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Nucleic acid sensing receptors in systemic lupus erythematosus: development of novel DNA- and/or RNA-like analogues for treating lupus

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Overview

Genetic, epigenetic, gender-related and environmental factors are believed to contribute to the pathogenesis of autoimmunity in systemic lupus erythematosus (SLE). Defective clearance of apoptotic cell debris [1] with release of nucleosomes and 'alarmins' [e.g. high mobility group box 1 (HMGB1)], increased bioavailability of type I interferon (IFN), evidence of up-regulated IFN-inducible genes along with multiple autoantibodies targeting DNA or RNA-

Summary

Double-stranded (ds) DNA, DNA- or RNA-associated nucleoproteins are the primary autoimmune targets in SLE, yet their relative inability to trigger similar autoimmune responses in experimental animals has fascinated scientists for decades. While many cellular proteins bind non-specifically negatively charged nucleic acids, it was discovered only recently that several intracellular proteins are involved directly in innate recognition of exogenous DNA or RNA, or cytosol-residing DNA or RNA viruses. Thus, endosomal Toll-like receptors (TLR) mediate responses to double-stranded RNA (TLR-3), single-stranded RNA (TLR-7/8) or unmethylated bacterial cytosine (phosphodiester) guanine (CpG)-DNA (TLR-9), while DNA-dependent activator of IRFs/Z-DNA binding protein 1 (DAI/ZBP1), haematopoietic IFN-inducible nuclear protein-200 (p202), absent in melanoma 2 (AIM2), RNA polymerase III, retinoic acid-inducible gene-I (RIG-I) and melanoma differentiation-associated gene 5 (MDA5) mediate responses to cytosolic dsDNA or dsRNA, respectively. TLRinduced responses are more robust than those induced by cytosolic DNA- or RNA- sensors, the later usually being limited to interferon regulatory factor 3 (IRF3)-dependent type I interferon (IFN) induction and nuclear factor (NF)-κB activation. Interestingly, AIM2 is not capable of inducing type I IFN, but rather plays a role in caspase I activation. DNA- or RNA-like synthetic inhibitory oligonucleotides (INH-ODN) have been developed that antagonize TLR-7- and/or TLR-9-induced activation in autoimmune B cells and in type I IFN-producing dendritic cells at low nanomolar concentrations. It is not known whether these INH-ODNs have any agonistic or antagonistic effects on cytosolic DNA or RNA sensors. While this remains to be determined in the future, in vivo studies have already shown their potential for preventing spontaneous lupus in various animal models of lupus. Several groups are exploring the possibility of translating these INH-ODNs into human therapeutics for treating SLE and bacterial DNA-induced sepsis.

Keywords: HIN-200, HMGB1, systemic lupus erythematosus, Toll-like receptors 7 and 9

associated nucleoproteins are immunological hallmarks of SLE.

SLE genetics

It is broadly accepted that SLE is a complex genetic disease with multiple genes contributing to the disease phenotype [2]. The concordance rate among monozygotic twins is \sim 30%, which is 10 times higher than the rate among dizygotic twins (\sim 3%) [3]. Recently established risk factors for

human SLE include allelic variants of genes with known immune function, such as human leucocyte antigen (HLA), interferon regulatory factor 5 (IRF5), signal transducer and activators of transcription 4 (STAT4), Fc gamma receptor 2a gene (FCGR2A)/3A, protein tyrosine phosphatase, nonreceptor type 22 (PTPN22), integrin alpha M (ITGAM), CTD-binding SR-like protein rA9 (KIAA1542), PX domain containing serine/threonine kinase (PXK), B cell scaffold protein with ankyrin repeats (BANK1), programmed cell death 1 (PDCD1), methyl cytosine (phosphodiester) guanine (CpG) binding protein 2 (MECP2) and tumour necrosis factor (ligand) superfamily, member 4 (TNFSF4) [4–6].

Epigenetic changes

The two most important epigenetic changes that can affect the gene functioning are histone modifications and DNA methylation. Environmentally driven epigenetic changes may explain partial discordance for SLE in monozygotic twins [7].

The role for abnormal DNA methylation in lupus has long been suspected. For example, lymphocytes from SLE patients exhibit globally hypomethylated DNA pattern [8,9]. Interestingly, many lupus-promoting drugs work through DNA demethylation (e.g. procainamide and hydralazine [10]).

A high-throughput approach was used to study monozygotic twins discordant for SLE, rheumatoid arthritis (RA) or dermatomyositis [7]. Only those discordant for SLE showed widespread changes in the DNA methylation status of a number of genes, particularly in those associated with immune function [e.g. interferon (IFN)- γ R2, matrix metalloprotease 14 (MMP), lipocalin 2 (LCN2), colonystimulating factor 3 receptor (CSF3R), platelet/endothelial cell adhesion molecule 1 (PECAM1), CD9 and absent in melanoma 2 (AIM-2)].

Infections and lupus: beyond molecular mimicry

It is well documented that infections coincide frequently with the occurrence of autoimmune diseases. The concept of molecular mimicry is one way of explaining this phenomenon because of the structural similarity between invading microbes and self-antigens [11]. A classical example of molecular mimicry is Guillain–Barré syndrome following infection with *Campylobacter jejuni* (reviewed in [11]. In relation to the lupus, Judith James found that autoantibodies against an epitope in 60 kD Ro antigen may cross-react with the peptide from the latent viral Epstein–Barr virus nuclear antigen-1 [12]. When animals are immunized with these cross-reactive epitopes they progressively develop autoantibodies which bind multiple epitopes of Ro autoantigens, a phenomenon known as epitope spreading.

