Fox transcription factors: from development to disease
Maria L. Golson and Klaus H. Kaestner*

ABSTRACT

Forkhead box (Fox) transcription factors are evolutionarily conserved in organisms ranging from yeast to humans. They regulate diverse biological processes both during development and throughout adult life. Mutations in many Fox genes are associated with human disease and, as such, various animal models have been generated to study the function of these transcription factors in mechanistic detail. In many cases, the absence of even a single Fox transcription factor is lethal. In this Primer, we provide an overview of the Fox family, highlighting several key Fox transcription factor families that are important for mammalian development.

KEY WORDS: Forkhead, Fox, Foregut development, Language acquisition, Pioneer factors, Transcription factors

Introduction

The forkhead (fkh) gene was originally identified in a random mutagenesis screen performed in Drosophila melanogaster (Weigel et al., 1989). This study showed that fkh is required for normal gut development, and that its absence results in a characteristic ‘forked head’ appearance resulting from the homeotic transformation of the foregut into a head structure. Soon after this discovery, a number of related genes – termed Fox genes – were identified in multiple organisms, ranging from yeasts to humans.

The Drosophila Fkh protein is characterized by a winged-helix DNA-binding domain ~100 residues long, termed the ‘forkhead box’. All Fox proteins share this distinctive DNA-binding domain but have divergent features and functions. Fox genes control a wide variety of biological functions and are broadly expressed both during development and in adult life. Their roles include, but are not limited to, the regulation of gut development (Ang and Rossant, 1994; Weinstein et al., 1994), stem cell and stem cell niche maintenance (Sackett et al., 2009; Aoki et al., 2016), the regulation of metabolism and cell cycle control (Hannenhalli and Kaestner, 2009). Indeed, Fox transcription factors are required for the normal specification, differentiation, maintenance and/or function of tissues such as the trophectoderm, liver, pancreas, ovaries, intestine, lung, kidney, prostate, brain, thyroid, skeletal and heart muscle, skeleton, vascular tissue and immune cells (Zhu, 2016).

Here, we first provide an overview of the Fox gene family and discuss how distinct Fox transcription factors regulate specific stages of development, tissue homeostasis and disease. Owing to their sheer number, we then concentrate on just four families: the FoxA factors to access closed chromatin (Fig. 3), thus allowing the recruitment of alternative histones and facilitating the subsequent binding of other transcription factors at nearby sites (Cirillo et al., 2002; Li et al., 2012b; Updike and Mango, 2006). Indeed, genome-wide mapping of FoxA binding sites and nucleosome architecture in the mouse liver has shown that FoxA binds both nucleosome-bound and nucleosome-free DNA targets with the same recognition site (Li et al., 2011). For this reason, FoxA family members have been shown to be important for mammalian development.

**Distinct protein domains, expression patterns and post-translational modifications contribute to the divergent functions of Fox family members**

Fox transcription factors bind a similar DNA sequence, albeit with different affinities, due to their highly conserved DNA-binding motif. How, then, do members of this large gene family have distinct roles? The divergent sequences outside of the conserved DNA-binding domain likely differentiate the function of these proteins, as do their distinct temporal and spatial gene activation patterns (Fig. 2).

The binding domains of FoxA transcription factors, for example, have structural similarity to linker histones H1 and H5 (Clark et al., 1993; Zaret et al., 2010). This feature allows FoxA transcription factors to access closed chromatin (Fig. 3), thus allowing the recruitment of alternative histones and facilitating the subsequent binding of other transcription factors at nearby sites (Cirillo et al., 2002; Li et al., 2012b; Updike and Mango, 2006). Indeed, genome-wide mapping of FoxA binding sites and nucleosome architecture in the mouse liver has shown that FoxA binds both nucleosome-bound and nucleosome-free DNA targets with the same recognition site (Li et al., 2011). For this reason, FoxA family members have been shown to be important for mammalian development.

termed ‘pioneer’ transcription factors (Cirillo et al., 2002). In this role, they help specify cell types by giving tissue-specific transcription factors access to their binding sites (Iwafuchi-Doi and Zaret, 2016). They also help maintain cell identity by acting as ‘place holders’ or ‘bookmarks’ at genes that are normally shut off during cell division; after cytokinesis is complete, cell type-specific genes previously marked by FoxA can be easily reactivated (Caravaca et al., 2013). Accordingly, a number of studies have shown that FoxA transcription factors are expressed in early development and play crucial roles in the development and homeostasis of various cells and tissues (see below).

Because of their actions as pioneer factors, FoxA proteins are required to facilitate the binding of many other transcription factors to their targets. This is especially evident for several nuclear receptors, such as androgen receptor (AR), glucocorticoid receptor (GR) and estrogen receptor (ER). This was first shown for the interaction between FoxA1 and AR in the prostate (Gao et al., 2003), then for ER and FoxA1 (Hurtado et al., 2011; Ross-Innes et al., 2012; Carroll et al., 2005; Lupien et al., 2008) and for FoxA2 and GR (Zhang et al., 2005). The consequences of this cooperative binding, particularly in the context of cancer, are discussed in detail below.

