

The exciting future for scleroderma: What therapeutic pathways are on the horizon?

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Abstract

Emerging evidence shows that a complex interplay between cells and mediators as well as extracellular matrix factors are likely to underlie the development and persistence of fibrosis in systemic sclerosis. Similar processes may determine vasculopathy. This article reviews recent progress in understanding the way in which fibrosis become profibrotic and how the immune system, vascular and mesenchymal compartment interest in disease development. This growing understanding can be exploited in forward translation to identify new targets for therapy. Similarly, early phase trials are informing about pathogenic mechanisms in vivo and reverse translation for observational and randomized trials is allowing hypotheses to be developed and tested. As well as repurposing drugs that are already available, these studies are paving the way for the next generation of targeted therapeutics.

Introduction

There has been major progress in understanding pathogenic mechanisms in systemic sclerosis at a molecular and cellular level. This has permitted key pathways, mediators and cell types that may be central to the disease to be better characterized. The disease can be regarded conceptually as one of dysfunctional connective tissue repair. This may arise due to ongoing injurious mechanisms or could reflect inability to harness the physiological regulators of tissue repair and growth. It seems likely that most of the mechanisms and pathways involved in disease progression are also implicated in normal growth and repair of connective tissue. This adds extra challenges for therapeutics that modify the disease as they might also impair normal wound healing or connective tissue homeostasis. Since SSc is an autoimmune disease a key mechanism that drive the pathology is likely to be immune mediated damage or cellular stimulation. The emerging biology and targets that could be exploited therapeutically are summarized in this article.

Pathways and mechanisms with central roles in fibroblast activation

Fibroblasts as key effector cells of fibrotic tissue remodeling in SSc

Single cell OMIC techniques demonstrated that fibroblasts are a highly heterogeneous population of cells composing of several subpopulations with distinct gene expression profiles and functional roles. Recent work from the Lafyatis laboratory identified 10 subpopulations of fibroblasts in SSc skin [1]. Fibrotic tissues in SSc are characterized by shifts from resting and homeostatic fibroblast subpopulations to inflammatory and profibrotic subpopulations. The proportions of several profibrotic and proinflammatory subpopulations such as COL11A1+, COMP+, PRSS23/SFRP2+, SFRP4/SFRP2+ fibroblasts and CCL19+ fibroblasts positively correlated with clinical and histopathological parameters of skin fibrosis, whereas immature, homeostatic populations such as CXCL12+ and PI16+ fibroblasts inversely correlated with progression of skin fibrosis (Honglin Zhu et al, manuscript submitted). The profibrotic pathogenic subpopulations include so-called myofibroblasts. Myofibroblasts are defined by the expression of contractile proteins such as alpha-smooth muscle actin (α SMA) with the ability to contract tissue. Myofibroblasts release abundant amounts of extracellular matrix (ECM) as well as numerous soluble mediators that maintain a local profibrotic milieu. A variety of different cell types can acquire at least a partial myofibroblast phenotype and may thus contribute to the accumulation of myofibroblasts in fibrotic tissues. These precursor cells include resident fibroblasts (e.g. a subpopulation of resident fibroblasts with high mRNA levels of SFRP2 [1]) and cells of the vascular wall, such as pericytes, endothelial cells and smooth muscle cells,

but also epithelial cells, tissue-resident progenitor populations and bone-marrow-derived fibrocytes that reach fibrotic tissues via the blood stream [2].

The characterization of functionally distinct subpopulations of fibroblasts and myofibroblast precursors may have therapeutic implications. Specific targeting of pathogenic subpopulations may not only provide increased antifibrotic efficacy and may also limit adverse events of antifibrotic therapies as they would not affect homeostatic subpopulations required for homeostasis. However, the molecular mechanisms that promote the expansion of these pathogenic fibroblast subpopulations in SSc require further studies. We are just beginning to understand the transcriptional networks that are active in individual fibroblast subpopulations.

