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Citation for published version:

Digital Object Identifier (DOI):
10.1242/dev.153163

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Development

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Wilms’ tumour 1 (WT1) in development, homeostasis and disease

Nicholas D. Hastie*

ABSTRACT

The study of genes mutated in human disease often leads to new insights into biology as well as disease mechanisms. One such gene is Wilms’ tumour 1 (WT1), which plays multiple roles in development, tissue homeostasis and disease. In this Primer, I summarise how this multifaceted gene functions in various mammalian tissues and organs, including the kidney, gonads, heart and nervous system. This is followed by a discussion of our current understanding of the molecular mechanisms by which WT1 and its two major isoforms regulate these processes at the transcriptional and post-transcriptional levels.

KEY WORDS: WT1, Developmental disorders, Homeostasis, Molecular mechanisms of disease

Introduction

The Wilms’ tumour 1 (WT1) gene was first identified in 1990 as a strong candidate predisposition gene for Wilms’ tumour (Call et al., 1990; Gessler et al., 1990), which is a paediatric kidney cancer that affects 1 in 10,000 children (Charlton and Pritchard-Jones, 2016). Since then, numerous studies have confirmed that WT1, which maps to chromosome 11p13, is mutated in the germline or somatically in ∼15% of Wilms’ tumour cases (Charlton and Pritchard-Jones, 2016). Wilms’ tumour has fascinated pathologists for over a century as it is one of the classic examples of how cancer arises through development gone awry (Hastie, 1994). WT1 behaves as an archetypal tumour suppressor gene, as both alleles need to be deleted or inactivated for tumours to develop (Knudson and Strong, 1972). However, it is not as simple as this because the majority of tumours with WT1 mutation also have gain-of-function mutations in the β-catenin (CTNNB1) gene and a proportion have a double dose of IGF2 through chromosome 11 loss of heterozygosity (Huang et al., 2016). Moreover, WT1 is expressed in a wide range of adult tumour types, including those derived from epithelial, mesenchymal, haematopoietic and neuronal tissue, even though it is not expressed in the corresponding healthy tissue, and this has led to the proposition that WT1 functions as an oncogene in these tumours. At present, there is scant evidence to support this concept. However, this widespread tumour expression has led to WT1 being the number one target for cancer immune therapy (Nishida and Sugiyama, 2016).

Although our understanding of the molecular and cellular mechanisms by which tumours arise through WT1 mutation is incomplete, studies of the WT1 gene over the past 25 years have led to broad insights into a number of phenomena. These include: (1) the mechanisms underpinning the development, homeostasis and disease of tissues arising from the intermediate and lateral plate mesoderm; (2) cellular switching events during development, particularly those involving mesenchyme-to-epithelial transitions (MET) and the reverse process, epithelial-to-mesenchyme transition (EMT); (3) the cellular origins of mesenchymal progenitors for a variety of tissue types, pinpointing the key role of the mesothelium; and (4) fundamental aspects of transcription and epigenetic regulation. WT1 is also an example of how protein isoforms differing by just a few amino acids may have profoundly different functions. Here, I provide an overview of the WT1 gene, highlighting how it functions in the development and homeostasis of various organs and tissues, and how its mutation can lead to disease.

WT1 structure, evolution and isoforms

The mammalian WT1 gene is ∼50 kb in length, encoding proteins from as many as ten exons. There are at least 36 potential mammalian WT1 isoforms, the diversity created through a combination of alternative transcription start sites, translation start sites, splicing and RNA editing (Fig. 1A). All isoforms include four C2H2 Kruppel-like zinc fingers similar to those found in the SP1 family of transcription factors. All non-mammalian vertebrates express only two isoforms, which differ by just three amino acids (lysine, threonine and serine; KTS) inserted by an alternative splice between zinc fingers 3 and 4 (Fig. 1B). Outside the vertebrates, there appears to be a WT1 orthologue in amphioxus but it is not clear whether invertebrates encode WT1 orthologues other than proteins with zinc fingers similar to those in the SP1 family.

