

**Transcription factors: Are they a real target
for future therapeutic strategies?**

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Introduction

Transcription factors have been identified as the major regulators of gene activity and therefore control the expression of most known proteins. Transcription factors *per se* do not exert any other function than to transform a message that was received by a cell via a receptor and its subsequent signalling molecules into the nucleus and onto the level of gene activity by either promoting or silencing gene transcription (1, 2).

The first transcription factors characterised had been often linked to malignant transformation and where e.g. termed “onco-genes” (3, 4), a misleading term as we know today. Today we have learned that transcription factors can be activated by most known growth factors and cytokines but also by hypoxia or oxidative stress (5, 6), lipids and polyunsaturated fatty acids (7), light (8, 9), stress (10, 11), or mechanical forces such as stretching (12, 13), as a response the expression of a whole array of genes is modified. Out of the function of certain transcription factors came the idea that if one can control their activity transcription factor modulation would be a tool to cure diseases (14-19). Such generalised conclusions are dangerous and ignore several basic aspects of cell biology.

The usual transcription factor resides in an inert inactive conformation associated to the cell membrane, the endoplasmatic reticulum, or at a less well characterised localisation in the cytosol. Upon activation a transcription factor undergoes a conformational change and attaches to specific carrier proteins that translocate it into the nucleus where it recognises a more or less specific DNA sequence to which it binds. Binding onto it specific DNA sequence affects the structural conformation of the DNA sequence and of some of the neighbouring nucleotides, the DNA un- or up-winds and becomes more accessible for binding of the RNA transcription machinery if the transcription factor activates a gene. However, transcriptional

regulation is dependent not only on transcription factor activation and chromatin remodeling, but also on co-regulators, co-activators, and co-repressors of the transcription factors.

Furthermore, transcription factors can only exert their function if they find a specific the DNA sequence and folding pattern that has to be associated with the right chromatin formation. There is an expanding array of additional modifications that titrate transcriptional regulation for the specific conditions of a particular cell type, organ system, and developmental stage, and such events are likely to be greatly influenced by upstream signalling cascades (1, 2, 20). While the basic mechanism as the proximal binding of essential transcription factors to the TATA-box and their interaction with the RNA polymerase II and co-activators has been studied for several transcription factors their function as a co-activator or transcription enhancer factor binding at a more distant location to the TATA-box is not well understood and is dependent on the folding and the relative location of the binding site to the TATA-box binding transcription factor (2, 21). A similar scenario accounts for the silencing function of transcription factors, where a single or multiple transcription factors bind to a defined DNA sequence and inhibit the action of the transcription machinery, e.g. the glucocorticoid receptor often silences genes which have no classical glucocorticoid response element in their promoter (22, 23).

Cell type specific transcription factors:

Beside general occurring and functioning transcription factors there are some cell type specific ones and those that exert a specific function under specific conditions or according in which cell type they are activated (24). Transcription factors Pax3 induced a mesenchymal to epithelial transition and the Pax3/FKHR complex affected the morphogenesis of human osteosarcoma cells (25). LEF1 affects cell survival in epithelial cells during tooth development where it mediates the Wnt signal (26). Several trophoblast specific transcription

factors have been reviewed by Knofler et al (27) but those have been mainly described in mouse models. However, since not all transcription factors have been identified yet “cell type specific” has to be used with caution as shown by a review regarding “organ specific” transcription factors including forkhead box A2 (HNF)-3beta, HNF-3/forkhead homolog-8 (FoxF1), HNF-3/forkhead homolog-4 (FoxJ1), thyroid transcription factor-1 (Nkx2.1), homeodomain box A5 transcription factor, the zinc finger protein Gli, and GATA transcription factors, as well as the basic helix-loop-helix Pod1 transcription factor (28). The family of MyoD transcription factors was described as myogenic differentiation factor triggering the maturation of smooth muscle cells (29). However, MyoD alone seems to be insufficient to control smooth muscle cell differentiation and needs the interaction with other related transcription factors (30). Therefore, it is often misleading to term a transcription factor cell type specific and more research is needed.

How to modify the action of transcription factors in therapy:

In order to use a transcription factor as a target in a new therapeutic strategy it seems to be unwise to block its function in an entire organism or to silence it for extended periods. There are several options to modify the action of transcription factors: (i) direct blocking of their activation by specific drugs, (ii) suppression of their expression by antisense oligo nucleotides, (iii) expression control by small inhibitory RNAs (siRNA), (iv) “catching away” activated transcription factors with decoy DNA oligo nucleotides of a specific DNA-binding sequence, (v) intercepting their interaction with other proteins, or (vi) transfection diseased organs/cells with overexpression vectors for a missing transcription factor. An overview of the current available methods that can be used to control the expression or function of transcription factors is provided in the following:

Antisense oligodeoxynucleotides can be used to induce a fast degradation of any gene of interest and use a natural occurring mechanism of the cells defence system based on the activation of RNase H that recognizes double stranded RNA-DNA strands and cleaves them (31). Most of the approaches to down regulate the expression of transcription factors by antisense oligonucleotides are in a trial phase which did not exceed the cell culture level or animal model. A major problem for antisense oligonucleotides is the delivery system. Antisense oligonucleotides are sensitive to a variety of enzymes present in the blood stream and in other body fluids (31 - 33).

