is often associated with hypocomplementemia, a result of the impaired clearance of immune complexes, which contributes to its immune-mediated manifestations (3). Intriguingly, both the diseases share common immunological abnormalities, particularly associated with B-cell hyperactivity, which can drive autoantibody production, tissue inflammation and damage (4, 5).

SjD occurring in patients with SLE has historically been defined as "secondary". Recent literature has highlighted that the term "secondary Sjögren"s syndrome" is a misnomer, emphasizing the need to recognize the unique clinical manifestations that emerge when Sjögren's disease overlaps with other autoimmune diseases, such as SLE. Although SjD and SLE are clinically distinct entities, their coexistence is increasingly recognized as more than a simple overlap of features. Instead, the SjD-SLE overlap represents a unique clinical and immunological phenotype with specific

implications diagnosis, prognosis, therapeutic for and management. Rather than merely exhibiting features of both conditions, these patients represent a distinct clinical entity with specific characteristics that differ from the individual disease when considered separately (Figure 1) (6). Indeed, SjD-SLE are predominantly female and tend to be older than typical SLE patients but younger than those with isolated SjD (7, 8). Clinically, they are characterized by prominent salivary gland involvement, including parotid gland enlargement and sicca symptoms, alongside mucocutaneous manifestations, joint involvement, renal complications, and serositis. Laboratory tests demonstrate elevated IgG levels, frequent hypocomplementemia and a characteristic autoantibody profile, including SSA, SSB, dsDNA, and rheumatoid factor. Moreover, SjD-SLE patients often present with evidence of systemic inflammation and a higher disease activity compared to patients with either condition alone (9-11). Finally, it has been suggested that overlapping patients may have a higher risk of lymphoma when compared to SLE alone (12, 13).



prevalence, and an equal sign (=) indicates similar prevalence or intensity. SjD, Sjögren's disease; SLE, systemic lupus erythematosus.

Despite its importance, the overlap phenotype remains underrecognized in clinical practice and is not adequately captured by current classification criteria. This under-recognition has important consequences. Diagnostic uncertainty can delay appropriate management, and the routine exclusion of overlap patients from clinical trials limits the applicability of emerging therapies to this subgroup. Furthermore, treatment decisions rarely account for the distinct immunopathological features of the overlap. Indeed, while the clinical phenotype of the SjD-SLE overlap is well-defined, research into its pathogenesis remains limited. Interestingly, emerging studies suggest that, despite differences in diagnosis, organ involvement, and disease presentation, autoimmune diseases often share common pathogenic mechanisms. However, these shared mechanisms alone are insufficient for differentiating between diseases, as a single disease can exhibit multiple molecular signatures, while distinct diseases may share similar ones (14). This complexity has led to growing interest in defining patient subgroups based on endotypes, biologically distinct mechanisms underlying similar clinical features. The SjD-SLE phenotype may represent an underlying unique endotype, emphasizing the need for targeted, personalized therapeutic strategies. However, specific studies focusing on the SjD-SLE overlap are rare, hence understanding pathogenetic information may also come from common pathways shared by the two diseases and their specific manifestations.

In this review, we investigate the pathogenetic basis of the SjD-SLE overlap, drawing insights from evidence specific to the overlap condition as well as shared mechanisms observed in SjD and SLE as separate disease. Specifically, we highlight recent advances in understanding the genetic background, interferon expression, and B-cell phenotypes. Finally, we also explore the potential for developing targeted therapies tailored to the unique SjD-SLE endotype, focusing on the specific pathogenetic processes that characterize this overlap.

Genetic

Few studies, often limited by small patient cohorts, have explored the genetic basis of the SjD-SLE overlap (15, 16).

Despite limited direct evidence, a shared genetic predisposition is strongly supported by indirect findings. Indeed, in families where one member is affected by SLE, there is a higher incidence of SjD, and vice versa (17, 18). This phenomenon, known as coaggregation, supports the concept of polygenic inheritance with condition-specific thresholds, rather than the existence rather than two entirely separate genetic backgrounds. Furthermore, there is considerable overlap in the genes identified as risk loci for Sjögren's Disease and for Systemic Lupus Erythematosus (19, 20). Research has revealed genetic risk factors within the HLA locus and in non-HLA loci (21, 22). Variants associated with SjD and SLE predominantly influence pathways of the innate and adaptive immune responses, notably involving the antigen presentation, type I interferon pathway and cytokine-mediated signaling pathway (23) (Table 1).