Although the functional relevance of the many WT1 isoforms is unclear, the importance of the +KTS and −KTS isoforms has been highlighted by the identification of splice site mutations in patients with Frasier syndrome (Barbaxou et al., 1997). These individuals have male-to-female sex reversal and suffer from focal segmental glomerulosclerosis (FSGS; i.e. scarring of the glomeruli) of the kidney. The dominant WT1 mutations create one allele that only produces the −KTS isoforms, leading to a reduced +KTS/−KTS isoform ratio. This suggests that both isoforms are essential and have different functions. Further support for this notion came from a study in which mice expressing only the +KTS or −KTS isoforms were created through gene targeting (Hammes et al., 2001). Mice lacking either of these isoforms die neonatally through incomplete kidney development, although the lack of −KTS isoforms leads to a more severe developmental phenotype than loss of +KTS isoforms (Hammes et al., 2001). By contrast, mice that specifically lack a mammalian-specific 17 amino acid insertion encoded by an alternative exon 5 exhibit no observable phenotype (Natoli et al., 2002). This is surprising, as the 17 amino acid domain acts as a transcriptional activator through interaction with the prostate apoptosis response factor PAR4 (PAWR) (Richard et al., 2001), and a mutation in this domain has been identified in a Wilms’ tumour (Schumacher et al., 1997), attesting to its importance in humans at least. Similarly, no phenotype is observed in mice lacking the extended isoforms of WT1, i.e. the isoforms produced via the use of a mammalian-specific alternative translation start site (Miles et al., 2003).
Diseases arising through germline WT1 mutations

Germline WT1 mutations may lead not only to the eponymous tumour but also to glomerulosclerosis of the kidney, gonadal dysgenesis and, in rare cases, congenital diaphragmatic hernia (CDH) and heart disease. There are several human syndromes resulting from WT1 hemizygosity or mutation and these have been very revealing about WT1 gene function. For example, deletions associated with WAGR syndrome (Wilms’ tumour, aniridia, genitourinary anomalies and retardation), which result in WT1 haploinsufficiency, lead to Wilms’ tumour in 70% of cases and a range of gonadal anomalies, most frequently undescended testes in males and streak gonads and bicornate uterus in females (Riccardi et al., 1978). On the other hand, heterozygous WT1 point mutations, predominantly in the zinc finger domain, lead to the more extreme phenotypes found in Denys-Drash syndrome (DDS) (Pelletier et al., 1991). Children with DDS often develop Wilms’ tumour and always suffer from mesangial sclerosis of the glomerulus, resulting in end-stage renal disease. Males with DDS have incompletely formed, ambiguous or female external genitalia; the testes may be normal, malformed, undescended or ambiguous. There is evidence to support the notion that the DDS mutations act in a dominant-negative mode, with the mutant WT1 protein dimerising with the wild-type protein, thus explaining the more severe phenotype compared with haploinsufficiency (Little et al., 1995). Patients with Frasier syndrome, which arises through an imbalance of the −KTS/+KTS WT1 isoforms (see above), have FSGS, and XY males with this condition exhibit female external genitalia and streak gonads (Barbaux et al., 1997). A fourth, less clear syndrome, and one that overlaps with DDS, is Meacham syndrome, which is characterised by CDH, ambiguous genitalia and complex congenital heart defects but no renal abnormalities. Surprisingly, two patients with Meacham syndrome have exactly the same WT1 missense mutations as seen in two cases of DDS with a different spectrum of anomalies (Suri et al., 2007).

The spectrum of phenotypic anomalies that result from WT1 mutations maps well onto the developmental expression domains of WT1. In mice, expression of WT1 is first detected in the proliferating coelomic epithelium and intermediate mesoderm at E9. Expression continues in the derivatives of the coelomic epithelium, the diaphragm, gonads and mesothelial lining of organs and in the kidney, which derives from the intermediate mesoderm (Armstrong et al., 1993). The phenotypes reported for the mouse Wt1 knockout are dramatic and concord well with the disease spectrum. Indeed, Wt1 null mice have no kidneys or gonads, exhibit CDH, and die at ~E13.5, presumably due to cardiac problems (Kreidberg et al., 1993). The mutant mice also suffer from hypoplastic lungs and have been shown to lack a spleen (Herzer et al., 1999) and adrenal glands (Moore et al., 1999; Bandiera et al., 2013).

