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Forkhead transcription factors in chronic inflammation

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Abstract

Forkhead (Fox) transcription factors have been increasingly recognized to play key roles in immune homeostasis, especially Foxp3 for its role in the development and function of regulatory T cells, and Foxo family members for their regulatory role in T and B lymphocytes as well as other leukocytes. Although these transcription factors positively regulate the expression of multiple target genes, a unique functional attribute of these genes is the maintenance of leukocyte homeostasis, such as the preservation of the naïve or quiescent T cell state and prevention of autoimmunity. As a result, many chronic inflammatory processes appear to reflect a relative loss of activity of one of these transcription factors, raising the possibility that therapeutic approaches which confer gain-of-function Fox activity may be beneficial. On the other hand, however, some of the Fox family members also appear to promote and/or maintain chronic inflammation by preserving inflammatory leukocyte survival and/or otherwise promoting the expression of inflammatory target genes, at least in some cell types such as neutrophils. Therefore, although the role of Fox in inflammatory disorders remains complex and incompletely understood, the continued study of these factors provides new insight into the initiation, maintenance, and propagation of inflammation.

Keywords

Autoimmunity; Transcription Factors; Forkhead; Neutrophils; Lymphocytes

Introduction

The forkhead (Fox) family comprises a large and diverse group of transcription factors that share a “winged helix” DNA binding domain, consisting of three alpha helices flanked by two “wings” of beta strands and loops, and play critical roles in multiple biological processes, including development, metabolism, aging and cancer (reviewed in Tran et al. 2003; Carlsson and Mahlapuu 2002). Several Fox family members have received increasingly growing attention in immunology due to their now well-recognized importance in the regulation of immune homeostasis (reviewed in Jonsson and Peng 2005). Interestingly, however, whereas traditional models for transcription factors in immunity have involved the positive regulation of pro-inflammatory or pro-proliferative target genes (e.g., Peng 2008b), many Fox genes control anti-inflammatory or anti-proliferative programs in cells, in an intrinsic or extrinsic manner. This review summarizes such current data, focusing upon potential implications for the pathogenesis of chronic inflammatory diseases, such as autoimmunity and allergy. For details regarding the specific mechanisms of some of these family members, the reader is

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directed to one of several recent reviews (e.g., Peng 2008a; Bacchetta et al. 2007; Jonsson and Peng 2005).

Foxp3 in the maintenance of chronic inflammation

Foxp3 (scurfin, sf, JM2) remains the currently most well-studied immunological Fox family member, largely because of its characteristic presence and function in the natural suppressor/regulatory (nTreg) subset of CD4⁺ T cells, which are produced in the thymus and are essential for the maintenance of immunological tolerance (Sakaguchi et al. 2008). Foxp3-deficient mice develop a fatal systemic autoimmune and allergic syndrome (Brunkow et al. 2001), and Foxp3 mutant humans develop multiple organ-specific autoimmune diseases such as type 1 diabetes, allergy and inflammatory bowel disease (Wildin et al. 2001; Bennett et al. 2001), all attributed to the lack of this Treg cell subset otherwise required to suppress the activity of autoaggressive leukocytes. The acquisition of an nTreg phenotype appears to require high and persistent expression of Foxp3 to stabilize and amplify a Treg genetic program, which consists of regulatory target genes such as CTLA-4, CD25, IL-10, TGF- β and IL-35 (Gavin et al. 2007; Nomura and Sakaguchi 2007; Campbell and Ziegler 2007). Loss of even partial expression of Foxp3, therefore, might play a significant factor in the initiation or maintenance of chronic inflammatory states by resulting in the loss of Treg numbers and/or function.

Some studies in both autoimmune and allergic diseases have in fact suggested that disease activity may be inversely related with Treg number, functionality, or both. For instance, in type 1 diabetes, autoimmune polyglandular syndrome II, multiple sclerosis and perhaps also asthma and allergy, nTreg appear to be similar in number to healthy control subjects but may exhibit reduced suppressive activity (Battaglia et al. 2006; Brusko et al. 2005; Putnam et al. 2005; Lindley et al. 2005; Shi et al. 2004a; Kriegel et al. 2004; Viglietta et al. 2004; Bellinghausen et al. 2003; Lee et al. 2007; Shi et al. 2004b; Karlsson et al. 2004; Putheti et al. 2004). On the other hand, several other inflammatory diseases appear to exhibit normal number and function of nTregs, including ulcerative colitis, thyroiditis, and sarcoidosis (Yu et al. 2007; Marazuela et al. 2006; Miyara et al. 2006). In rheumatoid arthritis, nTreg in the synovial fluid actually appears to be higher in number than the peripheral blood, suggesting the presence of a negative feedback system at the site of inflammation (Mottonen et al. 2005; van Amelsfort et al. 2004), consistent with a Treg model in which cytokines highly present at inflammatory sites inhibit Treg activity, as has been suggested for IL-21, TNF- α , and IL-17 (Stockinger and Veldhoen 2007; van Amelsfort et al. 2007; Peluso et al. 2007). Thus, altered nTreg homeostasis may indeed be responsible, at least in part, for chronic inflammation in these diseases.