FoxM1 is best known for its role in regulating the cell cycle. Its forkhead DNA-binding domain (FHD) shares only 18% sequence identity with that of FoxA1, and FoxM1 has lower affinity for the forkhead consensus binding site than other Fox proteins (Littler et al., 2010). Some investigators have shown that, instead of directly interacting with the DNA of its proliferative targets, FoxM1 attaches to proteins in the DREAM complex – a larger conglomerate of proteins that prevents the transcription of proliferative targets in the quiescent state, but promotes expression of the same targets during the cell cycle (Chen et al., 2013). However, other reports have demonstrated direct binding of FoxM1 to its targets (Sanders et al., 2013).

Given its crucial function in cell cycle control, FoxM1 expression and activity must be tightly regulated. Indeed, Foxm1 mRNA and protein are only usually expressed during the cell cycle (Korver et al., 1997). The activity of FoxM1 is also tightly controlled by several post-transcriptional mechanisms (reviewed by Golson et al., 2010): (1) FoxM1 is generally excluded from the nucleus, but phosphorylation by MAPK induces its translocation; (2) an intramolecular repressive domain inhibits the binding of FoxM1 to DNA until phosphorylation by Chk2 (Chk2); (3) FoxM1 only recruits co-factors for gene transactivation when phosphorylated by Cdk1/2; and (4) FoxM1 is targeted to the proteasome when phosphorylated by a presently unknown kinase.

Like FoxM1, the activity of FoxO proteins – a group of proteins that inhibit the cell cycle and regulate lifespan and metabolism – is regulated post-translationally. Phosphorylation by Akt, for example, leads to the nuclear exclusion of FoxO1 and sequestration away from DNA by the 14-3-3 scaffolding protein (Tzivion et al., 2011). Unlike many other Fox transcription factors, FoxO factors contain both a nuclear export signal (NES) and a nuclear localization signal (NLS) (Tzivion et al., 2011). FoxO proteins help to activate transcription of their targets by recruiting the SWI/SNF chromatin remodeling complex (Riedel et al., 2013). These transcriptional targets include antioxidants, cell cycle inhibitors and metabolic genes; in many ways, FoxO proteins act counter to FoxM1.

Fig. 1. Phylogenetic tree of mouse Fox family members. The entire sequences of mouse Fox transcription factors were aligned pairwise using Geneious software. The following parameters were employed: global assignment with free end gaps, the Jukes-Cantor genetics distance model, and unweighted pair-group method with arithmetic mean. Differences with other phylogenetic trees of Fox transcription factors are likely the result of grouping by homology to the FKH DNA-binding domain only. Scale indicates the relative number of amino acid changes between proteins.
### Table 1. Summary of the functions of Fox family members in mice and roles in human disease