WT1 function in kidney development, homeostasis and disease

The kidney diseases arising through WT1 mutation reflect the function of this gene at multiple stages of kidney development and tissue homeostasis (Fig. 2). Hence Wilms’ tumours involving WT1 mutations are likely to arise from the undifferentiated metanephric mesenchyme – a tissue that gives rise to the kidney – whereas WT1 mutations that give rise to glomerulosclerosis reflect a role for WT1 in the differentiation and maintenance of a fascinating specialised kidney cell type, the podocyte.
WT1 levels vary throughout this process of kidney development. WT1 is first expressed at low but detectable levels in the undifferentiated mesenchyme, and levels increase dramatically as the mesenchyme condenses around the bud prior to MET. Levels then stay high throughout nephrogenesis, becoming restricted to the proximal half of the S-shaped body and eventually the podocyte cells derived from this structure (Fig. 2). These expression levels correlate with a functional requirement for WT1 during kidney development; in Wt1 knockout mice the bud fails to invade the mesenchyme, which degenerates through apoptosis (Kreidberg et al., 1993). To explore the mechanism by which WT1 ensures mesenchyme maintenance, chromatin immunoprecipitation (ChIP) coupled to mouse promoter microarrays (ChIP-chip) was used to identify WT1 target genes using embryonic kidney extracts (Hartwig et al., 2010). Among the 1600 potential WT1 target genes were several known to be essential for kidney development within the mesenchyme (Fig. 2). These included Pax2, Sal1 and Bmp7, the expression of which was shown to depend on WT1 in nephrogenic organ culture (Hartwig et al., 2010). In an elegant study, it was further shown that WT1 is essential for mesenchyme survival and proliferation through direct transcriptional regulation of two cross-talking signalling pathways (Motamedi et al., 2014). WT1 transcriptionally activates the expression of several FGFs that are essential for mesenchyme proliferation, while repressing BMP/SMAD signalling, which induces an apoptotic response in the mesenchyme (Fig. 2). In line with this, it was shown that recombinant FGFs can rescue the survival of Wt1 null mesenchyme and suppress an apoptotic response induced by BMPs (Motamedi et al., 2014).

Key roles for WT1 during subsequent stages of kidney development can explain its function with respect to Wilms’ tumour and glomerulosclerosis. There are several subtypes of Wilms’ tumour, classified according to their pathology. The most common form is known as triphasic, comprising blastemal, epithelial and stromal elements. These tumours exhibit an architecture remarkably similar to that of the developing kidney. Wilms’ tumours arising through WT1 mutation, on the other hand, are mainly stromal and may often contain elements of heterotypic tissue, most commonly muscle but, more rarely, cartilage, bone and fat (Schumacher et al., 2003). WT1 is essential for the MET that underlies neprheon differentiation, partly through transcriptional activation of Wnt4 (Sim et al., 2002; Davies et al., 2004; Essafi et al., 2011). Furthermore, if Wt1 is deleted just prior to MET, the aberrant kidneys formed express a transcriptome similar to that observed in human Wilms’ tumours arising through WT1 mutation (Berry et al., 2011).
2015). It has therefore been hypothesised that WT1 mutant tumours arise through defective MET. However, this does not seem to equate with the stromal-predominant nature of the tumours. To address this, the origin of Wilms’ tumours was investigated by developing a series of mouse Wilms’ tumour models (Huang et al., 2016) using different Cre lines to delete Wt1 while simultaneously activating oncogenic Ctnnb1 or increasing the dose of IGF2, either in the nephron progenitors or the stroma. This approach revealed that tumours only develop when these genetic manipulations occur in the mesenchymal nephron progenitors, not in the stroma. Although tumour histology in these mice does not necessarily recapitulate that seen in humans with the same genetic alterations, tumours arising through Wt1 loss and increased IGF2 dose do express high levels of undifferentiated mesenchymal markers. Furthermore, deletion of Wt1 in the mesenchyme leads to activation of myogenic markers, providing a molecular explanation for the formation of ectopic muscle in Wilms’ tumours with WT1 mutation (Berry et al., 2015).