Alternatively, viral infections (similar to ultraviolet lights) may increase the supply of lupus autoantigens by inducing cellular injury and promoting apoptotic cell death. Slow disposal of apoptotic cells by mononuclear phagocytes may result in spontaneous release of lupus autoantigens from apoptotic blebs, initiating autoantibody production in genetically susceptible hosts.

However, the role of infectious agents may extend beyond promoting cell death. Certain microbial products may act as immune adjuvants inducing bystander activation of the innate immune system via Toll-like receptors (TLRs). Interestingly, the most common autoimmune targets in SLE, DNA and/or RNA-associated nucleoproteins, either alone or combined with autoantibodies, may trigger B cell activation through endosomal TLRs. Thus, common autoantigens in systemic autoimmune diseases such as chromatin, nucleosomes, Ku, topoisomerases, Sm/snRNP, ribosomes and Ro/La are not only passive targets of autoimmunity, but active triggers of innate immunity. In concordance with this hypothesis, injection of synthetic ligands for TLR-3, -7 and -9 could worsen spontaneous animal lupus [13–17].

Role for nucleic acid-sensing endosomal TLRs in lupus

Several lines of evidence support a role for TLRs in SLE. Of 13 known TLRs, endosomal single-stranded RNA- and hypomethylated DNA-sensing innate receptors TLR-7 and -9, respectively [18–21], but not double-stranded RNAsensing TLR-3 [22,23], have been implicated in the pathogenesis of SLE. These intracellular TLRs are responsible for activation of type I IFN-producing dendritic cells and autoreactive B cells upon recognition of immune complexes containing endogenous nucleic acids (RNA or DNA).

TLR-7 and -9 in lupus: in vitro studies

Transgenic AM14 B cells express a rheumatoid factor-like B cell receptor for antigen (BCR) which recognizes autologous IgG2a of the particular allotype. Because of the low affinity on a non-autoimmune background, AM14 B cells are not tolerized and can be found within the conventional mature B cell pool [24]. In vitro, AM14 B cells can be induced to proliferate upon exposure to immune complexes containing IgG2a antibodies directed against DNA or DNA-associated nuclear proteins [25], but not against unrelated haptens or proteins [26,27]. This proliferation depends heavily upon the presence of CpG motifs within the DNA [28]. RNAcontaining immune complexes can also activate AM14 B cells, especially following priming with type I IFNs [29]. In these examples, BCR-mediated capture and endosomal delivery of nucleic-acid containing immune complexes [30] induces B cell proliferation dependent upon TLR-9 or TLR-7, respectively [26,29]. In anergic B cells, however, effective BCR/TLR co-localization fails to happen, blunting responses to self-DNA [31].

In dendritic cells (DCs), stimulation with nucleic acidcontaining immune complexes induces IFN- α and proinflammatory cytokines. This requires a FcγR-mediated delivery of TLR ligands to TLR-7- or -9-expressing intracellular compartments [32,33].

TLR-7 and -9: in vivo studies

In Murphy–Roths large (MRL)-Fas^{lpr/lpr} mice, TLR-7 deficiency causes a significant drop in secretion of autoantibodies reactive with RNA-associated autoantigens, but not against chromatin. These animals also have a milder kidney disease [34]. A similar effect of TLR-7-deficiency was observed in pristane-induced SLE [35,36], and in glomerular injury induced with syngeneic late apoptotic cells [37].

Male BXSB mice develop a lupus-like disease because of the Y-linked autoimmune accelerator (Yaa). These mice represent a unique example how gene copy number variation may result in disease induction [38]. Noticeably, the Yaa phenotype is due to the translocation of X-chromosomal region that contains the TLR-7 gene (and 16 additional genes) to the Y chromosome resulting in TLR-7 gene duplication in males [39,40]. Deletion of the endogenous TLR-7 decreases autoantibody levels significantly and improves kidney disease in the Yaa strain [38,41].

B6 FcγRIIB^{-/-} mice develop an SLE-like disease where secretion of IgG2a and IgG2b antibodies requires a TLR-9 [42]. Lupus-like disease in these mice is accelerated upon acquiring the Yaa accelerator, through a mechanism that absolutely requires IRF5 but is independent of the type I IFN secretion [43]. Interestingly, the autoantibody profile in these mice changes from predominantly DNA-biased to RNA-related [44].

Contrasting with the lack of TLR-7, TLR-9-deficiency in MRL-Fas^{lpr/lpr} strain results in fewer anti-chromatin/antidsDNA antibodies, but causes exacerbation of the clinical disease [34,45]. A similar 'protective' role of TLR-9 was observed in other models of animal lupus [46]. While the logical explanation for this is lacking, one of the possibilities is that TLR-9-dependent anti-chromatin antibodies may have a role in apoptotic cell clearance. Alternatively, TLR-9 (but not TLR-7) signalling in autoreactive B cells and DCs may induce cytokines with regulatory properties [e.g. interleukin (IL)-10] [47,48] or may promote generation of forkhead box P3 (FoxP3)⁺ T cells. Interestingly, a TLR-7 by itself may play a role in acceleration of lupus in TLR-9-deficient mice [49]. While the deficiency of double-stranded RNA receptor TLR-3 does not affect the progression of spontaneous MRL-Fas^{lpr/lpr} disease, injection of viral dsRNA ligands aggravates lupus nephritis, presumably via TLR-3-expressing mesangial cells [50].