<table>
<thead>
<tr>
<th>Gene</th>
<th>Null mouse phenotypes</th>
<th>Developmental roles</th>
<th>Role in human disease</th>
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<tbody>
<tr>
<td><strong>Foxa1</strong></td>
<td>Early postnatal (P2-P14) lethality; hypoglycemia; dehydration</td>
<td>Establishes and maintains cellular identity in multiple endodermal-derived tissues including lung, liver, kidney, pancreas and prostate</td>
<td>Mutated or lost in prostate cancer; presence in ER-negative breast cancer correlates with a better prognosis but presence in ER-positive breast cancer correlates with a worse prognosis</td>
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<tr>
<td><strong>Foxa2</strong></td>
<td>Early embryonic lethality (E9-E10) due to lack of node; somite, neural tube, floor plate and motor neuron defects; heterozygote exhibits Parkinson’s-like phenotype due to loss of dopaminergic neuron maintenance</td>
<td>Establishes and maintains cellular identity in multiple endodermal-derived tissues</td>
<td>Downregulated or mutated in multiple cancers of epithelial origin</td>
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<tr>
<td><strong>Foxa3</strong></td>
<td>Hypoglycemia after long fast</td>
<td>Liver-specific gene expression maintenance</td>
<td></td>
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<tr>
<td><strong>Foxb1</strong></td>
<td>Variable embryonic lethality; high penetrance of postnatal lethality among survivors; motor weakness; midbrain abnormalities; lactation defect among female survivors</td>
<td>Neural tube and neuron process development</td>
<td></td>
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<tr>
<td><strong>Foxb2</strong></td>
<td>Uncharacterized</td>
<td></td>
<td></td>
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<tr>
<td><strong>Foxc1</strong></td>
<td>Perinatal lethality; hydrocephalus, edema, and eye, skull, cardiovascular system, kidney and skeletal defects</td>
<td>Skull, tooth, eye, cardiovascular, kidney, and hematopoietic stem cell development</td>
<td>Axenfeld-Rieger syndrome type 3; iris hypoplasia</td>
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<tr>
<td><strong>Foxc2</strong></td>
<td>Embryonic or neonatal lethality; thinned myocardium; abnormal spine and skull; distichiasis; increased brown fat; heterozygotes have lymphpatic node and vessel hyperplasia</td>
<td>Cardiac muscle, skeletal, iris and lymphatic system development</td>
<td>Lymphedema-distichiasis syndrome; promotes epithelial-to-mesenchyme transition and metastasis in breast, prostate and colon cancer</td>
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<tr>
<td><strong>Foxd1</strong></td>
<td>Embryonic lethality within 24 h of birth; defects in renal system development</td>
<td>Renal and eye development</td>
<td></td>
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<tr>
<td><strong>Foxd2</strong></td>
<td>Incompletely penetrant renal hypoplasia</td>
<td>Renal development</td>
<td>Autosomal dominant vitiligo</td>
</tr>
<tr>
<td><strong>Foxd3</strong></td>
<td>Embryonic (E6.5) lethality; lack of primitive streak; failure of gastrulation; expansion of extraembryonic tissue</td>
<td>Neural crest cell development and melanoblast differentiation; embryonic stem cell pluripotency</td>
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<tr>
<td><strong>Foxd4</strong></td>
<td>Uncharacterized</td>
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<td><strong>Foxe1</strong></td>
<td>Lethality within 48 h, with cleft palate, absent thyroid, and sparse, kinked hair</td>
<td>Thyroid development</td>
<td>Some mutations associated with thyroid dysgenesis, spiky hair and cleft palate; other mutations associated with thyroid cancer</td>
</tr>
<tr>
<td><strong>Foxe3</strong></td>
<td>Fusion of lens and cornea; other lens abnormalities</td>
<td>Lens development; proliferation, cell cycle, and apoptosis in lens</td>
<td>Anterior segment dysgenesis and congenital absence of a lens</td>
</tr>
<tr>
<td><strong>Foxf1</strong></td>
<td>Embryonic lethality at ∼E9; abnormalities in somite and posterior development as well as in extraembryonic tissues and lateral plate mesoderm; haploinsufficient mice on certain genetic backgrounds die perinatally with pulmonary defects</td>
<td>Pulmonary and gut development; liver stellate cell activation</td>
<td>Misalignment of pulmonary veins; gastrointestinal abnormalities</td>
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<tr>
<td><strong>Foxf2</strong></td>
<td>Lethality within first 2 h of life due to cleft palate</td>
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<td><strong>Foxg1</strong></td>
<td>Perinatal lethality due to lung defects; reduced cerebral size; eye defects</td>
<td>Neuronal differentiation; cell cycle progression</td>
<td>Rett syndrome and other forms of mental retardation; microcephaly and other brain abnormalities</td>
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<tr>
<td><strong>Foxh1</strong></td>
<td>Perinatal lethality with variable patterning defects; variable right isomerism leading to defects in heart, lungs and stomach and asplenia; cyclopia; microcephaly; absent jaw</td>
<td>Regulation of body patterning, including left-right asymmetry</td>
<td>Congenital heart disease and ventricular septal defects</td>
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<td><strong>Foxi1</strong></td>
<td>50% perinatal lethality; inner ear and renal defects; 25% of heterozygotes exhibit perinatal lethality</td>
<td>Renal and inner ear development</td>
<td>Pendred syndrome</td>
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<tr>
<td><strong>Foxi2</strong></td>
<td>Decreased circulating glucose</td>
<td></td>
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<tr>
<td><strong>Foxi3</strong></td>
<td>Lethality starting at E9.5 through perinatal life; lack whiskers and a mouth; absence of inner, middle and outer ear; increased cranial neural crest apoptosis</td>
<td>Differentiation of branchial arch-derived skeletal structures</td>
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<tr>
<td><strong>Foxj1</strong></td>
<td>Perinatal lethality; defective ciliogenesis and random left-right asymmetry; growth failure</td>
<td>Regulation of left-right asymmetry; T-lymphocyte quiescence</td>
<td>Allergic rhinitis</td>
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<tr>
<td><strong>Foxj2</strong></td>
<td>Uncharacterized</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Foxj3</strong></td>
<td>Decreased muscle mass and recovery after injury</td>
<td>Mitochondrial biogenesis</td>
<td></td>
</tr>
</tbody>
</table>

Continued
Although most Fox transcription factors are strictly transcriptional activators, some, such as FoxP, have dual activator and repressor functions; indeed, members of the FoxP family are thought to act primarily as repressors (Zuo et al., 2007; Shu et al., 2001; Li et al., 2004a). FoxP family members can bind as homo- or heterodimers through their leucine zipper and zinc finger domains, and this interaction is required for FoxP family members to repress their targets, perhaps because a conformational change occurs upon binding that allows a portion of the N-terminal domain to recruit co-repressors such as histone deacetylases, the lysine acetyltransferase TIP60 (Kat5), and the SMRT complex (Li et al., 2007; Wang et al., 2003; Lal and Bromberg, 2009; Jepsen et al., 2008). The proline-
rich track within the N-terminus of FoxP3 is essential for its function as a repressor (Xie et al., 2015), and this suggests that the glutamine-rich tracts in FoxP1, 2 and 4 are essential for their function. The structure of FoxP proteins when dimerized prevents them from binding the same strand of DNA on adjacent sites, suggesting that FoxP factors could also act to bring distal chromatin regions together (Stroud et al., 2006). Like FoxM1, recent reports have suggested that FoxP factors act in some cases by binding to other proteins rather than via direct interactions with DNA (Xie et al., 2015).

In addition to divergent protein domains, individual Fox factors have different binding partners and co-factors, which can influence both the specific DNA targets that are contacted and their downstream effects on transcriptional activity (Li et al., 2015b). Finally, many Fox transcription factors are expressed in distinct spatiotemporal patterns, allowing them to carry out distinct functions. However, it should be noted that, despite the well-known distinct roles of various families of Fox transcription factors, it is becoming clear that many of them regulate the same processes.