By contrast, glomeruloclerosis, for example that seen in children with DDS and Frasier syndrome, is due to abnormalities of kidney podocytes – specialised cells that form a filtration barrier with endothelial cells. It is now clear from several studies that WT1 is essential both for podocyte differentiation and podocyte maintenance throughout adult life (Moore et al., 1999; Hammes et al., 2001; Chau et al., 2011; Berry et al., 2015; Gebeshuber et al., 2013). Recent ChIP-seq studies have shown that WT1 binds to the promoters and enhancers of around half the 200 podocyte-specific genes identified (Kann et al., 2015a; Lefebvre et al., 2015; Dong et al., 2015). A subset of these target genes was shown to be downregulated upon Wt1 deletion, 11 of these specifically in mice lacking +KTS isoforms. Remarkably, WT1 bound to 18 of the 31 genes mutated in human podocyte disease, including Nphs1, Nphs2 and Actn4. Through bioinformatics analysis, it was proposed that WT1 is part of a podocyte transcription network that includes WT1, FOX-class transcription factors, LMX1B and TCF21 (Kann et al., 2015a; Lefebvre et al., 2015; Dong et al., 2015). Targets of this network include the Hippo signalling system, implicating this pathway in podocyte development or maintenance.

**WT1 and the adrenal-gonad axis**

As is the case for the kidney, WT1 plays roles at different stages during the development and homeostasis of the gonads and adrenal glands (Bandiera et al., 2015). These two steroidogenic organs develop from a common adrenogonadal primordium (AGP) arising from the coelomic epithelium. As discussed above, humans with WT1 mutations have a range of gonadal abnormalities but no adrenal anomalies to this author’s knowledge. Wt1 null mice completely lack gonads and adrenal glands, pointing to a crucial role in the formation/survival of the AGP. A vital factor for AGP survival, as in the kidney (Motamedi et al., 2014), is RA, the synthesis of which is reduced in Sertoli cells into foetal-like Leydig cells (Zhang et al., 2015). WT1 function in EMT: implications for heart and diaphragm development

Whereas WT1 plays key roles in MET during kidney and gonad development (as discussed above), in the developing heart and diaphragm it is required for EMT. In the developing heart, WT1 expression is mainly restricted to its epithelial component E-cadherin (von Gise et al., 2011). There is much evidence of cross-talk between the developing epicardium and myocardium, the former producing factors required for myocardial growth. One of these factors is RA, the synthesis of which is reduced in Wt1-deleted epicardium (Guadix et al., 2011). This can be explained by the finding that WT1 is required for full transcriptional activation of the gene encoding
RALDH2 (ALDH1A2), a key component of the RA synthetic pathway (Guadix et al., 2011). WT1 also represses, directly and indirectly through IRF7, the inhibitory chemokines CXCL10 and CCL5 that inhibit epicardial cell migration and myocardial proliferation, respectively (Velegela et al., 2013). Another key upstream factor in coronary vascular development is the neurotrophin receptor TRKB (NTRK2), which appears to be a direct WT1 transcriptional target in the epicardium (Wagner et al., 2005a).

As mentioned above, WT1 mutations can also lead to CDH, which is perhaps the most common serious birth defect, affecting 1 in 3000 births. CDH is characterised by incomplete formation or muscularisation of the diaphragm, which leads to herniation of the stomach, spleen, liver or intestines into the pulmonary cavities. The most prevalent form, observed in 90% of cases, is known as Bochdalek-type CDH and is characterised by a defect in the posterolateral area of the diaphragm, which is mostly lateralised to the left side. New insight into the mechanisms underpinning CDH has come from a recent study in which WT1 was deleted in the mesenchyme of the septum transversum (the tissue that gives rise to the diaphragm) of mice (Carmona et al., 2017). These mutant mice develop CDH with characteristics of the Bochdalek form. Using lineage tracing, it was shown that the post-hepatic plate coelomic epithelium normally gives rise to mesenchyme that populates the pleuropertoneal folds, thus isolating the pleural cavities prior to the migration of the somatic myoblasts. However, when WT1 is deleted from this region this process fails, seemingly owing to defective EMT. It has been known for some time that normal diaphragm development requires RA and that a deficit of RA can lead to CDH (Sugimoto et al., 2008). The recent Carmona et al. (2017) study showed that, as with the epicardium, the levels of RALDH2 are reduced specifically in the post-hepatic mesenchymal plate of the mutant mice. Importantly, supplementation of the maternal diet with RA can partially rescue the phenotype.