HLA risk loci

Among HLA class II alleles, the most robust genetic association identified so far is HLA-DR3. This association has been confirmed by several studies and still represents the strongest genetic risk factor for these conditions (24, 25). Specifically, HLA-DRB103:01* (DR3) is strongly associated with the presence of anti-SSA and anti-SSB autoantibodies in both SjD and SLE. This variant affects antigen presentation and immune tolerance, fostering autoantibody production. Importantly, HLA-DRB103:01* is also associated with reduced copy number of complement component C4A, which compromises immune complex clearance. These links illustrate how genetic variation contributes to both immune activation and defective clearance mechanisms, central to SjD-SLE pathogenesis (25-28). Furthermore, C4 and its effector, C3, are typically found at lower levels in the plasma of women compared to men possibly contributing to the higher incidence of autoimmunity in females. These sex-linked differences in complement protein expression may thus help explain the marked female predominance observed in both SLE and SjD (29).

TABLE 1 Key genetic loci associated with the SjD-SLE overlap syndrome.

Gene	Туре	Function of the encoded protein	Relevance to overlap
HLA-DRB103:01*	HLA class II	Antigen presentation	Associated with anti-SSA and anti-SSB antibody production
C4A	HLA class III	Part of the complement pathway	Impaired clearance of immune complexes
TNFAIP3	Non-HLA	Deubiquitinating enzyme; negative regulator of NF-κB signaling	Deficiency leads to B-cell hyperactivity
TNIP1	Non-HLA	Adaptor protein for TNFAIP3	Acts synergistically with TNFAIP3 in controlling inflammation
IRF5	Non-HLA	Transcription factor	Activate type I interferon expression
STAT4	Non-HLA	Transcription factor	Enhances cellular sensitivity to type I interferon
TYK2	Non-HLA	Tyrosine kinase	Mediates interferon signaling and lymphocyte activation
IL12A	Non-HLA	p35 subunit of IL-12	Promotes Th1 differentiation and IFN-γ release
TLR7	X-linked	Pattern recognition receptor (PRR)	Contributes to female predominance and interferon production
CXorf21	X-linked	Scaffold protein in SMOC complex	Contributes to female predominance and interferon production

The table summarizes selected genes implicated in the SjD-SLE overlap, including their classification (HLA, non-HLA, or X-linked), the function of the encoded protein, and their relevance to the clinical and immunological features of the overlap condition.

SjD, Sjögren's disease; SLE, systemic lupus erythematosus; HLA, human leukocyte antigen; IFN, interferon; IFN-I, type I interferon; NF-xB, nuclear factor kappa-light-chain-enhancer of activated B cells; PRR, pattern recognition receptor; SMOC, supramolecular organizing center; Th1, T helper type 1; IL, interleukin; TYK2, tyrosine kinase 2; STAT4, signal transducer and activator of transcription 4.

Non-HLA risk loci

Beyond the HLA region, several non-HLA genes also play crucial roles as modifiers of disease progression and severity in SLE and SjD. In this review, we will specifically examine the roles of the genes *TNFAIP3*, *TNIP1*, *IRF-5*, *STAT4*, *TYK2*, *IL-12A*, as well as the significance of genes located on the X-Chromosome (Figure 2) (21, 22, 24). *TNFAIP3*, encoding the A20 protein, and *TNIP1*, encoding the TNFAIP3-interacting protein 1, are both negative regulators of the NF-κB pathway, a crucial mediator of inflammation. This pathway is activated by several pattern recognition receptors (PRRs, such as Toll-like receptors), a key part of the innate immune response, and by the T-cell receptor (TCR) or B-cell receptor (BCR), vital for the

adaptive immune response (30). A20 deficiency leads to profound effects on B cells, which exhibit a hyperactive phenotype characterized by enhanced proliferation and the excessive production of immunoglobulins. This results in the overproduction of autoantibodies, such as double-stranded DNA (dsDNA) antibodies (31, 32). Furthermore, A20 impairment has been linked with primary Sjögren's syndrome (pSS) related lymphoma, suggesting that B cells continuously stimulated by autoimmunity may increase the risk of developing lymphoma (33).