Small inhibitory RNAs also use a natural occurring cellular virus defense system. Here a double stranded short (20-40 nucleotides) oligodesoxyribonucleotide sequence is introduced into the cell where it is recognised by specific enzymes. The double stranded RNA is bound, one of its strands is degraded and the remaining strand is used by the enzyme to find a new matching single stranded mRNA which binds and is degraded. Interestingly the detecting RNA strand is not degraded by the enzyme and is re-used to find and destroy target mRNAs (34, 35). The mRNA eliminating effect of siRNA seem to be very precise and target specific, however, the latter effect depends on the careful design of the to be used sequence. Similar problematic is the cell type specific delivery.

A more promising method was termed decoy oligonucleotides. Decoy oligonucleotides are synthetic double stranded oligonucleotides containing a transcription factor specific DNA consensus sequence and if present in the cytosol of any cell will bind active transcription factors and thereby prevent their migration into the nucleus. This method does not down-regulate the expression of a transcription factor but interferes with its function by competing with its natural target DNA sequence in the nucleus. Decoy oligonucleotides have been successfully used to suppress the action of e.g. nuclear factor-kappaB (NF-kappaB) and E2F to prevent the progression of several diseases including renal diseases (36). Tdecoy

oligonucleotides have been successfully used to control the activity of the activator protein-1 (AP-1), negative regulatory element (NRE) for the renin gene and angiotensinogen gene-activating element (AGE), and ets-1 (37 - 40). .

A major problem using any oligonucleotide construct is its short bio-stability, chemical modification in order to increase nuclease resistance often are accompanied by a decrease in the affinity for to the transcription factor or a loss of specificity of transcription factor binding. Neither circular dumbbell, nor chimeric decoy oligonucleotides changed the sensitivity to endonuclease cleavage. To address these problem so called “locked nucleic acids” of a decoy oligonucleotide for NF-kappaB have been designed with an increased stability compared to end-capped oligonucleotide (41). Such modified PNA-DNA are less sensitive to degrading enzymes and are still efficiently recognized by e.g. NF-kappaB, but their design and their safety in long term use as a drug has to proven (41 - 44).

Peptide nucleic acids-DNA chimeras, defined as a double stranded DNA sequence molecules that binds to transcription factors in a sequence-dependent manner. An example has been described for NF-kappaB and Sp1 and were used in vitro cultured in human cells and there efficacy was found to be comparable to those observed using double-stranded DNA decoys (45 - 47). The advantage of this method may be that based on peptide nucleic acids -DNA chimeras can be modified by the addition of short peptides that ease cell penetration and nuclear localization. This option may also hold the key to a cell type specific delivery of oligonucleotides.

Transcription factors as a target in therapy:

Activator protein-1 (AP-1): AP-1 controls proliferation and cytokine expression and therefore is involved in tumorigenesis and in inflammatory diseases. Together with histone

acetyltransferase CBP/p300 and the transcription factors CCAAT/enhancer binding protein (C/EBP), nuclear factor – AT (NF-AT) AP-1 controls the expression of the asthma associated cytokine IL-5 and can be activated also by rhinovirus infection (48 - 51). AP-1 can be blocked by either suppression of its activation or by inhibition of AP-1 binding to its DNA consensus sequence. Both methods concepts have been successfully used in animal and cell culture models but not yet in patients. A small-molecule AP-1 inhibitor, PNRI-299, targets the oxidoreductase, redox effector factor-1, was reported in human lung epithelial cells (IC₅₀: 20 microM) and reduced eosinophil infiltration in mice (52). MOL 294 blocks AP-1 and NF_κB inhibitor, controlling both factors at the transcriptional level (52). SP100030 inhibited AP-1 and NF_κB activation in Brown-Norway rats (53). Cyclosporin A, the adrenal steroid dehydroepiandrosterone, and the macrolide clarithromycin suppress DNA-binding of AP-1 (37, 54, 55). Decoy oligonucleotides have also been successfully used to block the action of AP-1 (35).

The CCAAT/enhancer binding proteins (C/EBP): Human C/EBPs consist of six known isoproteins (-α, -β, -γ -δ, -ε, and -ζ) which are all keep the balance between cell proliferation and cell differentiation and may even be expressed in a cell type specific pattern in the lung (56 – 58). The hyperplasia of smooth muscle bundles in the airways of patients with asthma seem to originate from a lack of C/EBP- α that leads to a less good growth control in this cells (59). Ceramide, a sphingolipid, inhibits the transport of activated C/EBP-α and NF-E2-related factor-2 (Nrf2) into the nucleus (60). Curcumin interfere with C/EBP-α and -β binding to their DNA consensus sequence (61). Trichostatin A inhibits C/EBP-α mRNA levels while valproic acid down-regulated its protein expression in adipocytes (62). Good control of smooth muscle cell differentiation was achieved by CCAAT-decoy oligonucleotide and were well tolerated in vivo in animal models and in pre-clinical studies (63 - 65). However, a

general blockade of all C/EBP-isoproteins by e.g. decoy oligonucleotides is not advisable since the various C/EBP-isoproteins exert distinct often opposing function (65). Here only cell type specific inhibition or induction of C/EBPs will help and has to be further investigated.