**WT1-expressing mesothelium: a source of mesenchymal progenitors**

A significant proportion of the vertebrate body comprises polarised epithelial cells, while another major component is non-polarised, more motile mesenchymal cells. These two cell types can switch between types via the processes of EMT and MET, and waves of EMT and MET are indeed vital for development. However, although often underappreciated, there are also stable cell populations that have an intermediate epithelial/mesenchymal state (Chau and Hastie, 2012). These cells are polarised, have adherens junctions but express high levels of mesenchymal markers including vimentin. Pre-eminent amongst these, as the name suggests, is the mesothelium that lines the body cavity and the organs therein. The mesothelium protects tissues from adhesion and plays key roles in fluid transport and inflammation (Kawanishi, 2016). However, over the past decade it has become clear that mesothelia are also a source of mesenchymal progenitors for diverse cell types within tissues, including fibroblasts and more specialised cells. In addition, it has been shown that WT1 is expressed at high levels in the proliferating coelomic epithelium and its mesothelial derivatives during development. Using lineage tracing, via a Wt1 locus-driven Cre recombinase to activate a reporter in mesothelial cells and their progeny (Zhou et al., 2008), the identity and fate of such mesothelial-derived cells has been investigated.

As discussed above, a role for the mesothelium as a source of mesenchymal progenitors was first shown in the heart, where the epicardium produces progenitors for vascular smooth muscle and some endothelium. Soon after, it was shown that the serosal mesothelium is a major source of progenitors for the smooth muscle component of the gut and lung vasculature (Wilm et al., 2005; Que et al., 2008). Furthermore, the lung mesothelium is a source of progenitors for endothelial cells, bronchial musculature and tracheal and bronchial cartilage (Cano et al., 2013), while in the liver, the mesothelium is the source of a subset of hepatic stellate cells that play a key role in tissue fibrosis (Ashina et al., 2011) (Fig. 3). WT1-expressing mesothelium also produces progenitors for the intestinal cells of Cajal, the intestinal pace makers (Carmona et al., 2013) (Fig. 3). Perhaps most surprising was the finding that visceral fat depots have a WT1-expressing mesothelial lining that provides progenitors for a significant proportion of visceral white adipose tissue (WAT) (Chau et al., 2014) (Fig. 3). There are two major classes of WAT: visceral and subcutaneous. Excess visceral fat predisposes to major diseases including heart disease, type 2 diabetes and cancer, whereas subcutaneous fat is thought to be protective. The nature and origin of progenitors for subcutaneous WAT and visceral fat depots have been the subject of much speculation (Billon and Dani, 2012), but it has now been shown that a significant proportion of all visceral WAT, but not subcutaneous WAT, arises from WT1-expressing progenitors and that these arise from the mesothelium (Chau et al., 2014) (Fig. 3).

In some tissues, WT1 expression is downregulated towards the end of gestation or postnatally; the timing of this downregulation varies depending on the organ, e.g. it is fast in the lungs (Cano et al., 2016), occurs at an intermediate rate in the heart (Smart et al., 2011) and is slow in the liver (Ijpenberg et al., 2007). Potentially interesting from a regenerative medicine perspective is that WT1 expression is reactivated in the adult epicardium following cardiac ischaemia, and this is associated with epicardial cell proliferation and the production of new EPDCs, which have the potential to generate new coronary vasculature and, controversially, cardiomyocytes (Smart et al., 2011).

It is also of interest that the other two major differentiated cell types that express WT1 at high levels – the kidney podocytes and gonadal Sertoli cells – are also epithelial with mesenchymal properties. It is unclear whether mutation of WT1 or other stresses leads to an epithelial-mesenchymal imbalance in these cells.

**WT1 in the nervous system: key roles in sensory neuron differentiation**

WT1 expression is not restricted to the mesoderm and its derivatives during embryonic development. It is also expressed in a small number of symmetrically placed neurons in the ventral spinal cord, the roof of the fourth ventricle of the brain and the developing sensory nervous system (Armstrong et al., 1993). Although the functional significance of WT1 expression in the ventricle and spinal cord is yet to be revealed, it has been shown that WT1 is essential for the development of retinal, olfactory and taste bud neurons, with the +KTS and −KTS isoforms appearing to play different roles.