**The FoxA family: regulators of development, differentiation and cell identity**

Mammalian FoxA transcription factors were first identified for their DNA-binding properties in rat liver nuclear extracts and were thus originally named hepatocyte nuclear factor 3 (HNF3) α, β and γ (Costa et al., 1989). Of all mammalian Fox genes, Foxa2 shares the most homology with the original fkh gene discovered in *Drosophila*. Its homolog in the nematode *C. elegans* is *pha-4* and, notably, studies of *pha-4* mutants have helped further our understanding of FoxA function by identifying FoxA targets (Gaudet and Mango, 2002), establishing their interactions with nuclear hormone receptors (Ao et al., 2004), demonstrating the recruitment of RNA polymerase II (Hsu et al., 2015) and the histone variant H2A.Z (Updike and Mango, 2006), and characterizing the regulation of PHA-4 by the TOR pathway.

**The expression of FoxA factors**

In mammals, FoxA1, 2 and 3 exhibit overlapping but distinct expression patterns in a variety of developing and mature tissues (Friedman and Kaestner, 2006). In the mouse, Foxa2 is the first member of the FoxA family to be expressed. At embryonic day (E) 6.5, Foxa2 expression can be detected in the primitive streak and in the node, both of which are important for gastrulation. By E7.5, Foxa2 is expressed in the mesoderm and definitive endoderm (Monaghan et al., 1993; Ang et al., 1993). Its expression is then maintained in endoderm-derived tissues, such as the pancreas, liver, thyroid, prostate and lung, throughout development and in adulthood (Friedman and Kaestner, 2006), and is also observed in ectoderm-derived neural tissues, such as the ventral midbrain, including in dopaminergic neurons and the hypothalamus (Bensard et al., 2004).

During early embryogenesis, the expression of Foxa1 is similar to that of Foxa2, but following a short temporal delay. For example, Foxa1 can first be detected at E7.0 in the primitive streak, and then later in the notochord, neural plate, floor plate and neural tube (Monaghan et al., 1993). However, the expression of Foxa1 and of Foxa2 differ in the adult. Although Foxa1 is initially highly expressed in the developing pancreas, its expression falls to <10% of Foxa2 levels in alpha, beta and acinar cells in the adult pancreas (Bramswig et al., 2013). In addition, Foxa1 is more widely expressed than Foxa2 in several adult tissues, including the respiratory system, brain and gastrointestinal tract. Foxa1 is also expressed in some tissues that lack FoxA2 entirely, such as male reproductive organs, the ureter and bladder (Friedman and Kaestner, 2006).

The expression of Foxa3 is more restricted than that of Foxa1 or Foxa2, and is more specific to the foregut endoderm than other family members. Foxa3 expression can first be detected at E8.5 and is maintained strongly in the liver but also in the pancreas and intestine throughout adulthood (Monaghan et al., 1993). It is the mostly highly expressed FoxA transcription factor in the adult liver (Kaestner et al., 1994).

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**Fig. 3. FoxA proteins function as pioneer factors.** The schematic depicts how FoxA transcription factors are able to function as pioneer factors that control gene expression via their interaction with chromatin.
The role of FoxA transcription factors

The earlier expression of FoxA2 compared with FoxA1 and FoxA3 is reflected in the severity of phenotypes in mice lacking these factors. Mice null for Foxa2 die between E10 and E11, exhibiting defects in all three germ layers (Weinstein et al., 1994; Ang and Rossant, 1994). Heterozygotes for Foxa2 are viable but display a Parkinson’s-like phenotype following aging (Kitappa et al., 2007). In contrast to Foxa2 null mice, those lacking Foxa1 survive until after birth, displaying lethality between postnatal day (P) 2 and 12 due to hypoglycemia and defects in kidney function (Behr et al., 2004; Kaestner et al., 1999); the hypoglycemia is likely to result from deficiencies in glucagon secretion, while the dehydration stems from abnormal kidney development (Behr et al., 2004; Kaestner et al., 1999). These mice also display defects in prostate morphogenesis (Gao et al., 2005). As might be expected from its limited expression pattern, among the FoxA family mice deficient for Foxa3 have the mildest phenotype. They are viable with a normal lifespan but do, however, display hypoglycemia after a prolonged fast because of defects in hepatic glucose production (Shen et al., 2001).

Since the embryonic lethality of Foxa2−/− mice precludes analysis of the role of FoxA2 in the organogenesis and function of many tissues, mice with conditional deletions of Foxa2 have been derived. Studies of these mutants reveal that FoxA2 on its own is not required for normal liver differentiation (Sund et al., 2000), although defects in lung morphogenesis are seen (Wan et al., 2004). In addition, severe defects in pancreatic islet formation and alpha and beta cell maturation that lead to alterations in glucose homeostasis are observed (Sund et al., 2000; Lantz et al., 2004). Interestingly, mice expressing an activated form of FoxA2 in neurons display an orexigenic (i.e. a stimulated appetite) phenotype (Silva et al., 2009). Although off-target effects of this mutated protein cannot be excluded, this study implicates FoxA2 in yet more aspects of metabolic regulation, namely food intake and energy output.