UNC93b1 shuttles TLR-3, -7 and -9 from endoplasmic reticulum (ER) to endosomes

Another layer of evidence supporting intracellular TLRs in the pathogenesis of SLE comes from autoimmune mice

lacking the UNC93b1 protein [51]. Unc93b1 is an ER protein that is involved in ligand-induced trafficking of TLR-3, -7 and -9 from the ER to the endosomes [52,53]. Under normal circumstances, Unc93b1 biases TLR responses towards DNA, not RNA sensing [54]. Amino acid D34 in UNC93b1 suppresses TLR-7-mediated responses and favours responsiveness to TLR-9 ligands. Conversely, D34A mutation renders DCs hyperresponsive to TLR-7 ligand, but hyporesponsive to TLR-9 ligand. This may help to explain heightened TLR-7 responsiveness in TLR-9^{-/-} lupus mice. Lupus-prone mice lacking the UNC93b1-sufficient counterparts [51].

TLR-7 and -9 expression and polymorphism in SLE

Several studies have suggested that TLR-9 may play an important role in human SLE. Papadimitraki found increased renal expression of TLR-9 in 50% of patients with SLE nephritis, particularly in those with higher activity index [55]. Moreover, antigen-presenting cells from SLE patients showed higher percentage of TLR-9+ cells as well as higher expression of TLR-9 compared to controls. However, response to CpG-ODNs correlated with disease activity, independently of the TLR-9 expression [56]. Another study by Wu [57] in untreated SLE patients showed increased percentages of both T and B cells expressing TLR-9. In addition to TLR-9, increased expression of TLR-7 was also documented, and this correlated with IFN- α transcription [58]. An interesting clinical observation linked acquired TLR-7/9 signalling defect and resulting antibody deficiency with long-lasting clinical remission in a patient with known history of SLE [59].

Several studies have investigated polymorphisms in TLR-7 and TLR-9 genes. A study in Chinese patients with SLE [60] explored the role of SNP (rs352140) in exon 2 of the TLR-9. A mild association between the T allele and susceptibility to SLE was found in a dominant model. A study in a Spanish SLE cohort revealed no significant difference in allele and genotype distribution of TLR-5 (rs5744168) and TLR-7 (rs179008) [61].

Is there a role for non-TLR DNA- and RNA-sensors in the pathogenesis of human SLE?

Over recent years several non-TLR proteins capable of binding and initiating responses to intracellular DNA or RNA molecules have been discovered. Indeed, increasing evidence suggests that TLR-9 engagement by DNA vaccines is not vital for the induction of immune responses *in vivo* [62–65]. Self-DNA may be delivered to cytosol under certain experimental conditions leading to increased IFN- β production. For example, DNAse II-deficient macrophages digest self-DNA poorly from engulfed apoptotic cells,

Table 1. Nucleic acid sensors.

Sensor	Ligand	Reference	
TLR-9	Hypomethylated CpG-DNA	[18]	
DAI/ZBP1	dsDNA	[82]	
RNA-Pol III	dsDNA (AT-rich)	[101,102]	
HIN-200 (p202)	dsDNA	[72]	
AIM-2	dsDNA	[73]	
TLR-3	dsRNA, poly I : C	[22]	
TLR-7	ssRNA, imiquimod, Loxoribine, R848	[20]	
TLR-8	ssRNA, R848	[20]	
RIG-I	dsRNA, 3P-ssRNA, short poly I : C	[104]	
MDA-5	dsRNA, long poly I : C	[105]	
LGP2	dsRNA, 3P-ssRNA	[104]	

AIM-2, absent in melanoma 2; DAI, DNA-dependent activator of IRFs/Z-DNA binding protein 1; HIN, haematopoietic IFN-inducible nuclear protein; LGP2, RIG-I-like RNA-helicase; MDA, melanoma differentiation-associated gene 5; RIG, retinoic acid-inducible gene-I; TLR, Toll-like receptor.

causing IFN- β production through the IRF3-dependent pathway [66,67].

A search for additional dsDNA-sensors has identified several candidate proteins, e.g. haematopoietic IFNinducible nuclear protein (HIN)-p202, AIM-2, DNAdependent activator of IRFs (DAI)/ZBP1, RNA polymerase III (Pol-III) and HMGB1. A similar search has identified RNA-helicases retinoic acid-inducible gene-I (RIG-I) and melanoma differentiation-associated gene 5 (MDA5) as TLR-7-independent cytoplasmic RNA sensors. Herein, we provide a brief summary about these novel nucleic acid sensors, particularly in relation to their putative role in lupus pathogenesis (Table 1).

IFI200 (HIN-200) family

At least two newly identified cytoplasmic DNA-binding receptors belong to the subset of the IFN-stimulated genes– IFI200 family. This family includes several structurally related proteins in mice and in humans (reviewed in [68,69]). IFI200 family members function by negatively regulating cell growth [70] and inhibiting lymphocyte apoptosis [71].