In the developing retina, for instance, WT1 expression becomes restricted to the presumptive retinal ganglion layer and is absent from adult retinas (Wagner et al., 2002a). WT1−/− mice exhibit much thinner retinas than control animals, and the number of proliferating cells in E12 mutant embryos is reduced by 90% relative to wild-type controls (Wagner et al., 2002a). Furthermore, a significant proportion of retinal ganglion cells is lost by apoptosis in mutant embryos, and the growth of optic nerve fibres is disturbed. This phenotype is reminiscent of that observed in knockouts for the Pou4f2 transcription factor (Gan et al., 1996). Accordingly, Pou4f2 transcript levels are reduced dramatically in Wt1 mutant retinas and...
WT1 was shown to transactivate the Pou4f2 promoter (Wagner et al., 2002a). Subsequently, it was shown that the retinal defects are more severe in mice lacking the −KTS than the +KTS isoforms (Wagner et al., 2005b).

WT1 is also expressed in the developing olfactory epithelium from E9.5 to E18.5, and both Wt1 null mice and those specifically lacking +KTS isoforms exhibit a thinner olfactory epithelium than wild-type animals (Wagner et al., 2002a). By contrast, animals lacking −KTS isoforms appear to have normal olfactory epithelia. Mechanistically, it was shown that the expression of two key transcription factors with crucial roles in olfactory neuron development, MASH1 (ASCL1) and neurogenin 1, is reduced in WT1 +KTS mutants. Moreover, the +KTS but not −KTS isoforms can induce the expression of these two neurogenic genes.

More recently, it was shown that the role of WT1 in sensory system development also extends to taste buds (Gao et al., 2014). In mammals, taste buds are located in specialised areas called papillae, of which there are three types: fungiform, foliate and circumvallate (CV). WT1 is expressed in the developing CV papillae located on the back of the tongue, and this expression continues into adult life, principally in taste buds. In mice lacking WT1, the CV papillae fail to form and the levels of three signalling molecules implicated in gustatory development (BMP4, PTCH1 and LEF1) are reduced. In line with this, WT1 was shown to bind to the promoter regions of the endogenous Ptc1 and Lef1 genes and their expression was shown to be dependent on WT1.

**WT1 in adult tissue homeostasis and disease**

Although early studies established that WT1 plays crucial roles during development, it was not clear whether the gene continues to function in adult life and whether it is implicated in adult disease. WT1 continues to be expressed in just a few locations in the adult mouse: kidney podocytes, supporting gonadal cells, the mesothelial lining of organs and 1% of bone marrow cells. To address the continuing requirement for WT1 into adult life, a ubiquitous deletion of the gene was induced in 6-week-old mice (Chau et al., 2011). The results were dramatic and unanticipated: the mice died ~10 days after the initiation of Wt1 deletion. These animals suffered from severe glomerulosclerosis with loss of podocyte foot processes, atrophy of the spleen and exocrine pancreas, and widespread fat and bone loss. Although the mechanisms underlying these dramatic phenotypes remain unclear, it was hypothesised that they reflect a combination of systemic, local paracrine and cell-autonomous factors operating downstream of WT1 (Chau and Hastie, 2012). Proteomic analysis revealed a 95% reduction in circulating IGF1 levels in these mice (Chau et al., 2011). As IGF1 regulates both bone and fat growth, it is reasonable to conclude that reduction in this key signalling molecule contributes to the widespread bone and fat reduction. However, the fat loss might also reflect a cell-autonomous role for WT1 as it continues to be expressed in visceral WAT progenitors in adult life. Furthermore, preliminary evidence suggests that WT1 deletion leads to a reduction in these progenitors (Chau et al., 2014).

A rare population of WT1-expressing cells also persists in the cortex of the adult adrenal gland, and lineage tracing has shown that these cells are able to differentiate into steroidogenic cells throughout life (Bandiera et al., 2013). These progenitors also express GATA4, GLI1 and TCF21. Importantly, gonadectomy activated this cell population, leading to their differentiation into gonadal steroidogenic tissue (Bandiera et al., 2013). This defines a novel paradigm whereby a response to organ loss is the recreation of hormone-producing cells at an ectopic site.

WT1 is also expressed at high levels in a variety of adult epithelial tumours and in some leukaemias, and this has led to much endeavour in the pursuit of immune therapies targeting WT1 epitopes (Nishida and Sugiyama, 2016). In the majority of cases, it is still unclear whether WT1 overexpression is helping to drive the carcinogenic state or is merely a consequence. However, in an shRNA screen for genes cooperating with KRAS, WT1 was identified as a key regulator of oncogenesis and senescence downstream of KRAS (Vicent et al., 2010). Moreover, Wt1 loss reduces tumour burden in a mouse model of KRAS-driven lung cancer.