The transcription factor PU.1, a member of the ETS family of transcription factors encoded by the *SPI1* gene, coordinates pro-fibrotic gene expression programs in fibroblasts required for differentiation into profibrotic fibroblast subsets [3]. The expression of PU.1 is upregulated in a subset of profibrotic fibroblasts in SSc, but not in resting fibroblasts. Forced overexpression of PU.1 in proinflammatory and resting fibroblasts converts them into profibrotic fibroblasts with increased expression of contractile proteins and enhanced release of ECM. Vice versa, genetic inactivation of PU.1 or pharmacologic targeting with heterocyclic diamidines enables re-programming of fibrotic fibroblasts into homeostatic fibroblasts with antifibrotic effects across different organs [3]. Although heterocyclic diamidines effectively inhibit PU.1 in vitro and ameliorate fibrosis in murine models, further pharmacological refinement will be required to yield candidates for clinical trials.

The transcription factor Engrailed 1 (EN1), a member of the family of homeodomain-containing transcription factors, is also involved into the differentiation of resting fibroblasts into profibrotic fibroblast subsets in SSc. A subset of fibroblasts in the skin that expressed EN1 during development can give rise to a subpopulation of fibroblasts with high capacity for extracellular matrix (ECM) production that is required for scar formation [4, 5]. Moreover, EN1 amplifies the profibrotic effects of TGF β in the skin of SSc patients. EN1 is induced in certain fibroblast subpopulations in a TGF β / SMAD3-dependent manner, and in turn facilitates the transcription of a subset of pro-fibrotic TGF β target genes to promote ROCK activation, cytoskeleton organization and fibroblast-to-myofibroblast transition. Knockdown of EN1 inhibited fibroblast-to-myofibroblast transition and ameliorated experimental skin fibrosis in murine models and human models of skin fibrosis. Pharmaceutical targeting of EN1 has not been investigated so far but might be achieved by cell permeable-peptides [6].

Nuclear receptors as potential targets for antifibrotic therapies

Nuclear receptors compose a superfamily of transcriptional regulators with 48 members. Several members of the nuclear receptor family have been implicated in the pathogenesis of SSc as they may regulate inflammatory processes, facilitate metabolic adaptation or regulate fibroblast activation. The role of selected nuclear receptors with future potential as therapeutic targets in SSc is discussed below.

NR4A1 (also referred to as Nur77, TR3) signaling is repressed by epigenetic and posttranslational mechanisms in SSc [7]. Under physiologic conditions with short-term upregulation of TGF- β , NR4A1 expression is induced and recruits a repressor complex comprising SP1, SIN3A, CoREST, LSD1, and HDAC1 to limit the transcription of profibrotic genes downstream of TGF- β [7]. However, in SSc and other fibrotic diseases, persistently high levels of TGF- β deactivate this feedback loop; prolonged stimulation of fibroblasts with TGF- β represses NR4A1 signaling by histone deacetylase-induced silencing and phosphorylation-induced inactivation of NR4A1 via AKT kinases [7, 8]. NR4A1 agonists prevent the inactivation of NR4A1 signaling, limit TGF- β -dependent fibroblast activation and exert antifibrotic effects in mouse models of SSc and other fibrotic diseases [7]. However, the pharmacologic profile of the NR4A1 agonist used in these studies (cytosporone B, a natural product) is not suitable for use in humans and the development of potent and selective agonists of NR4A1 remains challenging to date.

Vitamin D receptor (VDR, NR111) is also an antifibrotic receptor that could serve as a potential target for antifibrotic therapies. Activated VDR binds to phosphorylated SMAD3 to inhibit TGF- β -SMAD-signaling and fibroblast-to-myofibroblast transition [9]. In SSc, however, the expression of VDR is decreased in the skin of patients with SSc [9] and additionally vitamin D deficiency is common in SSc and other chronic diseases. The resulting downregulation of VDR signaling fosters fibroblast activation. VDR signaling can be activated by synthetic VDR agonists, which ameliorate TGF- β -induced fibroblast activation and tissue fibrosis. Multiple highly potent agonists of VDR are approved for clinical use and could be tested in SSc.