The HIN-200 family is a human homologue of murine Ifi200. It was shown recently that the HIN-200 family member, p202, binds stably transfected cytoplasmic dsDNA and works by inhibiting DNA-induced caspase (1 and 3) activation in macrophages [72]. Conversely, another HIN-200 protein, AIM2 (absent in melanoma 2, p210) was necessary for cytoplasmic dsDNA-induced caspase-1 and nuclear factor (NF)-κB activation and inflammasome formation (but not type I induction) [72,73]. Therefore, recognition of cytoplasmic dsDNA ligands by different members of the HIN-200 family may result in different biological outcomes.

In BL6 mice congenic for the Nba2 locus, Ifi202 gene has been identified as a candidate gene for SLE susceptibility [68]. These mice develop splenomegaly and produce hightitre immunoglobulin G (IgG) anti-nuclear antibodies. Polymorphism in the coding region of the Ifi202 genes in the NZB mice accounts for the increased level of this protein in B6.Nba2 mice. Interestingly, Ifi202a^{-/-} mice do not have any phenotype [74], probably because of the redundancy between Ifi202a and b proteins. Their B cells respond normally to various stimuli in vitro and to immunization with T-dependent antigens in vivo [75]. As well as B6.Nba2 mice, P202 protein levels are also elevated in the MRL-Fas^{lpr/lpr} strain [76], and correlate well with the development of lupus in these mice [77]. The way in which p202 protein in MRL-Fas^{lpr/lpr} contributes to the lupus pathogenesis is difficult to understand, as IFN- α appears to play a protective role in this strain. In relation to the known gender bias in SLE, steady state levels of Ifi202 mRNA were found to be higher in splenic cells from female mice than in males.

Human MNDA, IFIX, IFI16 and AIM2 proteins are increased in leucocytes from SLE patients [78], and increased MNDA expression was found in glomeruli from SLE patients [79].

A possible interplay between the TLRs and Ifi200 has not been studied in sufficient detail. Circumstantial evidence suggests that Ifi202 may cooperate with TLRs in cell activation. For example, overexpression of Ifi202 enhances lipopolysaccharide (LPS)-induced activation in Abelson murine leukaemia virus-transformed macrophage cell line 264.7 macrophages, presumably via TLR-4-dependent activation [80]. It remains to be determined whether Ifi202 and TLR-9 synergize or have antagonistic effects upon each other.

Similar to other nucleic acid associated proteins, IFI200 members may also serve as lupus autoantigens [81]. Antibodies against the IFI16 were found in both SLE and in Sjögren's syndrome [69,81]. These antibodies could differentiate further between patients with limited cutaneous systemic sclerosis and those with the systemic form [69].

DAI/ZBP1 (DNA-dependent activator of IRFs/Z-DNA binding protein 1)

DAI is another cytoplasmic DNA sensor [82] capable of activating IRF3 and NF-KB, resulting in type I IFNproduction. DAI interacts directly with dsDNA in vitro [83] and this interaction in turn enhances DAI association with IRF3 [82]. DAI-induced IRF3 phosphorylation is dependent on TANK-binding kinase 1 (TBK1) [84], while the NF-kB signalling depends on recruitment of RIP1 and either RIP2 or 3 (receptor interacting proteins) [85,86]. Once IRF is phosphorylated it undergoes dimerization and nuclear translocation promoting IFN- β secretion. In a positive feedback loop manner, IFN-β signals through JAK/STAT molecules inducing IRF7 and amplifying type I IFN secretion. However, DAI may not be the only cytosolic DNA sensor in human cells [87] and DAI-deficient mice still can make type I IFN in response to B form DNA [65]. The possible role of DAI in lupus has not been studied.

HMGB1 (high mobility group box 1)

HMGB1 is a non-histone, chromatin-associated nuclear protein that binds DNA, regulates transcription and functions as a proinflammatory cytokine when released outside the cell. By itself HMGB1 is only mildly proinflammatory, but it can synergize with other cellular activators including TLR ligands [88,89]. For example, TLR-9-dependent IL-6 secretion in response to type B(K) CpG-ODNs is enhanced by HMGB1 [90]. While HMGB1 binds preferentially complex forms of DNA, such as cruciform DNA [91] and class A(D) CpG-ODNs [92], it appears that HMGB1 binds DNA without sequence specificity [88,92]. HMGB1 is an excellent example of an alarmin: once released from necrotic (and possibly late apoptotic) cells it 'alarms' the immune system about the presence of tissue damage [93]. Extracellular HMGB1 may signal through TLR-2, TLR-4 or receptor for advanced glycation end-products (RAGE). HMGB1/ DNA complexes bind RAGE (or some other receptor on B cells) [94] which in turn causes recruitment of TLR-9 and enhances type I IFN secretion from pDCs and proliferation of autoreactive B cells [92]. The cross-talk between HMGB1 and TLR-9 appears to be a unique example of a synergistic interaction between two DNA receptors, resulting in cellular activation. HMGB1 does not affect the uptake of CpG-DNA into TLR-9 expressing early endosomes, but accelerates the recruitment of TLR-9 from the ER to endosomes [92]. While HMGB1 binds tightly to chromatin and is retained within apoptotic cells [88], novel data suggest that late apoptotic cells may release some HMGB1 [95]. This happens only after late apoptotic cells undergo secondary necrosis, when the permeability barrier breaks down [96]. The complex of HMGB1 with nucleosomes is more immunogenic and proinflammatory than naked nucleosomes and triggers more vigorous cell activation [97]. Highly relevant to the lupus, HMGB1 is expressed in skin lesions from patients with cutaneous lupus [98], and high levels of both HMGB1 and anti-HMGB1 antibodies can be found in patients with SLE [97,99,100]. HMGB1-containing nucleosomes from apoptotic cells, but not those from living cells, could induce anti-dsDNA and anti-histone antibody responses [97]. They were also capable of activating dendritic cells and macrophages to express co-stimulatory molecules and to secrete IL-1, IL-6, IL-10 and tumour necrosis factor (TNF)- α [97].