Additional susceptibility genes include *IRF5* and *STAT4*, transcription factors essential for type I and type II interferon signaling. Overactivity of the *IRF5* signaling pathway is a common observation across SLE and SjD and is intricately linked to Toll-like receptor pathways (24, 34, 35). Activation of *IRF*

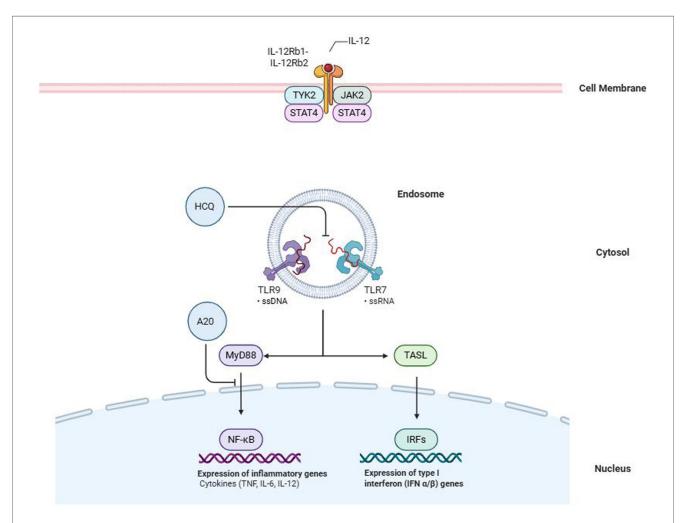


FIGURE 2

The image illustrates the intracellular signaling pathways involved in innate immune activation through Toll-like receptors (TLRs) and the interleukin-12 (IL-12) receptor. Within the endosome, TLR7 and TLR9 detect single-stranded RNA (ssRNA) and single-stranded DNA (ssDNA), respectively, triggering two downstream cascades: the MyD88-dependent NF- κ B pathway, which promotes the transcription of pro-inflammatory cytokines (e.g., TNF, IL-6, IL-12), and the TASL-mediated IRF pathway, responsible for the induction of type I interferons (IFN- α / β). The regulatory molecule A20 inhibits NF- κ B activation by targeting MyD88, while hydroxychloroquine (HCQ) blocks TLR activation, dampening both inflammatory and interferon responses. At the cell membrane level, IL-12 binds its receptor complex (IL-12Rb1/IL-12Rb2), initiating signaling via the kinases TYK2 and JAK2 and activating STAT4 to mediate transcriptional responses. HCQ, hydroxychloroquine; TLR, Toll-like receptor; ssRNA, single-stranded RNA; ssDNA, single-stranded DNA; NF- κ B, nuclear factor kappa-light-chain-enhancer of activated B cells; IRF, interferon regulatory factor; IFN, interferon; MyD88, myeloid differentiation primary response 88; TASL, TRAF3-interacting protein 2; IL, interleukin; TYK2, tyrosine kinase 2; JAK2, Janus kinase 2; STAT4, signal transducer and activator of transcription 4.

generally requires phosphorylation of IRF and its subsequent translocation to the nucleus. Once in the nucleus, IRF5 regulates the expression of various cytokines and its activity is associated with increased type I interferon (36). Another gene identified as a candidate for SjD and SLE development is *STAT4* (37, 38). The gene encodes a transcription factor that functions downstream of IL-12 and type I interferon receptor, therefore mutations in STAT4 are linked to type I interferons (39, 40). Intriguingly, *IRF5* and *STAT4* combined risk alleles exhibit additive effects in promoting the SjD-SLE phenotype, especially in anti-dsDNA-positive individuals (36, 41–43).

Another shared gene that encode for a protein of intracellular signaling is TYK2 (21, 44). This gene encodes a tyrosine kinase is crucial for downstream signals of several cytokine receptors, including type I interferon and IL-12, and is therefore central in both interferon signaling and the activation of lymphocytes (45). IL12A, is another risk gene implicated in both SJD and encodes the p35 subunit of interleukin-12 (IL-12). This subunit signals through the Janus kinase (JAK)–STAT pathway, involving, as mentioned before, TYK2 and STAT4 (46, 47). IL-12 serves multiple functions but is particularly crucial for the differentiation of naive T cells into T helper type 1 (TH1) cells and is essential for the production of interferon- γ (IFN γ) by these cells (48).

X-linked genes

The most relevant X-linked genes implicated in the SjD-SLE overlap are TLR7 and CXorf21. Activation of Toll-like receptors (TLRs) by nucleic acids initiates two primary transcriptional pathways: the NFkB pathway, which stimulates the production of cytokines like IL-6, TNF, and IL-12, and the interferon regulatory factor (IRF) pathway. IRF activation requires the assembly of a supramolecular organizing center (SMOC). In this context, TASL (encoded by CXorf21) acts as a scaffold protein within the SMOC downstream of TLR7, enabling IRF5 phosphorylation and translocation to the nucleus. This mechanism ultimately enhances type I interferon production. Importantly, increased expression or dysregulation of TASL has been associated with heightened interferon signatures, particularly in anti-SSA/SSB positive patients, suggesting a functional link between genetic risk, interferon amplification, and clinical phenotype (49). Finally, X-linked genes such as TLR7 CXorf21 may escape X-chromosome inactivation, contributing to the well-known female predominance of both diseases (50-52). Skewed X-inactivation may also arise as a consequence of chronic interferon exposure, particularly in hematopoietic progenitor cells, suggesting a dynamic interplay between genetic susceptibility and disease environment (53).