Other nuclear receptors that have been implicated into the pathogenesis of SSc include the constitutive androstane receptor (CAR)/NR113, the liver X receptors (LXRs) and the pregnane X receptor (PXR)/NR112. CAR is thought to directly regulate fibroblast activation, whereas LXR and PXR may rather regulate the release of profibrotic mediators from macrophages or T cells, respectively. CAR is a profibrotic nuclear receptor. Its activation by treatment with CAR agonists fosters activation of canonical TGF β signaling and exacerbates experimental fibrosis [10]. In contrast, LXRs limit macrophage activation and cytokine release and treatment with LXR agonists reduces macrophage influx and IL-6 release in murine models of SSc [11]. As for LXR, PXR activation also did not demonstrate direct inhibitory effects on fibroblasts, but

inhibited the release of IL-13 from Th2 cells to ameliorate fibrosis in inflammatory mouse models of SSc [12].

Targeting the reactivation of developmental pathways in SSc

Several lines of evidence in complementary models demonstrate that hedgehog- and WNT signaling are central pathways of fibroblast activation in SSc and other fibrotic diseases [13-22]. These pathways are essentially required for embryonic development and are thus referred to as developmental pathways. After embryonic development, these pathways are silenced in most cell types except rapidly cycling stem cells. However, hedgehog signaling and WNT signaling can be reactivated upon injury to promote proliferation and differentiation of target cells. Persistent activation of those pathways in fibroblasts drive fibroblast-to-myofibroblast differentiation and fibrotic tissue remodeling.

The expression of the ligand sonic hedgehog (SHH) is upregulated in the skin of patients with SSc with consistent accumulation of the downstream transcription factor GLI2 [23, 24]. Moreover, SHH levels are increased in the blood of SSc patients [23]. This upregulation might at least in part be mediated by TGF- β as TGF- β induces the expression of SHH and of GLI2 in fibroblasts [24]. Activation of hedgehog signaling stimulates fibroblast-to-myofibroblast transition and promotes experimental skin fibrosis [24], whereas pharmacologic or genetic inactivation of hedgehog signaling e.g. by selective genetic or pharmacologic inactivation of GLI2 or by treatment with inhibitors of the receptor Smoothed ameliorates experimental fibrosis in murine models of SSc [25].

β -catenin-dependent WNT signaling, also referred to as canonical WNT signaling, is active in and multiple other fibrotic diseases. Activation of canonical WNT signaling occurs as a consequence of deregulation on multiple levels with upregulation of WNT proteins, downregulation of endogenous WNT inhibitors and by transcriptional synergism with other profibrotic mediators [17, 18, 26-30]. As for hedgehog signaling, TGF- β can activate canonical WNT signaling, i. p. by epigenetic downregulation of the expression of endogenous WNT antagonists such as dickkopf-1 (DKK1) or secreted frizzled-related protein-1 (SFRP1) [31-33]. Canonical WNT signaling is sufficient and required for fibrotic tissue remodeling and targeted inhibition of WNT signaling exerts potent antifibrotic effects in various preclinical models of SSc and other fibrotic diseases [3, 17, 21, 22, 26, 28, 31, 34-40].

Despite their crucial role in embryonic development and stem cell maintenance, hedgehog and WNT signaling are both assessable for pharmacologic intervention. For hedgehog signaling, Smoothed inhibitors are already in clinical use for neoplastic diseases and GLI2 inhibitors are clinical development [41]. Compounds with WNT inhibitory activity such as pyrvinium are

also in clinical use and more selective and potent WNT inhibitors such as porcupine- or tankyrase inhibitors are in clinical development. Indeed, clinical trials with WNT targeting strategies are currently in preparation for interstitial lung diseases and are also discussed for sclerodermatous chronic graft-versus-host diseases. However, potential concerns of these approaches may include toxicity associated with impaired regeneration of stem cells upon long-term treatment. Given the crucial roles of WNT and hedgehog signaling in stem cell regeneration, specific strategies might be required to minimize the effects on the stem cell compartment associated with long-term use.