RNA polymerase III [101,102]

The RIG-I dependent pathway plays a role in recognition of viral RNA (see below), and also mediates responses to cytosolic dsDNA. In a recent study, AT-rich dsDNA served as a template for RNA polymerase III and was transcribed into dsRNA with a 5'-triphosphate moiety. dsRNA in turn engaged RIG-I resulting in type I IFN production and NF- κ B activation [101,102]. Pol-III functions normally to transcribe 5S rRNA, tRNA and other small non-coding RNA. This Pol-III-mediated conversion of transfected cytosolic poly (dA-dT) (but not other forms of dsDNA) into 5'-pppRNA was also seen by Chiu [102]. However, because of the apparent redundancy between cytosolic DNA sensors, dsDNA could induce IFN production in mouse cells lacking RIG-I [103].

RNA-sensors: RIG-I, MDA5 and LGP2

Viral RNA induced IFN- α production in cell types other than pDCs is not dependent on TLR expression, but rather requires RIG-I family cytoplasmic RNA-helicases. Two family members, RIG-I [104] and MDA5 [105], are recently identified RNA sensors that recognize distinct viral and synthetic RNA patterns leading to the production of type I IFN and proinflammatory cytokines via IRF3, IRF7 and NF- κ B. Single-stranded 5'-triphosphate RNA is a well-characterized RIG-I and RIG-I-like RNA-helicase (LGP2) ligand [106], while dsRNA synthetic analogue poly I : C can activate either MDA5 or RIG-I depending on its length [107]. LGP2 binds dsRNA, but functions as a negative regulator of the RIG-I/ MDA5 signalling pathway [104]. Transient exposure of prediseased MRL-Fas ^{lpr/lpr} mice to 3P-RNA aggravates lupus nephritis via IFN-signalling [108].

Evidence for the role of type I IFN system in SLE

One common feature of all nucleic acid sensing receptors (with the possible exception of AIM-2) is their ability to induce type I IFN secretion upon recognition of their cognate ligands. We will therefore summarize recent evidence that links type I IFNs with the pathogenesis of SLE (reviewed in [109,110]).

Treatment of patients with chronic viral infections and certain types of malignancies with IFN- α may result in SLE-like clinical manifestations in patients without prior history of SLE [111]. Increased serum concentrations of IFN- α can be found in human SLE [112] and IFN- α levels correlate with disease activity and severity in human SLE [112,113]. Higher IFN- α levels are found in earlier stages of SLE. Nevertheless, some SLE patients never develop high IFN- α levels, not even during disease flares.

Type I IFN-inducible gene expression signature was found in peripheral blood mononuclear cells in approximately 50% of adult SLE patients, particularly in those with more severe disease [2,114], and in almost all paediatric SLE patients with recent onset [115]. Gene expression profile of peripheral blood mononuclear cells from SLE patients was suggestive of an active type I IFN signalling [2,116]. However, an extended longitudinal study in 11 SLE patients failed to show any association between IFN response scores and changes in disease severity or in risk for SLE flares [117]. This suggests a very limited usefulness of IFN-inducible gene profiling as a biomarker for lupus.

IFN- α inducers

TLR-7 and -9 ligands are very strong inducers of type I IFNs both *in vitro* and *in vivo*. TLR-7- [118] and TLR-9-mediated [119] induction of early IFN-inducible genes in pDCs is dependent on p38-mitogen-activated protein kinase (MAPK) signalling, STAT1 phosphorylation and IRF7 translocation but is, interestingly, IFN- α/β -independent. DNA-containing immune complexes are capable of inducing dendritic cell activation and type I IFN secretion both in humans and in rodents. This activation is dependent on the presence of unmethylated CpG dinucleotides within the dsDNA [120].

In vivo treatment of NZB autoimmune mice with complex TLR-9 agonists induces abnormally high levels of serum IFN- α [17]. Treatment with IFN- α accelerates disease and induces early lethal lupus in New Zealand black/white (NZB/W)-F₁ mice [121]. Several investigators have shown that deficiency of the type I IFN receptor may protect lupus-prone mice from developing a lupus-like disease [122,123].

One way in which IFN- α may contribute to the SLE pathogenesis could be via up-regulation of TLR7 [124] and TLR-9 [125]. Type I IFN may also promote B cell activation and plasma cell differentiation with isotype switching to complement-fixing IgG2a, IgG2b, IgG3 antibodies in mice. IFN- α from SLE patients could induce differentiation of monocytes into potent DC-like antigen-presenting cells which may then present antigens derived from apoptotic cells to T cells [126]. In T helper cells, type I IFN promotes TH1 differentiation. They can also increase cytotoxic T cell and NK cell activity along with increased IFN-y production. Therefore, there are multiple ways how type I IFN may contribute to the lupus pathogenesis. Attempts to block this activity, either by using neutralizing monoclonal anti-IFN- α/β antibodies, soluble IFNAR-Fc constructs, or by blocking the activity of nucleic acid inducers at the level of TLRs may provide a better control of disease activity in human SLE. Indeed, a recent phase Ia clinical trial in patients with mild to moderate SLE with skin involvement showed that an anti-IFN- α monoclonal antibody (MEDI-545) could (partially) reverse the overexpression of type I IFN-inducible genes in peripheral blood and lesional skin [127]. However, specific data on safety were not provided. As adequate type I IFN response is critical for fighting viral infections, it could be speculated as to whether blocking type I IFN activity may result in serious immunodeficiency. This could be a problem in patients with SLE whom suffer from acute or chronic viral infections or were vaccinated recently with live attenuated viruses [128].