Epigenetic regulation

In addition to genetic variation, epigenetic regulation appears to be a key modulator of interferon activity. Hypomethylation of interferon-stimulated genes has been observed in both SLE and SjD, especially in patients with SSA/SSB autoantibodies, contributing to sustained interferon gene expression (54). These findings reinforce the view that genetic and epigenetic mechanisms converge to promote a self-perpetuating interferondriven immune response in the SjD-SLE overlap.

In summary, both HLA and non-HLA loci—along with epigenetic and sex-linked mechanisms—converge to promote a pathogenic immune landscape in SjD-SLE overlap. These factors enhance B-cell activation, disrupt immune complex clearance, and amplify interferon signaling, providing a strong rationale for viewing this overlap as a biologically distinct entity.

Interferons

Interferon signaling is a well-known hallmark of both SLE and SjD and recent data indicate that patients with SjD-SLE overlap exhibit a stronger type I interferons and type II Interferon signature than those with either disease alone (11, 55).

Type I interferon (IFN-I)

An elevated type I Interferon (IFN-I) signature in SLE has been proposed as a predisposing factor for the development of overlapping SjD (56). While IFN- α is the dominant type I interferon in most autoimmune diseases differences in subtype-specific effects (e.g., IFN- α vs. IFN- β) have begun to emerge. For instance, IFN- β may exert more tolerogenic effects in certain contexts, while IFN- α is more potent in driving autoreactive B-cell responses (57). The specific IFN-I subtype distribution in SjD-SLE overlap remains to be fully characterized, but a higher total burden of IFN-I signaling may underlie the increased immunopathology observed in these patients.

As previously discussed, genetic risk variants contribute to this heightened interferon activity. There is a strong interplay between genetic risk factors, interferon signatures and specific autoantibodies, both in SjD and SLE. These genetic factors are closely linked to the production of autoantibodies such as anti-SSA/Ro, SSB/La, and dsDNA. However, in patients lacking an IFN signature, associations between HLA-DRB1*0301 and SSA disappear, further emphasizing the centrality of interferons in shaping the autoimmune phenotype. A similar observation can be made for IRF5, IFN-I and dsDNA, associations in SLE (14, 24, 58, 59). Indeed, type I interferons influence B-cell function through various mechanisms, driving autoreactive B-cell activation and the subsequent production of autoantibodies (60, 61). In turn, autoantibodies can induce type I interferon through several mechanisms. One key process involves Fcy receptor (FcγR)-mediated internalization of immune complexes, where IgG antibodies potentially leak from phagolysosomes into the cytosol (62). These immune complexes deliver dsDNA and single-stranded RNA into endosomal compartments, activating and TLR9, respectively (63-65). Additionally, autoantibodies can intensify innate immune responses, inhibiting

TRIM21 (Ro52) and possibly Ro60 which are normally responsible for damping interferon responses. TRIM21 acts as a negative regulator of TLR signaling by ubiquitinating (inactivating) interferon-regulating factors (IRFs), whereas when Ro60 is deleted there is an increase in interferon-induced proinflammatory cytokine production (59, 66-69). Ultimately, SjD patients anti-Ro/SSA and/or anti-La/SSB positive pSS patients exhibited hypomethylation in type I interferon induced genes (54, 70). Collectively, these findings suggest a feed-forward loop where IFN-I induces B cell activation and autoantibody production, leading to immune complex formation and further escalation of IFN-I production (71). Clinically, patients with high interferon present with high levels of dsDNA and SSA autoantibodies, increased circulating free light chains, decreased C3 levels, reduced lymphocyte counts ultimately corresponding to increased disease activity (72-74).