Epigenetic changes and the establishment of a profibrotic tissue memory

The chronic profibrotic milieu in affected tissues of SSc patients induces epigenetic modifications in fibroblasts[42-44]. These epigenetic modifications consolidate an activated myofibroblast phenotype and render them at least in part independent of external stimuli. Epigenetic modifications establish self-sustaining activation loops to promote chronic fibroblast activation and progressive fibrotic tissue remodeling in SSc. This is best evidenced by the activated phenotype of SSc fibroblasts even upon long-term culture: Fibroblasts explanted from fibrotic skin of SSc patients exert a myofibroblast-like phenotype with increased expression of contractile proteins and enhanced release of collagen, which persists for several passages *in vitro*. Epigenetic modifications are critical to maintain the profibrotic phenotype of SSc fibroblasts. This stabilization of an activated phenotype by epigenetic modifications is often referred to as profibrotic tissue memory. The tissue memory is encoded by a complex pattern of different epigenetic alterations. Epigenetic alterations including DNA methylation, histone acetylation, histone methylation, bromodomain (BRD) dependent regulation and non-coding RNAs such as microRNAs (miRNAs) or long non-coding RNAs (lncRNAs) are well established as drivers of progressive fibrotic tissue remodeling in SSc, but also in other fibrotic diseases [45-52] [48, 53]. Selected examples and potential approaches for therapeutic intervention are discussed below.

DNA methylation

DNA can be methylated at position C5 of the pyrimidine ring of cytosine by a family of three DNA methyltransferases (DNMTs): DNMT1, DNMT3A and DNMT3B [54]. Methylation of cytosine residues generates binding sites for methyl-CpG-binding domain (MBD) proteins, in particular when methylated cytosine residues are clustered in so-called CpG islands. Binding of MBD proteins promotes the recruitment of repressor complexes to silence transcription of

the associated genes [55]. Several studies demonstrated a role of altered DNA methylation in fibrotic diseases including SSc [35, 48, 56-58]. The first and best studied target regulated by DNA methylation in SSc is the Friend leukemia integration factor 1 (FLI1) gene, which encodes for a transcription factor of the ETS family [48, 59, 60]. FLI1 limits TGF- β -signaling to inhibit fibroblast activation under homeostatic conditions [61]. However, in the profibrotic milieu of SSc, FLI1 expression and activity are repressed by epigenetic and posttranslational mechanisms. TGF- β induces DNA methylation of the FLI1 promoter to silence its expression and also promotes FLI1 degradation via PKC δ -mediated phosphorylation [62]. Moreover, DNMT-induced silencing of the suppressor of cytokine signaling 3 (SOCS3) facilitates prolonged activation of JAK2 / STAT3 signaling to facilitate TGF- β -induced fibroblast activation (PMID: 31990678). Aberrant DNA methylation also facilitates activation of canonical WNT signaling by silencing of the endogenous WNT antagonists Dickkopf-1 (DKK1) and secreted frizzled-related protein 1 (SFRP1) [35]. Treatment with the DNMT inhibitor 5-aza-2'-deoxycytidine (5aza), which is in clinical use for myelodysplastic syndromes, has exerted antifibrotic effects in murine models of SSc and other fibrotic diseases [35, 46, 63]. As treatment with 5aza is relatively well tolerated, 5aza may offer potential for testing in clinical trials in SSc.

Histone acetylation

Histone modifications include acetylation and methylation at various sites. First evidence for a role of histone modulations in the pathogenesis of SSc was provided by the observation that treatment with histone deacetylation inhibitors reduced the activation of SSc fibroblasts and ameliorated bleomycin-induced skin fibrosis [64]. As HDAC inhibitors such as SAHA are in clinical use for malignant diseases, targeting of HDACs may offer therapeutic potential for SSc.