Cooperativity and compensation among FoxA transcription factors

The conditional deletion of genes encoding individual FoxA transcription factors revealed little requirement for any one FoxA family member in the liver (Lee et al., 2005b; Kaestner et al., 1999; Shen et al., 2001). Gross pancreatic morphology was also unaffected when only one FoxA transcription factor was missing (Lee et al., 2005b; Kaestner et al., 1999). These studies suggest that FoxA family members are dispensable in these organs or, alternatively, that they can compensate for each other. Both in vivo and in vitro studies suggest that the latter possibility is likely: both Foxa1 and Foxa2 transcription factors must be suppressed to abolish expression of Muc2, which encodes a protein important for intestinal function (van der Sluis et al., 2008), and both Foxa1 and Foxa2 are upregulated in Foxa3 null livers (Shen et al., 2001). In addition, several different analyses using the conditional, simultaneous deletion of Foxa1 and Foxa2 demonstrated that these two transcription factors can compensate for each other in a number of tissues. For example, their combined absence results in complete liver agenesis (Lee et al., 2005a), near-complete pancreatic agenesis (Gao et al., 2008), and altered allocation of enteroendocrine cells within the intestine (Ye and Kaestner, 2009), but, as outlined above, deletion of only one FoxA transcription factor leads to a less severe phenotype in these tissues. Finally, mice with a late-gestation deletion of both Foxa1 and Foxa2 demonstrate upregulation of Foxa3, with Foxa3 also being observed to bind FoxA targets in the double-null animal that were bound only by FoxA1 and FoxA2 in wild-type mice (Iwafuchi-Doi et al., 2016).

FoxM1: a key cell cycle control factor

FoxM1 was identified nearly simultaneously by three groups and hence was originally given three names: Trident (Korver et al., 1997), hepatocyte nuclear factor 3/fork head homolog 11 (Ye et al., 1997) and WIN (winged helix protein in the INS1 cell line) (Yao et al., 1997). All three groups identified FoxM1 by homology to FoxA proteins, but whereas the Clevers group discovered it within the thymus, the Costa lab cloned it from the colon carcinoma cell line Caco-2, and the Wong group identified it in a cell line derived from an insulinoma.

FoxM1 is widely recognized for its role in driving the cell cycle (Fig. 4). Its direct transcriptional targets function at both the G1/S and G2/M transitions, as well as during karyokinesis and cytokinesis (reviewed by Wierstra, 2013; Wierstra and Alves, 2007). Accordingly, FoxM1 expression is mostly confined to actively replicating cells; its expression is thus broad in embryos and declines in differentiated tissue as well as with age (Ye et al., 1997).

FoxM1 exists in various genera and species, including Xenopus, Danio, Mus, Ratius and Homo sapiens, but not in C. elegans or Drosophila. The role of FoxM1 in Drosophila and C. elegans might be filled by other forkhead transcription factors, but at this time the only reports associating forkhead with proliferation in these two organisms is the increased replication in the absence of FoxO homologs. In humans, although one FOXM1 gene exists, splice variants produce three different FOXM1 proteins: FOXM1A, FOXM1B and FOXM1C. Both FOXM1B and FOXM1C are transcriptional activators, whereas FOXM1A is a transcriptional repressor. In mice, only one FoxM1 protein splice variant is produced; it is most similar to human FOXM1B and is likewise a transactivator.

The crucial role of FoxM1 in development is highlighted by studies perturbing its expression. For example, mice lacking FoxM1 display embryonic lethality between E14.5 and E16.5 due to failed liver and heart expansion (Krupczak-Hollis et al., 2004). Mice with conditional deletions of Foxm1 display profound proliferation defects in tissues such as the liver (Krupczak-Hollis et al., 2004), heart (Bolte et al., 2011), pancreas (Zhang et al., 2006), intestine (Yoshida et al., 2007), lungs (Kalin et al., 2008) and smooth muscle...
transplantation-quality donor tissue by rejuvenating older donor tissue. However, as is the case for other proteins involved in the cell cycle, the benefits of activating or attenuating FoxM1 activity must be carefully considered. Drug treatments are currently not targeted to any one tissue, and activating FoxM1 endogenously to rejuvenate the replicative potential in a tissue of interest without targeting it to a specific cell type could potentially cause existing malignancies to become more prone to growth or metastasis. Conversely, inhibiting FoxM1 in cancer therapy could have negative impacts in tissues that are likely to require FoxM1 activity and exhibit high cellular turnover, such as the intestine.

**FoxO factors: from cell cycle control to metabolism and longevity**

FoxO proteins play multiple crucial roles: they regulate the cell cycle, apoptosis, metabolism and lifespan. Recently, interest in FoxO proteins has also been spurred on by their functions in mediating insulin and insulin-like signaling (Fig. 5) (reviewed by Golson et al., 2010). In short, insulin binding to the insulin receptor causes phosphorylation of insulin receptor substrate 1/2 (IRS1/2), resulting in a phosphorylation signaling cascade that involves phosphoinositide 3-kinase and Akt, and ultimately leads to the phosphorylation of FoxO. In the absence of insulin signaling, FoxO proteins reside in the nucleus; however, active insulin signaling causes them to translocate to the cytoplasm, where they are no longer able to bind or transactivate their targets. In addition, Akt-phosphorylated FoxO proteins are stabilized in the cytoplasm through interactions with 14-3-3 scaffolding proteins (reviewed by Tzivion et al., 2011). This stabilization can be disrupted by the phosphorylation of 14-3-3 by Jun kinase and the dephosphorylation of FoxO by protein phosphatase 2A. FoxO protein stability is also regulated by ERK1/2 (Mapk3/1), which phosphorylate FoxO proteins and target them for degradation (Yang et al., 2008).