Type II interferon (IFN-II)

Similar to IFN-I, IFN-γ (type II Interferon, IFN-II) also plays a significant and perhaps earlier role. Interestingly, temporal analyses reveal elevated IFN-γ levels in patients with preclinical SLE before the appearance of most autoantibodies and before increases in IFN- α activity (75). This suggests that IFN- γ may be an early factor in breaking immune tolerance, leading to autoreactive B-cell, autoantibody production and IFN-α activity. This cascade establishes a feedback loop between autoantibodies and IFN-α, ultimately contributing to the full development of an autoimmune disease. Indeed, there is significant crosstalk between type I and type II interferons and many signaling pathways and inducible genes are shared between them. Additionally, each type induces the other's production, leading to a mutual stimulation and a combined interferon signature (76). Despite this overlap, IFN-y remains functionally distinct. IFN-y is associated with specific genetic risks, notably with IL-12A, which drives its production, and with genes like STAT4, encoding a protein involved in shared interferon signaling pathways (46, 47, 77). Moreover, IFN-II significantly enhances MHC complex expression, as demonstrated on salivary gland epithelial cells (SGECs) (66, 78). Furthermore, IFN-γ has a profound impact on B cells by stimulating T cells and antigenpresenting cells (APCs) to produce B lymphocyte stimulating factor (BLyS), crucial for B cell activation (79). Within B cells, instead, IFN-γ and its downstream signaling molecules, STAT1 and T-bet, drive inflammatory cytokine production (80). IFN-y-STAT1 signaling pathways activate critical processes in B cells, fostering their differentiation into autoreactive, antibodyproducing cells, with type I IFN signalling providing only moderate support to these processes (80). Instead, T-bet is essential for antibody class switching, with IFN-γ promoting a shift toward more pathogenic IgG subclasses, such as IgG2a and IgG3 in mice (81). Elevated IFN-γ correlates with high antidsDNA and RF levels, as well as with higher disease activity scores in both SjD and SLE, as reflected in SLEDAI and ESSDAI scores (82, 83).

In summary, in the SjD-SLE overlap, simultaneous upregulation of both IFN-I and IFN-II pathways likely accounts for the co-occurrence of high-titer autoantibodies, severe systemic inflammation, and multi-organ involvement. Thus, while interferons contribute to pathogenesis in both diseases, their combined and sustained activity may define the unique clinical and immunological features of the overlap phenotype.

B-cell

B-cell activation is a prominent feature of the SjD-SLE overlap, and despite very few differences in immunological architecture, a recent study has demonstrated that patients with SjD-SLE overlap, SjD alone, and SLE alone share a similar immunological profile (84). However, unique features of B-cell subsets and activation pathways suggest a distinct pathogenic mechanism in the overlap condition. Historically, germinal centers (GCs) were considered the primary sites for generating pathogenetic somatically-mutated and high-affinity autoantibodies autoimmune patients (85). However, more recent data challenge this view, pointing instead to extrafollicular (EF) B-cell responses as central drivers of autoimmunity (85-87). EF responses refer to antibody-producing pathways that occur outside GCs, typically in regions such as the red pulp of the spleen, the medullary cords of lymph nodes, and importantly, in tertiary lymphoid structures (TLS), ectopic lymphoid aggregates found in inflamed nonlymphoid tissues, such as the salivary glands of SjD patients (88). Notably, in this scenario, two distinct B-cell subsets have been identified: double-negative 2 (DN2) B cells in SLE and FcRL4+ intraepithelial B cells in SjD.

Double-negative 2 (DN2) B cells

DN2 B cells are characterized by a hyperactivated, proinflammatory phenotype and are expanded in active SLE. These cells are distinguished by the absence of both IgD and CD27 markers (IgD-, CD27-), differentiating them from conventional memory and naive B cell populations. Key markers for DN2 cells include T-bet, CD11c, FcRL5, along with the absence of CXCR5 (89). DN2 cells are characterized by the expression of the transcription factor T-bet, as well as high levels of CD11c (CD11chi), which guide their migration to inflammatory sites (90). Another marker of DN2 B cells is FcRL5, a member of the Fc receptor-like (FcRL) family, which shares structural similarities with the classical Fc gamma receptor I (FcγRI). FcRL5 binds IgG of all subclasses, with strongest binding by IgG1 and IgG2, and its interaction with IgGcontaining immune complexes can mediate either stimulatory or inhibitory signaling (90). CXCR5, a chemokine receptor commonly expressed on B and T cell subsets, is notably absent in DN2 cells. The CXCR5-CXCL13 axis plays a pivotal role in recruiting immune cells to germinal centers and ectopic lymphoid structures further confirming the extrafollicular origin of DN2 cells (91, 92). Furthermore, unlike germinal center (GC)

B cells, which depend on robust B cell receptor (BCR) signaling for survival and selection, DN2 cells are unresponsive to BCR-mediated survival signals and are instead highly responsive to TLR7 stimulation, reflecting a distinct mechanism of activation (86, 93–95). DN2 cells differentiate into autoantibody-secreting plasma cells under the influence of IFN-γ, IL-21, and IL-2, cytokines typically derived from Th1-skewed T cells (96). In lupus-prone mouse models, EF responses producing anti-dsDNA and RF autoantibodies rely heavily on TLR7/TLR9-mediated activation—confirming the pathological potential of DN2-like cells (63, 97, 98). These cells have been correlated with decreased complement levels and increased disease activity, and may contribute to tissue damage in organs such as kidneys and skin (90).