No studies to date, however, have demonstrated that significant alterations in Foxp3 expression levels or *FOXP3* polymorphisms account for Treg defects in these diseases. However, since most methods for Treg identification rely upon high, constitutive expression of Foxp3 (e.g., Tang and Bluestone 2008)), this lack of evidence may reflect limitations of current techniques. Conventional T cells may acquire a regulatory T cell phenotype in the periphery, generating induced or adaptive Treg (iTreg), which include at least IL-10 secreting Tr1 and TGF- β -secreting Th3 subsets (Roncarolo et al. 2006; Chen et al. 2003; Weiner 2001), and are associated with only a transient induction of Foxp3 – a phenomenon which has also been observed during the pro-inflammatory activation of conventional T cells (Allan et al. 2007; Walker et al. 2005). Furthermore, both Treg formation and optimal effector T cell (Teff) activation require the cytokine IL-2, suggesting the presence of a complex interplay between the pathways which induce and maintain suppressor versus effector activities (Stockinger 2007; Bettelli et al. 2007; Davidson et al. 2007; Laurence et al. 2007; Wang et al. 2007; Zorn et al. 2006). Therefore, several potentially Foxp3-independent pathways for the generation of iTregs exist, and yet Foxp3 appears to be at least part of an effector T cell (Teff) program; however, its importance in these non-nTreg populations remains largely unclear. Its role in

chronic inflammation therefore may extend beyond simply a fate-inducing or –maintaining gene for nTregs, but also to the homeostasis of aTregs and/or perhaps Teff function.

Foxo family members in chronic inflammation

The three most well-studied Foxo family members include Foxo1 (Fkhr), Foxo3a (Fkhr1) and Foxo4 (Afx), which are all mammalian homologues of the *Caenorhabditis elegans* longevity gene DAF-16 (reviewed in Peng 2008a). Their transcriptional activity is generally regulated by phosphorylation-dependent nuclear export, initiated upon cellular exposure to stimuli such as mitogens via the phosphoinositide 3-kinase (PI3K)-protein kinase B (PKB, Akt) pathway. In immune cells, Foxo1 in particular plays critical roles in the regulation of several effector functions, such as T cell homing by regulating the expression of L-selectin and other trafficking-related receptors such as Edg, CCR7 and IL-7R α (Ouyang et al. 2009; Kerdiles et al. 2009; Fabre et al. 2008). In B cells, Foxo1 is required to express IL-7R α at the pro-B cell stage, to induce recombinase activating gene (Rag)-1 and Rag-2 at the pre-B cell stage, and to mediate homing and class switch recombination in peripheral B cells via expression of L-selectin and activation-induced cytidine deaminase (Dengler et al. 2008; Amin and Schlissel 2008). As such, it is intriguing to speculate that upregulation of Foxo family members might participate in the pathogenesis of multiple inflammatory diseases.

However, studies in gene-targeted mice indicate that the role of the Foxo family members in inflammation is more complex, involving both regulatory and effector functions. Despite the findings above, Foxo1 deficiency also leads *in vivo* to spontaneous T cell activation and effector differentiation, as well as the enhanced ability to induce inflammatory bowel disease in a transfer model of (Ouyang et al. 2009). Likewise, Foxo3a deficiency leads to spontaneous lymphoproliferation, T cell hyperactivation, and a Sjögren's-syndrome like inflammation, especially of the salivary glands, in association with hyperactivity of the pro-inflammatory transcription factor NF- κ B and related pro-inflammatory target genes such as IL-2 and IFN- γ (Lin et al. 2004a). In the 16/6ld murine model of lupus, the inhibitory peptide hCDR1 ameliorates the disease in association with the induction of Foxo3a (Sela et al. 2006), and disease activity in at least some lupus patients correlates inversely with Foxo1 expression levels (Kuo and Lin 2007). Finally, in a mouse model of multiple sclerosis, the pro-inflammatory chemokine osteopontin appears to promote autoaggressive T cell activity by inhibiting Foxo3a (Hur et al. 2007). Thus, Foxo family members play critical roles in the suppression of T cell activation, at least of naïve autoreactive cells.

Mouse models of neutrophilic inflammation, including acute arthritis and peritonitis, require Foxo3a to suppress pro-apoptotic Fas ligand; without Foxo3a, the pro-inflammatory environment of the synovium elicits an apoptotic response in neutrophils (Jonsson et al. 2005). Analogously, neutrophils in rheumatoid arthritis patients express elevated levels of Foxo3a compared to healthy controls (Turrel-Davin et al. 2009). Rheumatoid arthritis synovium, however, exhibits differential phosphorylation of the Foxo family members among different cell types, such as fibroblast-like synoviocytes and macrophages, with a strong negative correlation between inactivation of FoxO4 in RA synovial tissue and increased serum C-reactive protein levels and a raised erythrocyte sedimentation rate (Ludikhuize et al. 2007). Such findings indicate that Foxo3a may play different functions in T cell versus neutrophil versus other inflammatory cell subsets.