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**Fig. 3. Specialised cell types arising from the mesothelium.** WT1 expression (red) is observed in the mesothelium and the mesenchymal progenitors it produces, but not in the differentiated progeny of these progenitors. For instance, WT1 is expressed in: (A) the mesothelial lining of the heart (the epicardium) and epicardium-derived cells (EPDCs); (B) the liver mesothelium and its mesenchymal progenitors that give rise to a subset of hepatic stellate cells; (C) the mesothelial lining of visceral white adipose tissue and the mesenchymal progenitors that give rise to adipocytes; and (D) the intestinal mesothelium and its progenitors that form interstitial cells of Cajal.
cancer (Vicent et al., 2010). Consistent with this, WT1 loss was shown to lead to decreased proliferation and to senescence in a human lung cancer cell line dependent on oncogenic KRAS (Vicent et al., 2010). Much evidence has been published to suggest that WT1 can increase the survival of various cancer cells through anti-apoptotic functions. For example, a mechanism by which WT1 anti-apoptotic function can be modulated in response to cytotoxic drugs in cell lines and cell-free systems has been reported (Hartkamp et al., 2010). WT1 is cleaved into unstable fragments by the protease HTRA2, the expression of which is induced by anti-cancer drugs. This leads to downregulation of WT1 and a resulting increase in cell survival through upregulation of C-MYC and JUNB, which are normally repressed by WT1. It has also been reported (Wagner et al., 2014) that WT1 is often expressed in the vasculature and stroma of a variety of adult cancers, rather than in the epithelial components themselves. Using lung cancer and melanoma xenograft models, it was shown that the host vasculature and stroma invading the tumour express WT1 but that the nearby vasculature and stroma do not express detectable levels. In addition, when Tie2-Cre was used to delete WT1 in the host endothelial, haematopoietic and myeloid suppressor cells, tumour growth and metastases are impaired, and pre-existing tumours regress (Wagner et al., 2014). Mechanistically, WT1 was shown to transcriptionally activate both Pecam1 and c-Kit explaining, at least in part, its proangiogenic functions.

Surprisingly little is known about the pathways and factors that act upstream to regulate WT1 expression. However, it has been shown that WT1 expression is induced in coronary vasculature following ischaemia (Wagner et al., 2002b). It was then reported that WT1 is induced by hypoxia, with compelling evidence showing that the hypoxia-inducible factor HIF1 transactivates WT1 directly (Wagner et al., 2003). The possibility that WT1 plays a physiological role in response to ischaemia remains to be explored.

**Molecular mechanisms of WT1 action**

Although there is much evidence that WT1 functions as a transcription factor, several studies support post-transcriptional functions, via RNA interactions, for WT1. Furthermore, as summarised below, the data suggest that the +KTS isoforms may function mostly as transcriptional regulators, whereas the −KTS isoforms act predominantly post-transcriptionally, although this is not black and white as the +KTS isoforms can bind DNA and regulate transcription and the −KTS isoforms can bind RNA and shuttle to the cytoplasm. Genetic studies have shown that the two isoforms function differently at the later stages of genitourinary development and in sensory organ differentiation (Hammes et al., 2001; Wagner et al., 2005b). However, mice lacking the −KTS or +KTS isoforms do not, unlike null mice, exhibit defects in the early stages of genitourinary development or cardiovascular development (Hammes et al., 2001). This suggests that the two isoforms perform identical or compensatory functions during these processes.

**Effects on transcription and chromatin**

WT1 is a transcription factor that binds to DNA targets through its four zinc fingers. Early cell-free studies showed that WT1, the −KTS isoforms in particular, binds to a consensus site, 5'-GGCGGGGGCGG-3' (Rauscher et al., 1990). This consensus is identical to that found for EGR1, which has only three zinc fingers, very similar to WT1 zinc fingers 2-4. Crystallographic and NMR analyses of WT1 zinc finger interaction with DNA confirmed that only zinc fingers 2-4 insert deeply into the major groove, where they make base-specific contacts (Stoll et al., 2007). The first zinc finger does not contribute to binding specificity but helps anchor WT1 to the DNA. Cell-free studies also showed that the +KTS isoform binds to a slightly different sequence (Bickmore et al., 1992). A molecular explanation for this came through NMR analysis, which showed that the KTS insertion increases the flexibility of the linker between zinc fingers 3 and 4, thus abrogating binding of finger 4 to its cognate site in the major groove (Laity et al., 2000).