**FoxO in C. elegans**

The role of FoxO proteins in longevity was first revealed by studies in the nematode *C. elegans*. During periods of high stress, such as a low food supply, *C. elegans* enter a ‘dauer’ state that allows them to survive and also extend their lifespan (reviewed by Fielenbach and Antebi, 2008). In such times of nutrient shortage, expression of insulin receptor homologs such as DAF-2 is low. The sole *C. elegans* FoxO homolog, DAF-16, is therefore not phosphorylated and is thus able to enter the nucleus and transactivate its targets, a full list of which was recently published (Kaletsky et al., 2016). The effect of DAF-16 on longevity is primarily manifested in the intestine (Murphy et al., 2007; Libina et al., 2003), and its effects on lifespan are likely to be related to the regulation of genes involved in countering oxidative and thermal stress (Nemoto and Finkel, 2002). DAF-16 also regulates multiple neuronal processes, including many different learning processes, sleep, morphology maintenance and axon regeneration (Kauffman et al., 2010; Tank et al., 2011; Toth et al., 2012; Murakami et al., 2005; Byrne et al., 2014; Nagy et al., 2014). A recent study delineated the neural targets of DAF-16 in *C. elegans* by comparing the transcriptomes of neurons that had been FACS sorted from wild type and insulin signaling-deficient (daf-16;daf-2) mutants (Kaletsky et al., 2016). Since many FoxO targets are conserved from *C. elegans* to humans (Webb et al., 2016), it has been proposed that understanding the mechanisms by which FoxO regulates aging in the nematode might provide a basis for extending human lifespan. However, given the fundamental differences in the aging process between these very distantly related species, caution is warranted.

**Box 1. Anti-FOXM1 agents as potential cancer therapies**

Owing to the association of FOXM1 with aggressive tumors, and because of direct evidence highlighting the importance of FoxM1 in tumor progression in mice, there is intense interest in developing anti-FOXM1 agents as therapies for a variety of cancers. The downregulation of FOXM1 by siRNA in vitro decreases DNA replication as well as angiogenic and metastatic potential (Wang and Gartel, 2011; Wu et al., 2010; Halasi and Gartel, 2012; Halasi et al., 2013). A number of proteasome inhibitors have been shown to decrease FOXM1 levels, probably by stabilizing an unidentified negative regulator of FOXM1 (Gartel, 2010), and many of these inhibitors are currently used in cancer treatments; most of their effects are likely to be due, at least in part, to FOXM1 downregulation. However, these drugs are also associated with serious side effects (Adams et al., 1999), so more specific inhibitors of FOXM1 have been sought. Recently, a high-throughput screen identified a small molecule, FDI-6, that makes direct contact with the DNA-binding domain of FOXM1, blocks the interactions of FOXM1 with its transcriptional targets, and suppresses the expression of those targets (Gormally et al., 2014). FDI-6 is specific enough that it does not affect the binding or function of other Fox transcription factors, and it also does not affect proteasomal activity. This novel molecule thus has exciting potential therapeutic applications for a variety of cancers.
FoxO in mammals

Mammals have four FoxO proteins: FoxO1, FoxO3, FoxO4 and FoxO6. FoxO6 shares the least sequence homology with other FoxO family members. FoxO1 is the most thoroughly studied of the family but, like FoxO1, FoxO3 and FoxO4 have roles in regulating lifespan and metabolism and in mediating cell cycle arrest.

Regulation of metabolism by FoxO1

FoxO1 is the most highly expressed FoxO family member in insulin-responsive tissues such as the liver, adipose tissue and skeletal muscle (Armoni et al., 2006). Consistent with this broad expression pattern, FoxO1 regulates multiple metabolic processes. In the liver, FoxO1 contributes to the activation of gluconeogenic targets (Nakae et al., 2002; Matsumoto et al., 2007; Titchenell et al., 2015; Haesler et al., 2010), and deleting one copy of Foxo1 corrects the insulin resistance phenotype in insulin receptor-deficient mice (Nakae et al., 2002). In skeletal muscle, FoxO1 appears to control whether carbohydrates or lipids are used as fuel by regulating the expression of genes such as those encoding pyruvate dehydrogenase kinase and lipoprotein lipase (Bastie et al., 2006). Consistent with this broad expression pattern, FoxO1 regulates multiple metabolic processes.

In addition to liver, muscle and adipose tissue, FoxO1 is highly expressed in insulin-secreting beta cells, where it may act in a protective capacity in times of stress. Several reports have indicated that FoxO proteins activate the expression of antioxidant enzymes, and FoxO1 protects beta cells against the effects of reactive oxygen species, since it and family members activate the expression of antioxidant enzymes (Kitamura et al., 2005; Kops et al., 2002; Nemoto and Finkel, 2002). FoxO1 has also been implicated in preventing beta cell de-differentiation during stress by suppressing neogenic genes, such as the early endocrine development factor neurogenin 3 (Neurog3), which is not normally expressed in the adult endocrine pancreas (Talchhai et al., 2012). Protection by FoxO1 occurs in the presence of many metabolic stressors, such as multiple pregnancies, chemical ablation of beta cells, and when insulin resistance is conferred by leptin receptor (Lepr) deficiency. However, a contradictory study of mice deficient for Lepr in all tissues or for FoxO1 specifically in beta cells indicates that FoxO1 promotes the expression of the same genes (Kobayashi et al., 2012). The reason for this discrepancy is not apparent at this time, and both studies demonstrated more severe hyperglycemia in Lepr−/− mice lacking FoxO1 compared with those with FoxO1 expression. Previous work demonstrating the induction of the beta cell maturity marker MafA by FoxO1 also supports a role for FoxO1 in preventing de-differentiation (Kitamura et al., 2005). FoxO1 may thus protect beta cells from dysfunction during the period of insulin resistance that precedes type 2 diabetes.