GATA-: GATA-3 a cell lineage-specific factor expressed in Th2 cells subsequent to STAT-6 activation in the context of inflammatory diseases (66, 67). GATA-3 function was successfully suppressed by antisense oligonucleotides (68).

Nuclear Factor_κB (NF_κB): The NF_κB transcription factor family is involved in the pathology of many diseases including AIDS, atherosclerosis, arthritis, asthma, cancer, diabetes, inflammatory bowel disease, muscular dystrophy, stroke, and viral infections (66, 67). Its ubiquitous action is important in host defence and in chronic inflammatory diseases and therefore, NF_κB control was early suggested as a potential therapeutic approach for (69, 70). Glucocorticoids have been reported to inhibit NF_κB activity but the mechanism is unclear (71 - 74). Pranlukast, pyrrolydine dithiocarbamate, and fosfomycin have been reported to inhibit NF_κB activity (74 - 76). Isoprenoids such as the kaurene diterpenoid and sesquiterpene lactone class and also the flavonoid silybin inhibit NF_κB activity, but their mode of action is unknown (77, 78). In an animal model decoy oligodeoxynucleotides NF_κB blocked its activity efficiently in airway immune cells, but not in structural lung cells which may indicate a cell type specific delivery mode of decoy oligonucleotides (77, 78).

Nuclear factor E2 p45-related factor 2 (Nrf2)/ antioxidant response element (ARE): Nrf2/ARE is involved in the oxidative stress response in a beneficial manner that would protect the affected cell from stress and therefore not inhibition but activation would be of interest for therapy (79 - 81). As for C/EBPs ceramide inhibited the transport of activated

Nrf2 into the nucleus (60) which indicates its low transcription factor specificity. Moreover, if curcumin would be used to block the pro-inflammatory action of NF κ B at the same time it would block the beneficial action of Nrf2/ARE.

Peroxisome Proliferator-activated Receptor (PPAR): PPAR ($-\alpha$, $-\beta$, $-\gamma$, $-\delta$) interact with the glucocorticoid receptor and with several C/EBP-isoproteins and therefore participate in cell proliferation and differentiation. They therefore have a similar critical role in the pathogenesis of several diseases (82, 83). PPAR γ agonists, glucocorticoids, and β_2 -agonists synergistically suppress cytokine expression at the transcriptional level (83). In regard to therapy there are already specific PPAR-isoform inhibitors and activators available (84). 15-deoxy-Delta(12,14)-PGJ(2) (15d-PGJ(2)) and troglitazone both activate PPAR γ inhibited the pro-inflammatory action of TNF α (85). Ciglitazone and GW9662, two other PPAR α agonists decreased airway hyperresponsiveness, basement membrane thickness, mucus production, collagen deposition, and TGF α synthesis in a mouse model (85, 86). PPAR- δ , in contrast, acts as a pro-inflammatory factor and binds to the same target DNA sequences as PPAR α , $-\gamma$, and its enhanced expression would be no benefit for asthma (82, 84 - 86). However, there could be a cell type or species specific effect of PPARs action since under certain conditions troglitazone counteracts the inhibitory effect of rapamycin on the PPAR γ -C/EBP- α interaction (87).

The signal transducer and activator of transcription 6 (STAT6): The role of the JAK-STAT system in health and inflammatory lung diseases was reviewed by Pernis and Rothman 2002 (88). TNF α , TGF- β , IL-4, and IL-13 are known activators of STAT6 (89, 90), and a polymorphism in the human STAT6 promoter could explain the genetic pre-disposition of high IgE levels in asthma patients and their siblings (91). Up to date the action of STAT6 is

only known to be inhibited by glucocorticoids (92, 93) and no other inhibitors for STAT6 have so far been reported.

Conclusion

Transcription factors are important regulators for immune response, inflammation and tumorigenesis their inhibition or stimulation may cure a disease without the side effects of standard drugs if they can be applied in a cell type specific mode, but a practical application of the bench work that has been done may take some more years. A major point of concern is that most transcription factors are central control factors of tissue and organ homeostasis and each longterm inhibition or activation will most likely cause severe side effects in other organs. Cell type specific application of decoy or antisense oligonucleotides for NF κ B, Nrf2 or STAT6, or specific agonists for PPAR α and $-\gamma$ have been attempted but not yet proven to be harmless over long period application. The key to success with such anovel therapeutic approach using transcription factors as medication comes with the cell type specific delivery system, a well known and not yet solved problem with the existing drugs.

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