Follow-up studies revealed that the expression of the profibrotic transcription factor PU.1 (see above) is also controlled by a complex network of epigenetic mechanisms that include histone modifications [3]. In resting fibroblasts, PU.1 expression is silenced and the promoter and the upstream regulatory element of the PU.1 locus is dominated by repressive H3K9me3 and H3K27me3 marks. In fibrotic environments, however, the upstream regulatory element of the PU.1 locus becomes permissive with increased H3K27 acetylation and loss of H3K9me3 and H3K27me3. These epigenetic alterations at the PU.1 locus promote expression of PU.1 protein in fibrotic fibroblasts. As discussed above, PU.1 inhibitors with improved pharmacological profile are currently in development.

Moreover, histone acetylation at H4K16 has recently been shown to modulate the outcome of fibrotic diseases by fine-tuning autophagy [65]. Autophagy describes the catabolic cellular

process of degradation of unnecessary or dysfunctional cellular organelles in particular during starvation or in response to cellular stress [66]. However, components of the autophagy machinery are also involved in unconventional secretion of proteins [67-69]. Autophagy is activated in a TGF β -dependent manner in SSc fibroblasts [65]. TGF β represses the expression of the H4K16 histone acetyltransferase MYST1 via SMAD3-dependent mechanisms to promote the expression of core components of the autophagy machinery. The resulting increase in the autophagic flux induces activation of human dermal fibroblasts and fibrosis in murine skin and lungs. Re-establishment of the epigenetic control of autophagy by forced expression of MYST1 in fibroblasts impairs myofibroblast differentiation and ameliorates experimental dermal and pulmonary fibrosis. However, pharmaceutical approaches to selectively promote MYST1 activation are currently not available and further studies are required to best transfer these findings from bench to bedside.

Other epigenetic modifications: miRNAs and BRDs

miRNAs are small non-coding RNAs. Binding of miRNAs to their respective target mRNAs promotes degradation of target mRNAs [70]. More than 50 miRNAs have been implicated in the pathogenesis of fibrotic diseases [70]. Most of these miRNAs are expressed in a highly cell-specific and/or context-specific manner. However, miR-21 and miR-29 are broadly expressed miRNAs that have been implicated in fibrotic remodeling of multiple organs and might thus be particularly relevant for a multi-systemic disease such as SSc. TGF- β induces the expression of miR-21, which in turn downregulates SMAD7 to promote canonical TGF- β signaling [71]. Antagomirs against miR-21 attenuated experimental pulmonary, myocardial and renal fibrosis [71-73]. In contrast to miR-21, miR-29 is an antifibrotic miRNA that is downregulated in fibrotic diseases including SSc. miR-29 inhibits the translation of multiple collagen genes and of several enzymes involved in ECM turnover [74]. miR-29 mimics may thus offer potential for the treatment of SSc and other fibrotic diseases. Of note, miRNA-based therapies are currently evaluated for the treatment of cardiac fibrosis.

Bromodomain proteins (BRDs) bind acetylated lysines in histone tails and regulate gene transcription by the recruitment of molecular partners. BRDs have recently been implicated in aberrant fibroblast activation in SSc. Chromatin accessibility and transcriptome profiling revealed constitutive activation of a TGF- β 2 enhancer in SSc fibroblasts [75]. The constitutive activation of this enhancer required BRD4 and targeted inhibition of BRD4 reduced the TGF β 2 enhancer activity and the expression of profibrotic TGF- β 2 target genes. Moreover, small molecule inhibitors of BRD2/4 ameliorated experimental fibrosis in preclinical models of SSc (unpublished data). BRD inhibitors are actively investigated in multiple clinical programs for

malignant diseases. Although these studies faced obstacles including toxicity, modified application schemes, e.g. with intermittent dosing, may limit concerns and offer opportunities for BRD inhibitors in fibrotic diseases.