Selective TLR-7 and TLR-9 antagonists as potential lupus therapeutics

There is a growing interest for developing TLR-7- and/or TLR-9-specific antagonists as therapeutics for human SLE. Anti-malarial agents such as hydroxychloroquine work, in



Fig. 1. Toll-like receptor (TLR)-9 ligand cytosine (phosphodiester) guanine oligonucleotide (CpG-ODN 2084) (100 nM) induces rapid nuclear factor kappa-B (NF- κ B) and activator protein-1 (AP-1) nuclear translocation as detected by electrophoretic mobility shift assay which can be inhibited by equimolar concentrations of inhibitory oligonucleotides (INH-ODNs) 2088 and 2114, but not with the control ODN 2310.

part, by blocking endosomal acidification and TLR-7/9dependent signalling. Hydroxychloroquine reduces frequency and severity of lupus flares and has a favourable therapeutic effect on lupus arthritis, serositis and skin disease [129]. However, its use is limited by suboptimal efficacy and toxicity. Therefore, selective TLR-7- and/or TLR-9specific antagonists may be more beneficial, assuming a broadened therapeutic safety window.

Pisetsky's group was the first to discover that synthetic inhibitory oligonucleotides (INH-ODN) containing poly-G sequences could block bacterial DNA-induced activation [130,131]. However, this effect required relatively high micromolar concentrations of INH-ODNs and was not specific for TLR-9, as these INH-ODNs could also block other signalling pathways [132].

Krieg's group noticed that certain CpG sequences, including methylated CpG-ODNs [133,134], have not only lost the ability to stimulate TLR-9-responsive cells, but acted as antagonists when added to bacterial DNA-stimulated cultures [134].

Our group discovered that at the signalling level, the earliest steps in NF- κ B [135] and MAPK-activation were potently inhibited [136] suggesting a very proximal place of INH-ODN action (Fig. 1), possibly at the level of TLR-9 itself [137]. Detailed mapping studies in mouse B and non-B cells [138,139] determined the following rules for TLR-9inhibition: (i) the CpG motif is not required for inhibition; (ii) a stretch of three consecutive G nucleotides is necessary for inhibition; (iii) the 5' end of an INH-ODN is important for inhibition: CCT triplet is optimal. An INH-ODN containing multiple CCT repeats could inhibit TLR-7/9 activation [140]; (iv) the optimal distance between the 5' CCT and the downstream GGG triplet is 3–5 nucleotides long; (v) the order of 5'CCT \rightarrow GGG-3' is critical, as ODNs with the reverse order are non-inhibitory; (vi) the spacing between the CCT and GGG triplets has a minor impact on INH-ODN activity and can accept multiple substitutions; (vii) the overall length of an INH-ODN has an impact on activity; and (viii) inhibition of the TLR-9-pathway does not require G-rich segments to form intrachain or interchain Hoogsten bonds between the adjacent Gs [141].

INH-ODNs are active in human peripheral blood B cells, B cell lines, pDCs [142,143] and in TLR-9-transfected HEK cells [144]. Our recent mapping studies showed that extending INH-ODNs for 4-5 bases at their 5' end significantly enhanced their inhibitory activity in human cells. Similar to mouse studies, activity was not dependent on the ability of INH-ODN to self-aggregate [144]. TLR-9 bound (PO) INH-ODNs similarly to CpG-ODNs and the affinity for TLR-9 did not correlate with the biological activity (Ashman et al. submitted for publication). These results concur with the recent observation that sugar backbone 2-deoxyribose determines DNA recognition by TLR-9 [145]. Phosphorothioatemodified deoxyribose has much higher affinity for both TLR-7 and -9 compared to PO-deoxyribose, transforming these molecules into TLR-7 and TLR-9 antagonists [145]. Therefore, some other molecule, not TLR-9, must be responsible for sequence-specific recognition of INH-ODNs (unpublished data and [144]).

Concept of class R and class B INH-ODN

For our mapping studies we used INH-ODN-2114 ([141]; Table 2). This ODN is a very potent TLR-9-inhibitor in both

Table 2. Inhibitory oligonucleotides.

human and mouse settings *in vitro* [138,139,141]. It also works in the MRL-Fas ^{lpr/lpr} strain of lupus *in vivo* [146]. INH-ODN-2114, and very similar ODNs developed by two other groups have no inhibitory activity on TLR-2, -3, -4 and -5 and BCR-induced stimulation when used at concentrations up to 1 μ M [141,147,148].

Because INH-ODN-2114, similar to poly-G ODNs [149], has four consecutive Gs and at higher concentrations can make G4-stacks, this ODN may have some non-specific effects on immune activation. In order to avoid any contribution from G4 aggregates we created INH-ODN 4024 (Table 2) [142]. This ODN contains canonical CCT and GGG triplets, but does not make G4-stacks and is as potent as INH-ODN 2114 for human and mouse TLR-9-expressing cells [139,142]. We further truncated INH-ODN-4024 to create a shortest active 12-mer INH-ODN 4084-F (Table 2) [150].