FcRL4+ B cells

On the other hand, FcRL4+ B cells, found in salivary gland epithelium in SjD, exhibit a phenotype similar to DN2 cells (99). These FcRL4+ B cells exhibit an activated phenotype, characterized by elevated expression of T-bet, CD11c and TACI, along with reduced expression of CXCR5 and CD40. FcRL4 is an immunoregulatory receptor that belongs to the Fc receptor-like (FcRL) family. Evidence suggests that when soluble IgA binds to FcRL4, it triggers a functional switch in B cells from BCRmediated activation to TLR-mediated activation, similar to what was observed for DN2 (100, 101). Unlike DN2 B cells in systemic lupus erythematosus, glandular FcRL4+ B cells in SjD do not express plasma cell markers, suggesting a distinct, possibly more regulatory or tissue-resident role. Their localization is guided by CXCR3, which responds to CXCL10, an IFNinduced chemokine produced by the inflamed ductal epithelium. Persistent stimulation by IFN-γ, IL-27, BAFF, and APRIL, as well as CD40-independent signals, supports their maintenance in situ. Notably, FcRL4+ cells are strongly associated with RF positivity and are believed to serve as a precursor pool for MALT lymphoma, given their activated and persistent phenotype (66, 102).

B cells in SjD-SLE overlap

Importantly, even though direct evidence is lacking, it is plausible that in the SjD-SLE overlap, elements of both DN2 and FcRL4⁺ B-cell pathways coexist. The frequent presence of both anti-dsDNA and RF autoantibodies in these patients suggests a broad extrafollicular response that may encompass both systemic and tissue-resident features. Moreover, given the high prevalence of TLS in the salivary glands of SjD patients, it is reasonable to speculate that such structures could support the persistence and expansion of these B-cell subsets in the overlap condition.

In summary, EF B-cell responses—occurring in both secondary lymphoid tissues and TLS—are likely to be key orchestrators of the SjD-SLE overlap phenotype. DN2 and FcRL4+ cells may represent two ends of an EF continuum, contributing to distinct but converging autoantibody profiles, tissue localization, and clinical

manifestations. Their chronic activation and persistence may also underlie the increased lymphoproliferative risk observed in these patients.

Treatment

Therapeutic options for SLE and SjD remain limited despite extensive research in recent years (103-105) (Table 2). A significant barrier is patient heterogeneity, which has led to increasingly strict inclusion criteria in clinical trials. As a result, patients with overlapping SiD-SLE features are often excluded from studies of either disease, leaving them without evidencebased treatment options. To address this challenge, future trials should adopt more inclusive designs based on molecular signatures (e.g., interferon-high or BAFF-dependent endotypes) rather than rigid diagnostic categories. This approach would facilitate the enrolment of overlap patients and enhance the generalizability of trial results. Notably, only one trialinvestigating epratuzumab, an anti-CD22 antibody—has demonstrated efficacy in this population, albeit based on post hoc analysis (106). However, given the distinct clinical profile of SjD-SLE overlap, including prominent inflammation, high interferon activity, and intense B-cell dysregulation, specific therapeutic approaches should be considered (Figure 3).

TABLE 2 Therapies in Sjögren's disease and systemic lupus erythematosus.

Drug	Target/ Mechanism	Trial
HCQ (hydroxychloroquine)	TLR modulation; immunomodulatory effects	Approved for SLE and SjD based on long-term use
Anifrolumab	IFNAR1 blockade (type I IFN receptor)	Approved for SLE; Phase II trial ongoing in SjD
JAK-STAT inhibitors (e.g., baricitinib)	JAK1/2 inhibition	Trials failed in SLE and SjD
TYK2 inhibitors (e.g., deucravacitinib)	TYK2 kinase inhibition	Phase III trials ongoing in SLE and SjD
Rituximab	CD20 B-cell depletion	Phase III trials failed in SLE and SjD; approved in refractory cases in SLE; off-label SjD
Obinutuzumab	Glyco-engineered anti- CD20	Phase III positive in lupus; not tested in SjD
Epratuzumab	Anti-CD22 B-cell modulation	Phase III failed in SLE; post hoc data suggests benefit in SjD-SLE overlap, not tested in SjD
Bispecific antibodies	Dual B-cell targeting	Phase II trial ongoing in SLE; not tested in SjD
CAR-T	CD19-targeted CAR-T cells	Case reports in SLE and SjD
Belimumab	BAFF inhibition	Approved for SLE; used off-label SjD

This table summarizes the mechanisms of action and current clinical development status of selected therapeutic agents targeting key immune pathways in SjD, SLE, and their overlap. SjD, Sjögren's disease; SLE, systemic lupus erythematosus; TLR, toll-like receptor; IFNAR, interferon alpha/beta receptor; JAK, Janus kinase; TYK2, tyrosine kinase 2; BAFF, B-cell activating factor; CAR-T, chimeric antigen receptor T cells; CD, cluster of differentiation.