Extracellular ligand-receptor targeting of fibrosis in systemic sclerosis

Targeting the extracellular space in systemic sclerosis

Biological therapies have transformed outcomes in immune mediated inflammatory diseases by harnessing the specificity and binding affinity of antibody molecules or soluble receptors to trap or block the biological effects of pathogenic cytokines. This was first demonstrated in rheumatoid arthritis using monoclonal antibodies that bound to TNFalpha and later with recombinant receptors fused to IgG heavy chains or other molecules. This approach has proven safe and effective and has been applied to many different clinical settings for TNFalpha and other ligands. As well as providing effective therapeutics this has provided important insight into pathogenesis and permitted exciting reverse translational studies.

Some of the established biological agents have been applied to different diseases including systemic sclerosis and have demonstrated some efficacy. This has included targeting cell types as well as cytokines and growth factors.

In addition to targeting cells and cytokines or growth factors through binding to ligand or receptor there is the possibility to bind other extracellular or matricellular proteins and this is an area of current investigations. Systemic sclerosis represents dysfunction or dysregulated connective tissue repair, and this may be normalised by modifying the cellular microenvironment through binding to extracellular proteins that are important regulators of fibroblast activation and differentiation as outlined earlier in this review article.

Cytokines, growth factors, and matrix proteins in SSc pathogenesis

Cellular networks and fibroblasts activation by cytokines and ECM proteins

The hallmark pathological processes in systemic sclerosis are fibrosis and structural vasculopathy. These are likely to reflect the processes that are normally recruited for tissue repair and wound healing. A plausible explanation for the detrimental changes that develop and persist in SSc is that these usually coordinated and self-limiting biological processes occur excessively and are not appropriately resolved. This is likely to reflect imbalance between profibrotic and pro-resolution pathways and mediators. Much of this regulation is likely to occur

in the extracellular space and involve cytokines, growth factors their receptors and associated matricellular proteins. It is notable that many of these entities are identified as hallmarks of the SSc disease phenotype in recent gene and protein expression studies [76]. It is therefore logical to target these extracellular proteins using biological therapeutics or small molecule inhibitors. Some of the candidates that have been tested or are emerging in SSc are summarised below.

Targeting cytokines and receptors

TNFalpha.

Although targeting TNFalpha was enormously effective as a treatment for inflammatory disease including rheumatoid arthritis, seronegative spondylarthritis and inflammatory bowel disease it has not been shown to be very effective in fibrotic disease [77]. This may reflect that it is a less critical driver in diseases that are less characterised by persistent inflammation or that pathways are redundant. A review of use did not suggest major benefit and a small open label clinical trial pointed towards only modest improvements that did not reach statistical significance [78].

IL6

Although also considered a proinflammatory mediator, IL6 was first defined as a lymphocyte regulator especially important for B cells [79]. It appears to have a much broader role and it was reported that patients with elevated IL6 levels in the circulation had a worse outcome [80]. In addition, the markers for elevated IL6 activity including acute phase markers appeared to predict poor outcome in several observational studies [81]. The availability of tocilizumab as an inhibitor of both cis and trans signalling was attractive for clinical evaluation and a phase 2 trials (faSScinate) was supportive [82]. The subsequent phase 3 trial that included milder skin disease showed only a trend of benefit for skin but a very convincing signal for clinically meaningful impact on lung fibrosis [83]. Indeed, the worsening of lung function over 48 weeks was essentially prevented at a group level in the trial. This led to FDA approval for tocilizumab as a treatment to reduce worsening of lung function in SSc. Parallel mechanistic studies from the phase 2 trial highlighted that the activated phenotype of explant cultured fibroblasts could be almost entirely reversed after 6 months treatment with tocilizumab [84]. This is notable as the clinical impact on skin was just a trend of benefit suggesting that other mechanisms or fibroblast populations may be important in determining the outcome and progression of skin fibrosis but that in early-stage lung fibrosis in SSc the population of fibroblasts that are attenuated but tocilizumab are critical.