In order to understand the contribution from defined secondary structures other than G4 stacks, e.g. ability to make DNA duplexes or hairpins, we created 24 mer-ODNs in which the INH-ODN 4084F sequence was positioned either at the 5' or the 3' end, and was followed (or preceded) by 12 nucleotides complementary to the INH-ODN 4084F sequence, making a complete palindrome (INH-1, INH-4, Table 2) [150]. Based on their biological activity we named these new TLR-9-antagonists class R INH-ODNs (where 'R' stands for restricted activity [151]), as they showed similar inhibitory potency for TLR-9-activated IFN- α producing dendritic cells as their linear analogues (class B, broadly active, INH-18, INH-13, Table 2), but were between 10- and 30-fold less inhibitory in human and mouse B cells [150]. This difference in activity between classes R and B INH-ODNs in B cells could depend on the ability of these ODNs to reach different TLR-9expressing compartments, e.g. early versus late endosomes

No.	Sequence	Class	Effect in lupus	Reference	
2088	TCCTGGCGGGGAAGT	B/G	Not tested	[141]	
2114	TCCTGGAGGGGAAGT	B/G	++	[141]	
4024	TCCTGGATGGGAAGT	В	Not tested	[138]	
4084F	CCTGGATGGGAA	В	Not tested	[150]	
INH-1	CCTGGATGGGAATTCCCATCCAGG	R	++	[150]	
INH-4	TTCCCATCCAGGCCTGGATGGGAA	R	Not tested	[150]	
INH-13	CTTACCGCTGCACCTGGATGGGAA	В	Not tested	[150]	
INH-18	CCTGGATGGGAACTTACCGCTGCA	В	—/+	[150]	
Poly-G	GGGGGGGGGGGGGGGGGGGG	G	Not tested	[130]	
A151	TTAGGGTTAGGGTTAGGGTTAGGG	G	++	[137]	
GpG	TGACTGTGAAGGTTAGAGATGA	В	+	[170]	
G-ODN	CTCCTATTGGGGGTTTCCTAT	B/G	Not tested	[148]	
IRS-869	TCCTGGAGGGGTTGT	B/G	Not tested	[143]	
IRS-661	TGCTTGCAAGCTTGCAAGCA	R/TLR7	+	[147,180]	
IRS-954	TGCTCCTGGAGGGGTTGT	B/TLR7/9	++	[147]	
SAT05f	CCTCCTCCTCCTCCTCCTCCTCCT	B/TLR7/9	Not tested	[140]	
6	$\mathrm{CTATCT}G_{2\text{-}0\text{-}mr}A_{2\text{-}0\text{-}mr}\mathrm{C}\mathrm{G}\mathrm{T}\mathrm{T}\mathrm{C}\mathrm{T}\mathrm{C}\mathrm{T}\mathrm{G}\mathrm{T}$	B/TLR7/9	Not tested	[174]	

Nucleic acid sensors in SLE



Fig. 2. Superior efficacy of class R INH-1, compared to class B inhibitor-18 (INH-18) in preventing renal damage in MRL-Fas^{/pr//pr} mice. Periodic acid-Schiff (PAS) staining. Magnification: ×50 (upper panels); ×200 (lower panels).

[150,152-154]. In B cells, class R INH-ODNs, similar to mammalian DNA, have a restricted access to late endo/ lysosomes. Because the BCR engagement allows B cells to respond to a wider range of TLR-9 ligands, including complex TLR-9-agonists [125,154-158], we hypothesized that the same principal may apply to class R TLR-9antagonists. In order to test this hypothesis, we used autoreactive AM14 B cells as a model for BCR/TLR-9 crosstalk [24]. When AM14 B cells were stimulated with linear CpG-ODN ligands, similar to non-autoreactive B cells, class R INH-ODNs were still 10-fold less potent inhibitors compared to class B INH-ODNs [150]. However, when DNAcontaining immune complexes were used for stimulation, the potency of class R INH-ODN increased and equalized that of class B INH-ODNs [150]. We wondered whether this selectivity could be advantageous for treating lupus. Indeed, studies in the MRL-Fas Ipr/Ipr strain showed that linear class B INH-18 was surprisingly less effective, while treatment with palindromic class R INH-1 improved survival, diminished renal pathology and restored the B cell phenotype (Figs 2 and 3) [150]. Furthermore, levels of anti-dsDNA and anti-Sm/RNP antibodies were reduced

significantly in mice treated with INH-1. These results re-emphasized the fact that TLR-9 may have some protective effects in the MRL-Fas^{lpr/lpr} strain of lupus mice.

Telomeric TTAGGG repeats

Klinman's group created oligonucleotides containing telomeric TTAGGG repeats (A151 in Table 2). These INH-ODNs had multiple effects on immune activation [129]. For example, A151 blocked cytokine production induced by a variety of polyclonal activators and antigens, including TLR-9-ligands [129,159,160]. In vivo, these ODNs showed a remarkable potential for preventing inflammatory arthritis induced by intra-articular injection of CpG-ODNs [161], SLE in the NZB/W strain [162], uveitis [159], silicosis [163] and LPS-induced toxic shock [164]. Their activity depended on the ability to make G4-stacks. There is evidence that TTAGGG repeats may selectively bind STAT1 and STAT4 and block their phosphorylation [160,164]. Similar G-rich ODNs can also target STAT3 [165,166], scavenger receptors [149], nucleolin [167] and lupus autoantigen - Ku [168].