A second role proposed for FoxO1 is in regulating beta cell mass. FoxO proteins have been shown to upregulate cell cycle inhibitors (Martins et al., 2015). In mice lacking one copy of the insulin receptor in all tissues, beta cell proliferation is reduced compared with that in wild-type mice, but deletion of one copy of Foxo1 partially rescues beta cell division (Nakae et al., 2002). Conversely, Foxo1 overexpression attenuates the increased beta cell mass normally observed in mice overexpressing the insulin receptor (Okamoto et al., 2006). However, contradictory reports have called the generality of these observations into question. Mice lacking Foxo1 either in beta cells or throughout the entire pancreas show no increase in beta cell proliferation either on a chow or high-fat diet (Kobayashi et al., 2012), and mice overexpressing FoxO1 fed a high-fat diet actually showed increased beta cell proliferation (Zhang et al., 2016). These results suggest that FoxO1 might inhibit beta cell replication only when the insulin receptor is completely absent, which is a unique and rare state.

FoxO in mammalian longevity

Like DAF-16 in C. elegans, FoxO transcription factors together with calorie restriction and insulin signaling have been reported to regulate lifespan in rodents (Mulvey et al., 2014; Shimokawa et al., 2015). For example, decreased insulin signaling correlates with human longevity (Kojima et al., 2004; Pawlikowska et al., 2009), as do several genetic variants in FOXO3 (Willcox et al., 2008; Pawlikowska et al., 2009; Flachsbart et al., 2009; Li et al., 2009). In mice, FoxO3, but not FoxO1, is required for an expanded lifespan due to calorie restriction (Shimokawa et al., 2015). However, a meta analysis calls this conclusion for calorie restriction into question (Swindell, 2012). First, in some mouse strains, life expectancy was actually shortened in cohorts with calorie restriction (Liao et al., 2010; Swindell, 2012). Second, ad libitum fed controls might not be an ideal comparison for rodents with calorie restriction; ad libitum access to normal chow leads to weight gain and associated detrimental health effects (Sohal and Forster, 2014). Mixed results have also been reported for non-human primates (Colman et al., 2009; Bodkin et al., 2003; Mattison et al., 2012), and studies correlating calorie restriction and longevity are hard to perform accurately in humans and thus far have been inconclusive (Heilbronn and Ravussin, 2003).

At present, the mechanisms by which FoxO3 or other FoxO transcription factors influence lifespan, if at all, in humans is still unknown. However, one could envision that the multiple processes in which FoxO plays a role, such as stress resistance, cell cycle regulation and control of apoptosis, could pleiotropically influence healthy aging.
The FoxP family: language acquisition and cognitive function

In mammals there are four FoxP genes (Foxp1-4), and the transcription factors that they encode have been shown to play a role in the development of multiple cell types, including cardiomyocytes (Wang et al., 2004), neurons (Shu et al., 2005), lung epithelial secretory cells (Li et al., 2012a) and regulatory T-cells (Fontenot et al., 2003). Accordingly, FoxP null mice display varying phenotypes. Foxp1−/− (Wang et al., 2004) and Foxp4−/− (Li et al., 2004b) mice display embryonic lethality by E14.5 due to a thinning of the cardiac ventricular myocardium. Foxp2−/− mice display severe cerebellar defects and motor impairment; they usually die by 3 weeks of age (Shu et al., 2005). Foxp3−/− mice have a defect in regulatory T-cells and elevated lymphocyte proliferation rates; these combined abnormalities lead to an immune attack on multiple cells and organs, including pancreatic beta cells, resulting in a disease resembling type 1 diabetes (Fontenot et al., 2003), and Foxp3−/− mice die by 4 weeks of age (Fontenot et al., 2003). Tissue-specific deletions of FoxP factors also result in developmental defects. For example, mice with a deletion of Foxpl in neurons are viable but display a morphological change in the striatum and hippocampus (Bacon et al., 2015).

Members of the FoxP family, notably FoxP1 and FoxP2, have also generated interest because of their roles in regulating cognitive development processes such as speech acquisition. FoxP2 was the first of this transcription factor family to be associated with language deficits (Lai et al., 2001) but, more recently, FoxP1 has also been implicated in speech development (Horn et al., 2010; Hamdan et al., 2010). Mutations in both FOXP1 and FOXP2 are associated with other cognitive dysfunctions, such as autism spectrum disorder (ASD) and intellectual disability (Bacon and Rappold, 2012). However, disorders associated with the two genes do not have completely overlapping symptoms, indicating that the two transcription factors might regulate different but related brain functions. For example, language deficits caused by alterations in Foxp2 are generally accompanied by deficits in orofacial movements, whereas impairments in language acquisition associated with Foxp1 variants are always accompanied by another cognitive impairment (Bacon and Rappold, 2012). Currently, no known connections between cognitive function and Foxp3 or Foxp4 exist.