IL4/IL13

There are multiple ways in which IL4 and IL13 may be implicated in pathogenesis of SSc [85]. This included effects on fibroblast, perhaps in concert with TGFbeta and driven by IL13 as well as key roles related to immune cell activation [86]. In addition, these cytokines are critical for macrophage polarisation an in vitro can induce and M2 like phenotype that is considered pro-fibrotic [87]. It is encouraging that a phase 2 trial of romilkimab, a novel bispecific antibody targeting IL4 and IL13 was positive with greater improvement in mRSS and some encouraging signals in other relevant endpoints [88]. This requires further confirmation.

Targeting the adaptive immune system

Autologous stem cell transplantation (ASCT) as maximal immunosuppressive therapy has shown to improve skin sclerosis, quality of life and predicted forced vital capacity, a surrogate marker for interstitial lung disease and/or lung fibrosis, and 5-years survival rate. So far, this is the most effective therapy in SSc as shown by three different studies. However, as recently elucidated for patients fulfilling the criteria to be eligible for ASCT, overall, 10-years survival by ASCT is nowadays equivalent to the current best clinical practice indicating that less aggressive therapies are currently successfully been applied [89]. Transfer of peripheral blood mononuclear cells (PBMCs) from SSc patients induce interstitial lung disease as well as inflammation of other organs, which is not present when PBMCs were transferred from rituximab treated patients [90]. Those studies indicate an important role of B cells at least in the early inflammatory part of SSc. In line with this, a recent placebo-controlled phase II study on patients with early diffuse SSc patients revealed improvement of both the predicted FVC and skin fibrosis as assessed by the modified Rodnan skin score (mRSS) [91].

As well as the attenuation of agonist antibodies that may be pathogenic. there is now convincing support for targeting B cells in SSc. This is based upon biological studies of the disease that highlight the potential role of abnormal B cells, especially transitional cell populations that may demonstrate a failure of peripheral tolerance [92].

The putative role of agonistic autoantibodies in pathogenesis have now been further appreciated, having first been suggested some years previously [93]. Transfer for IgG purified from SSc patients induced interstitial lung disease and obliterative vasculopathy in mice suggesting the potent role of antibodies in the development of inflammation and vasculopathy in SSc [94]. In vitro, purified IgG from SSc patients induced an inflammatory and fibrotic proteome in monocytic cells lines and induced proteins show associations with the mRSS of the corresponding donors. Specifically, antibodies induced several cytokines and chemokines known to be important biomarkers for ILD in SSc [95]. The transfer of fibrotic signals by IgG from SSc patients also induced a fibrotic transcriptome and proteome in fibroblasts also

supporting the ability of IgG to induce disease mechanisms [96]. Indeed, very recent studies identified antibodies directed to the angiotensin receptor type-1 (AT1R) as causative factors for interstitial lung disease and skin fibrosis (Yue). The generation of these abs require T cell help also supporting the use of immunosuppressive therapies in the therapy of SSc. In vitro, these abs induced TGF β and adhesion molecules in endothelial cells, collagen-1 in fibroblasts and CCL18 or other cytokines in monocytes. AT1R abs often correlate with antibodies directed to the endothelin receptor type-1 (ETAR).

Other natural regulatory antibodies such as antibodies against the thrombin receptor 1 (PAR-1) were recently show to biological activity which further supports the potential for targeting antibodies therapeutically.

The use of B cell depleting treatments is further supported by a multi-centre cohort analysis [97] and by a recent meta-analysis [98].

Costimulatory molecules

Abatacept, a fusion protein composed of the Fc region of the immunoglobulin IgG1 fused to the extracellular domain of CTLA-4 has been tested in a small phase 2 trial and showed only a trend of benefit at a group level [99]. However certain subgroups of patients appeared to be driving the effect of abatacept on mRSS and this was especially in those patients with an inflammatory gene expression signature in their skin biopsy [100]. More encouragingly, all patients showed a meaningful impact on HAQ-DI. This was a phase 2 study, but it seems likely that if a phase 3 trial confirmed the results for HAQ-DI that this is a treatment that might be very helpful for some patients with SSc.