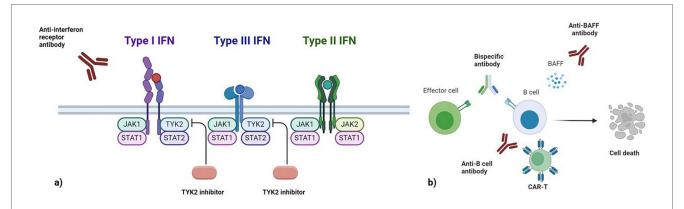


FIGURE 3

This image illustrates therapeutic approaches targeting interferon signaling and B cells. (a) Interferon-targeting strategies include anti-interferon receptor antibodies that block signaling for type I interferon. The associated signaling pathways involve TYK2, JAK1, and STAT transcription factors for type I and III IFNs, and JAK1/JAK2 for type II IFNs. TYK2 inhibitors specifically disrupt pathways shared by type I and III interferons, offering a selective approach to modulate their activity. (b) B-cell depletion strategies employ various mechanisms, such as anti-B-cell antibodies (e.g., anti-CD20), bispecific antibodies that engage effector cells to eliminate B cells, and CAR-T cells engineered to target B-cell-specific markers. Additionally, anti-BAFF antibodies inhibit BAFF-dependent B-cell survival, leading to cell death and suppression of pathogenic B-cell activity. IFN, Interferon; TYK2, Tyrosine Kinase 2; JAK, Janus kinase; STAT, signal transducer and activator of transcription; BAFF, B-cell activating factor; CAR-T, chimeric antioner receptor T-cell.

Several therapeutic strategies have been explored to target the activation of interferon pathways, including TLR inhibitors, interferon receptor blockers, and JAK-STAT signaling inhibitors (Figure 3a). Hydroxychloroquine, a TLR7 and TLR9 inhibitor, reduces type I interferon (IFN-I) levels and is widely used in clinical practice for both SjD and SLE (Figure 2). However, in these diseases results from randomized clinical trials of hydroxychloroquine remains contradictory (107, Anifrolumab, a monoclonal antibody targeting type I interferon receptors, has been approved for SLE and is currently being evaluated in clinical trials for SjD (109, 110). Interestingly, Anifrolumab has shown greater efficacy in patients with a high interferon signature, making it a promising option for patients with this feature, including those with SjD-SLE overlap (111). JAK-STAT inhibitors, which interfere with interferon signaling, have also been investigated. However, multiple trials of JAK inhibitors in both SLE and SjD have not yet demonstrated consistent efficacy (112, 113). It is important to note that different interferons rely on distinct JAK signaling pathways. For instance, while type I and III interferons signal through TYK2 and JAK1, IFN-γ relies exclusively on JAK1 and JAK2 (114). Consequently, not all JAK inhibitors may have equal effectiveness across all interferon pathways. A novel drug, Deucravacitinib, a TYK2 inhibitor, is currently undergoing trials in both SLE and SjD (115, 116) (Figure 3a). TYK2 is a genetic risk factor for the SjD-SLE overlap and plays a pivotal role in IL-12 signaling, which impacts IFN-y expression as well as IFN-I and IFN-III pathways.

B-cell-targeted therapies include direct depletion (e.g., anti-CD20/anti-CD19 antibodies, CAR-T cells, bispecific antibodies) and indirect modulation via BAFF inhibition (Figure 3b). Rituximab reduces dsDNA and RF levels and has been shown to deplete DN2 and FcRL4⁺ B cells in SLE and SjD, respectively (117–120). Despite its success in rheumatoid arthritis,