Additional insight regarding the importance of Foxo family members in inflammation can be derived from its emerging role in the CD4 lymphopenia observed in chronic HIV infection. There, activity of Foxo3a appears responsible for the apoptosis of CD4⁺ T cells and macrophages, probably via the Tat-dependent activation of the Egr1-PTEN and/or PI3K-Akt1 pathways (Cui et al. 2008; Dabrowska et al. 2008). This likely involves specifically central

memory CD4 cells, which in turn may correspond with overall host fate to become an HIV+ elite controller versus an aviremic successfully treated subject (van Grevenynghe et al. 2008b). In one model, HIV-mediated immune suppression and/or leukopenia, perhaps associated with breakdown of the lymph node microenvironment, leads to decreased survival signals to T cells and perhaps B cells, leading to Foxo3a dephosphorylation and activation (reviewed in van Grevenynghe et al. 2008a). In this sense, Foxo3a appears to contribute to the potential for chronic inflammation by perpetuating viral pathology but at the same time, delimits overall inflammation by arresting or killing its host cell(s). Such observations indicate that the pro-versus anti-inflammatory roles of the Foxo family members therefore are highly cell- and context-dependent, but nonetheless mediate critical fate decisions within each specific context.

Other Fox family members

Increasing data with other Fox family members suggest potentially analogous roles in immunoregulation. Foxj1 (HNF4, FKHL13) and Foxd1 (BF-2, FREAC4, Hfh10, Hfhbf2), for instance, have been implicated in the homeostasis and suppression of naïve T cell activation, since mice with lymphoid deficiencies in either gene exhibit spontaneous, multiorgan, systemic inflammation associated with T cell hyperactivity and increased activity of NF- κ B and or NFAT and their target genes such as IL-2, IFN- γ and IL-4 (Lin et al. 2004b; Lin and Peng 2006), and Foxj1 deficiency further results in spontaneous and accentuated B cell activation and spontaneous autoantibody production (Lin et al. 2005). In addition, overexpression of Foxj1 ameliorates inflammation in the MRL/lpr lupus model (Srivatsan and Peng 2005), and polymorphisms in FOXJ1 have been implicated in susceptibility to lupus and possibly rheumatoid arthritis (Li et al. 2007). Indeed, in lymphocytes, Foxd1, Foxj1 and Foxo appear to participate in a regulatory network that maintains naïve lymphocyte quiescence and prevents spontaneous autoimmunity (Lin and Peng 2006). As a result, a growing number of Fox genes may turn out to play critical roles in the homeostasis of immune cells, and therefore be subject to dysregulation in chronic inflammatory diseases.

Conclusions and Future Prospects

These accumulating studies demonstrate highly varied roles for the forkhead transcription factors in the regulation of immunity and therefore likely also highly varied roles in chronic inflammatory diseases. Whereas Foxp3 may primarily play an “extrinsic” role in the regulation of inflammation by supporting the development of and maintaining the activity of Treg cells, potential “intrinsic” roles in the modulation of inflammatory genes, even in T_H17 cells, seem theoretically possible as supported by circumstantial expression data. Indeed, Foxo family members, especially Foxo1 and Foxo3a, appear to play key roles in the development, homing, and/or differentiation of lymphocytes, yet at the same time are required for the maintenance of T cell quiescence. Similar findings have emerged for two other Fox genes, Foxj1 and Foxd1, which also regulate the quiescence of mature T and/or B cells. These concepts are further supported by findings in human autoimmune diseases such as lupus and rheumatoid arthritis, where genetic polymorphisms and/or variations in expression of Fox genes appear to correlate with disease susceptibility and/or activity.

Although intriguing, such diverse pathways and mechanisms of activity suggest that the deliberate therapeutic manipulation of Fox genes may prove difficult in the clinical treatment of inflammatory diseases. For instance, inhibition of Foxo3 activity might be highly desirable for inflammatory arthritis (Jonsson et al. 2005), but may bear the risk of lymphoproliferative disease (Lin et al. 2004a). On the other hand, such risk-benefit issues are familiar to clinicians experienced with immunosuppressive therapies, such as with the TNF- α antagonists which are effective in inflammatory arthritis yet may convey an increased risk for lymphoma (e.g.,

Geborek et al. 2005); and at the same time, it may be possible to direct immunomodulation at specific cell types, such as has been accomplished for photodynamic therapy with antibody conjugates (e.g., van Dongen et al. 2004). Therefore, future studies will hopefully further elucidate the many context-specific roles of the Fox genes in inflammation, enabling further insight into the pathogenesis of and hopefully also future avenues for therapeutic intervention upon chronic inflammatory diseases.

Abbreviations

Fox	forkhead
PI3K	phosphoinositide 3-kinase
PKB	protein kinase B
RAG	recombinase activating gene
aTreg	adaptive regulatory T cell
nTreg	natural regulatory T cell
Teff	effector T cell
Treg	regulatory T cell

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