Future candidates for targeted therapy in the extracellular compartment

There are a number of promising future candidates for targeting extracellular proteins and ligands. These are likely to emerge based on current studies and preclinical and supportive translational data.

OSM

Despite strong theoretical rationale [101], a well-conducted phase IIa trial of anti-OSM has recently been completed and unfortunately did not show evidence of benefit in SSc based upon prespecified markers of biological or clinical effect. This was an early-stage study that was primarily testing the safety of the antibody and there was meaningful impact on

haematological parameters including anaemia and thrombocytopenia in some cases. On this basis it is not being pursued further as a treatment for systemic sclerosis [102, paper in press].

CTGF

This prototypic member of the CCN family of matricellular proteins has long been a hallmark marker of the profibrotic SSc fibroblast phenotype [103]. It appears to promote or augment fibrosis and may work as a downstream mediator or co-factor related to TGFbeta [104]. There have been encouraging phase 2 data for targeting CTGF in IPF and in the future it may be a promising target in SSc [105].

S100A4

This protein was originally identified as a fibroblast expressed protein marker (FSP-1) based on differential display data for cells undergoing epithelial-mesenchymal transition [106]. It is now clear that this protein is a member of the S100 protein family [107] is expressed by several cell types and that it is an important extracellular matrix protein that can activate innate immune pathways [108]. Promising preclinical data support its potential as a target for treatment for fibrosis and in SSc [109].

Interferon

An elevated IFN signature is seen in SSc as well as many other rheumatic diseases [110]. Although not present in all patients it seems to be associated with poor outcome and with an overlap phenotype [111]. Since targeting IFN using anifrolumab is now an approved treatment for SLE [112] and because early phase studies showed attenuation of IFN signature in SSc patients this is a potential treatment for evaluation in SSc [113].

TGFbeta

This profibrotic master regulator is an obvious candidate for ligand directed therapy in SSc and other forms of fibrosis [114]. However, the very broad roles in connective tissue and immunological development and homeostasis together with potential roles in protecting for neoplastic transformation have raised legitimate concerns about targeting TGFbeta and the balance between risk and benefit [115]. The first trials using weak monospecific antibody against TGFbeta1 suggested safe but showed no signal of efficacy [116]. An open label study of fresolimumab was more encouraging [117]. There are several ongoing trials evaluating TGFbeta directed antibodies or ligand traps. The recent promising data for PAH targeting active pathways provide support for the potential of this approach [118] and the results of ongoing trials are eagerly awaited.

Reverse translation and insights into pathogenesis

Trials of targeted treatment offers a unique platform for experimental medicine studies as was shown for tocilizumab and these give real insights into treatment mechanism, target engagement and biology of SSc. There have been exciting results from studies and insights that may allow more targeted or stratified approaches in future trials to advance clinical trial development and pave the way for a more stratified approach to clinical practice.

Preclinical models

It has proven challenging to use preclinical models to conform treatment benefit, but they are very valuable in highlighting clinical potential and identifying the stage and type of SSc that may be most informative in a subsequent clinical trial.

Concluding remarks

It is an exciting time for SSc therapeutics because the benefits of background treatments are being established and so it is possible to design trials that add more targeted approaches on top of standard immunosuppression. The trials on nintedanib and romilkimab are excellent examples of this approach and it has been helpful in confirming the benefits from standard treatments as well as additive value of new drugs. The powerful effect of HSCT provides a gold standard of what can be achieved therapeutically, albeit with a mortality that has high morbidity and treatment related mortality. In addition, it is unsuitable for many cases and indeed those most in need are excluded from current trial protocols despite having a demonstrably worse outcome than those that are eligible. In the future it is a legitimate goal to achieve the therapeutic impact of HSCT through combination targeted therapies with much less treatment related toxicity. Emerging data suggest that an individual approach may be rewire and that tools such as skin subset, disease duration and ANA profile as well as skin biopsy intrinsic subset or peripheral blood IFN signature may be valuable tools in developing an optimal approach to treatment for SSc.

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