Combined TLR-7/TLR-9 antagonists

Barrat-Coffman's group created a novel TLR-9 inhibitor, IRS 869 [143]. Noticeably, this ODN differs from INH-ODN 2114 by having two $A \rightarrow T$ substitutions at the 3' end where the ODN length but not the primary sequence counts [138,139]. This ODN was capable of preventing d-galactosamine plus CpG-ODN-induced systemic inflammation and cytokine storm [143].

The same group subsequently developed INH-ODNs suppressive for the TLR7-pathway. Their prototype IRS 661 contained five GC motifs buried within the complete palindrome [147]. This ODN was capable of blocking TLR-7/8 agonist (R848)-induced IL-6 secretion, but was ineffective against TLR-9-ligands. The same group combined TLR-7 and TLR-9 sequences and developed IRS 954 which blocked stimulation through TLR-7 and TLR-9. *In vivo*, IRS 954 proved efficacious in the NZB/W-F₁ strain of lupus mice [169]. Interestingly, several groups have shown that (PS) ODNs including TLR-9-antagonists, control ODNs and CCT repeats [140], may have backbone-dependent and sequence-independent effects on TLR-7-induced activation [29,150,170–173].

Finally, Idera pharmaceuticals has developed INH-ODNs containing 2'-O-methylribonucleotide modifications but lacking the poly-G motif. These INH-ODNs were capable of blocking TLR-7 and TLR-9-induced activation, both *in vitro* and *in vivo* [174].

What is the mechanism of INH-ODN action?

There is a possibility that various types of INH-ODNs may work through different mechanisms. For example, INH-ODNs may compete for receptor-mediated endocytosis in a sequence-independent manner. This effect may depend on the length of an INH-ODN, as well as on its ability to make G4 stacks [149,175]. Longer and G-rich ODNs are taken up more effectively by macrophages than shorter ODNs. The opposite is true for primary B cells [175]. The next possibility is that INH-ODNs block TLR-9-trafficking from the ER to the endosomes or prevent TLR-9-processing into a functionally active product [176,177]. INH-ODNs may bind TLR-9 and prevent it from undergoing a conformational change critical for recruiting MyD88 [178]. INH-ODNs may promote Rab7-dependent degradation of TLR-9 in LAMP1⁺ late endosomes [179]. Certain INH-ODNs may work downstream of the TLR-7/9, e.g. at the level of STAT signalling.

Revised classification of INH-ODNs

We classified INH-ODNs into two major categories: class B and class R [151]. Class B are linear ODNs that potently block CpG-induced activation in all TLR-9-expressing cells. They also block TLR-7 activation in a sequence-independent manner. Interestingly, they are less protective in the MRL-Fas lpr/lpr strain. They may find applications for prevention/ treatment of TLR-9-dependent microbial sepsis and chronic inflammation. On the other hand, class R INH-ODNs contain complete palindromes or short 5' or 3' singlestranded overhangs. Class R INH-ODNs are typically longer (20-28 mer) ODNs capable of either dimerizing or making hairpins. BCR cross-linking increases their potency for TLR-9-activated B cells for at least 10-fold, making them good candidates for targeting dsDNA-, nucleosome- or RF-specific autoreactive B cells. We initially included all complex INH-ODNs, including those capable of making G4 stacks, into the class R category [151]. However, it is now clear that G4-stacking ODNs and palindromic ODNs have different signalling targets. Therefore, we now propose a new category of INH-ODNs: class G (Table 3). We include into this class all INH-ODNs which are capable of making larger G-aggregates. These ODNs are much less specific for the TLR-7/9 pathway, and may have direct pro-apoptotic effects in tumour cells. They can block phosphorylation and nuclear translocation of multiple members of the STAT family. Besides TLRs, they can also interact with other cellular targets such as scavenger receptors Ku and nucleolin. Because of their promiscuity they can be more immunosuppressive than other classes of INH-ODNs.

All three classes of TLR-9-antagonists have sequenceindependent phosphorothioate backbone-dependent effects on TLR-7 activation. TGC triplets may additionally increase their potency for the TLR-7 pathway [147]. Classes B and G INH-ODNs and combined TLR-7/9 inhibitors are effective in animal models of lupus [146,150,162,169,180]. These ODNs are very potent upstream inhibitors of TLR-7- or TLR-9-induced type I IFN secretion. However, it remains to be determined whether any of these INH-ODNs can interfere with the type I IFN-production induced following engagement of cytosolic DNA and RNA receptors and what

 Table 3. Classification of inhibitory oligonucleotides.

Distinguishing			TLR-9 inhibition	TLR-9 inhibition	TLR-7 inhibition	Effect	
Class	feature	Example	in B cells	in DC	(backbone effect)	in lupus	Reference
G	G4-stacking	A151	+	+++	++	++	[137]
R	Palindromic	INH-1	+	+++	++	++	[150]
В	Linear	INH-18	+++	+++	++	—/+	[150]

TLR, Toll-like receptor.

the exact role of these nucleic acid sensors in the lupus pathogenesis might be. We envision application of INH-ODNs as therapeutic agents for human lupus and for DNAdependent bacterial sepsis.

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Disclosure

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