randomised clinical trials for rituximab in SjD (TEARS and TRACTISS) and SLE (EXPLORER and LUNAR) failed to demonstrate significant efficacy (121-123). Indeed, a major challenge with B cell-depleting therapies lies in their inability to uniformly target all B cell subsets, allowing residual B cells to perpetuate autoimmunity. Two key reasons may explain this limitation. First, the kinetics of B cell depletion in tissues is slower than in peripheral blood, leaving tissue-resident subsets in the spleen, lymph nodes, and tertiary lymphoid tissues incompletely depleted (124). Second, certain pathogenic B cells or plasma cells may lack CD20 expression or express it at low levels, reducing their susceptibility to CD20-targeted therapies (63, 125). Moreover, as B cells differentiate into plasma cells, they sequentially downregulate CD20 and CD19, rendering longlived plasma cells largely refractory to anti-CD20 treatment (124). Indeed, autoantibody production reflects multiple B-cell sources: long-lived plasma cells from germinal centers (resistant CD20 therapies) vs. short-lived plasmablasts from extrafollicular pathways (sensitive to therapy) (63, 125). One promising approach is second-generation anti-CD20 agents, like obinutuzumab have shown promise in lupus nephritis and may provide more effective tissue depletion. Moreover, emerging B-cell-depleting therapies, such as CAR-T cells targeting CD19 and bispecific T-cell engagers (TCEs), are under active investigation and could offer deeper and more sustained B-cell depletion. These methods may overcome limitations seen with rituximab, particularly in depleting autoantibody-producing extrafollicular B cells and may offer additional therapeutic options for patients with SjD-SLE overlap (125-127).

Another indirect depletion of B cells involves BAFF-blocking antibodies. Transitional and naive B cells rely heavily on BAFF (B cell-activating factor of the tumor necrosis factor family) for survival and are effectively targeted by BAFF-blocking therapies (66, 124, 126). Targeting BAFF with belimumab may be

particularly useful in SjD-SLE overlap, especially given the BAFF-dependence of DN2 and FcRL4⁺ cells (66, 126). Accordingly, belimumab, a BAFF inhibitor, has demonstrated efficacy in SLE and has shown potential when used in combination with rituximab for the treatment of SjD (127–130). Given the complementary mechanisms of action, combining B-cell depletion with BAFF inhibition—such as rituximab followed by belimumab—has shown synergistic effects in depleting both mature B cells and their precursors (131). This approach may be particularly relevant in SjD-SLE overlap, where extrafollicular and tissue-resident B cells are simultaneously active.

Despite these advances, SjD-SLE overlap patients remain systematically excluded from most trials. To address this, future clinical studies should incorporate dedicated overlap subgroups, stratify patients by immunological endotype (e.g., IFN-high, BAFF-high), and explore combination regimens tailored to dual interferon/B-cell axis dysregulation. In conclusion, targeting interferons and B cells remains the cornerstone of therapy in SjD-SLE overlap. However, the heterogeneity and dual-pathway activation in these patients necessitate personalised strategies. Emerging therapies, including interferon receptor antagonists, next-generation B-cell depletors, CAR-T cells, and BAFF inhibitors, offer new hope for this challenging subgroup.

Conclusions

The SjD-SLE overlap represents a distinct clinical and immunological phenotype that cannot be fully explained by either disease alone. Genetic predisposition—particularly involving somatic HLA alleles and non-HLA variants affecting interferon and cytokine signalling—creates a permissive background that shapes the immunological landscape. This is further amplified by epigenetic dysregulation and X-linked gene activity, which together enhance interferon responsiveness and female predominance.

A common pathogenic axis emerges in this overlap condition, where aberrant extrafollicular B-cell activation intersects with heightened interferon signalling. These mechanisms reinforce each other, contributing to autoantibody production (e.g., anti-dsDNA, RF, SSA/SSB) and sustained inflammation in both systemic and tissue-specific compartments. Integrating these pathways provides a more cohesive model of disease pathogenesis and opens the door for a precision medicine approach.

Despite these insights, overlap patients remain systematically underrepresented in clinical trials, limiting the evidence base for effective treatments. Addressing this gap requires both the inclusion of immunologically stratified overlap cohorts in future studies and the development of diagnostic criteria that reflect their unique biology.

Promising therapies—such as interferon receptor inhibitors, BAFF-blocking agents, and next-generation B cell-targeted strategies—may yield synergistic effects when used in combination. Ultimately, the integration of genetic, molecular, and cellular findings into clinical practice could enable earlier diagnosis, better risk stratification, and more personalised treatment of patients with SjD-SLE overlap.

Author contributions

GF: Conceptualization, Investigation, Methodology, Writing – original draft, Writing – review & editing. GL: Writing – review & editing. MM: Writing – review & editing. CB: Writing – original draft, Writing – review & editing.

Funding

The author(s) declare that no financial support was received for the research and/or publication of this article.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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