How FoxP1 and FoxP2 contribute to neural function has also been investigated in animal models. Normally, mouse pups subvocalize when separated from their mother; Foxp2−/− pups do not exhibit this behavior, and Foxp2−/− pups show a reduction (Shu et al., 2005). No alterations in vocalization were reported for mice with a brain-specific deletion of Foxp1; however, these mice exhibit abnormal cognitive and social behavior, echoing phenotypes in patients with FOXP1 mutations (Bacon et al., 2015). In a striking example of evolutionary conservation, FoxP1 function has been studied in songbirds. Mouse subvocalization is innate, whereas human speech and birdsong share the necessity that they must be learned from older members of the species. After a FOXP2 mutation was identified in a family with inherited impaired speech acquisition, the expression patterns of Foxp1 and Foxp2 were investigated in zebra finch brains (Teramitsu et al., 2004). Similarities in the expression patterns of Foxp1 and Foxp2 were observed between songbird and human brains, and Foxp2 was upregulated during the period when adolescent finches actively learned song patterns (Haesler et al., 2007). When Foxp2 gene activity was suppressed during adolescence, the affected birds copied their tutors with less precision than controls. These studies highlight a remarkable conservation of function in Fox transcription factor function between disparate species.

Shared and cooperative roles for Fox transcription factors

Although Fox transcription factors have distinct expression patterns and are known for fulfilling different roles in regulating biological processes, many of these transcription factors often have similar roles. As mentioned above, FoxA and FoxO transcription factors both regulate glucose homeostasis and metabolism. However, FoxM1 (Golson et al., 2015) as well as FoxP1, FoxP2 and FoxP4 (Spaeth et al., 2015) were recently reported to contribute to these processes as well. Another overlap is the action of these proteins as pioneer factors; both FoxO (Hatta and Cirillo, 2007) and FoxE (Cuesta et al., 2007), in addition to members of the FoxA family, can act in this capacity.

Notably, a number of Fox transcription factors have been implicated in regulating cell proliferation. FoxM1 and FoxO, for example, have long been known to have opposing roles in the cell cycle and tumorigenesis. Many other Fox transcription factors, such as FoxC2, FoxE3, FoxF1, FoxF2, FoxN1 and FoxN3, also regulate proliferation (Tuteja and Kaestner, 2007b; Tuteja and Kaestner, 2007a). FoxA2 acts as a tumor suppressor by maintaining a differentiated state and decreasing metastasis in liver, lung and breast tissue (Tang et al., 2011; Wang et al., 2014b; Zhang et al., 2015), while FoxA1 acts as an oncogene in breast and prostate cancer (Yamaguchi et al., 2008; Imamura et al., 2012). Remarkably, in the liver, the FoxA proteins act as both repressors and promoters of hepatic carcinogenesis, dependent on the sex of the animals (Li et al., 2012c). Thus, while male mice deficient for both FoxA1 and FoxA2 develop fewer tumors, the situation is opposite in female mice, demonstrating the key role of FoxA factors in the action of the sex steroid hormone receptors.

Diverse Fox transcription factors also interact with estrogen receptor α (ERα; also known as ESR1) to regulate multiple aspects of tumorigenesis. In the MCF7 human breast cancer cell line, FOXA1 acts as a pioneer transcription factor and opens up chromatin, allowing the nearby binding of ERα (Hurtado et al., 2011). At cell cycle loci, FOXM1 can then displace FOXA1 and transactivate cell cycle genes. FOXM1 binds 70% of the same genes as FOXA1 in this breast cancer line (Sanders et al., 2013). Interestingly, FoxO transcription factors act as ERα status-dependent tumor suppressors in breast cancer. In ERα-positive breast cancer, FOXO3 is associated with less invasiveness, whereas in ERα-negative breast cancer, FOXO3 is associated with more invasive tumors (Sisci et al., 2013). Finally, the FoxA homolog PHA-4 contributes to increased longevity in C. elegans (Panowski et al., 2007). As with FoxO proteins, higher nutrient levels lead to the repression of PHA-4 activity and a decreased lifespan, and in this function FoxA is negatively regulated by the TOR pathway (Sheaffer et al., 2008).

Because many Fox transcription factors are required for life, they clearly are unable to compensate completely for each other. However, their highly related consensus binding sites suggest that they can substitute for each other to some degree. It is likely that some of the overlapping roles for Fox proteins reflect differences in expression patterns, such that one Fox protein might perform the same role in the gut that another performs in neural tissues. In other cases, it is likely that distinct Fox proteins act in somewhat divergent ways at the same loci, for example by recruiting different co-factors.

Conclusions

Fox transcription factors are remarkably well conserved DNA-binding proteins and regulators of gene expression. In mammals,
diverse Fox factors share multiple roles. This ancient class of transcription factors contributes to the control of all aspects of development, from before gastrulation to the prevention of adult disease. Indeed, Fox transcription factors constitute a promising drug target considering their involvement in so many diseases. However, because they are transcription factors and hence are not accessible at the cell surface, or even generally in the cytoplasm, they have thus far largely remained unalterable, whether at the expression or activity level. Future studies to target Fox transcription factors should be aimed in the following directions: (1) the cell type-specific delivery of a drug payload that would be internalized; (2) gaining an understanding and then targeting of the regulatory mechanisms of Fox expression; (3) the identification and targeting of Fox target genes. Such approaches will, no doubt, further our understanding of Fox transcription factors in human biology and disease.

Competing interests
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