Recent studies identifying physiological target genes (summarised in Table 1) using ChiP-Chip and ChiP-seq have brought much clarity to this area. Several slightly different genomic binding sites have been identified, one identical to that shown to interact with the +KTS isoforms in vitro (Motamedi et al., 2014; Kann et al., 2015a; Lefebvre et al., 2015; Dong et al., 2015). So far, most of the validated transcriptional targets appear to be −KTS specific, with few genuine +KTS targets identified. Through ChiP-Chip and ChiP-seq, several thousand potential WT1 transcriptional targets during kidney development have been identified. However, so far, only a small subset of these have been validated as genuine targets, the expression of which changes as a result of WT1 mutation in developing tissue.

WT1 can act as either a transcriptional activator or repressor (Fig. 4A) depending on its binding partners (for a review see Toska and Roberts, 2014). Accordingly, there are repressor and activator regulatory domains at residues 71-101 and 180-250, respectively (Fig. 1). The repression domain was used to isolate a novel co-repressor, BASP1, that clearly plays a role in the downregulation of some WT1 targets in vivo (Carpenter et al., 2004; Essafi et al., 2011). Several other co-activators, co-repressors and transcription factors, including p53 (TRP53), have been shown to interact with WT1, modulating its target sites and activities, at least in cell lines (Toska and Roberts, 2014). Furthermore, several post-translational modifications, including sumoylation and phosphorylation, have been shown to regulate WT1 subcellular localisation and function (reviewed by Toska and Roberts, 2014).

Recent studies have revealed that WT1 can also regulate gene expression by modulating the epigenetic landscape, and this is relevant for disease progression (Rampal et al., 2014; Wang et al., 2015). Loss-of-function WT1 mutations are observed in a subset of acute myeloid leukaemia (AML), as are mutations in the genes encoding TET family proteins, including TET2 and IDH1/2 (Rampal et al., 2014; Wang et al., 2015). These enzymes are involved in converting 5-methylcytosine (5mC) in the genome to 5-hydroxymethylcytosine (5hmC), often leading to increased gene expression. Importantly, it was noted that WT1 and TET gene mutations are mutually exclusive and this led to the hypothesis that WT1 might work in the same pathway as TETs. Indeed, it was shown that WT1 interacts with TET2, recruiting it to target genes to activate their expression (Rampal et al., 2014; Wang et al., 2015). Accordingly, loss of function of WT1, TET2 or TET3 leads to a reduction in 5hmC and a similar impaired haematopoietic differentiation phenotype.

WT1 also seems to modulate the state of chromatin domains far beyond its binding sites. For example, WT1 is a transcriptional activator of Wnt4 in developing kidney mesenchyme undergoing MET, but a repressor of Wnt4 in epicardial cells poised for EMT, and these roles appear to involve global changes in chromatin access (Essafi et al., 2011). Transactivation and repression require the co-activator CBP/p300 (CREBBP/EP300) and co-repressor BASP1, respectively (Essafi et al., 2011). Deletion of Wt1 in kidney mesenchyme leads to loss of Wnt4 expression and the switching of the whole 130 kb Wnt4 locus, which lies between two CTCF binding sites, from an active chromatin configuration to a repressed
Table 1. Validated WT1 transcriptional targets that are relevant for developmental processes in different tissues

<table>
<thead>
<tr>
<th>Gene</th>
<th>Cell/tissue type</th>
<th>Activated (A) or repressed (R)</th>
<th>Biochemical activity of protein</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fgf16/20</td>
<td>Kidney mesenchyme/nephron progenitors</td>
<td>A</td>
<td>Signalling upstream of MAP kinase/PI3 kinase</td>
<td>Motamedi et al., 2014</td>
</tr>
<tr>
<td>Bmpr</td>
<td></td>
<td>A</td>
<td>Inhibits BMP signalling</td>
<td>Motamedi et al., 2014</td>
</tr>
<tr>
<td>Bmp7</td>
<td></td>
<td>A</td>
<td>Usually signals via SMADS</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Sal1</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Pax2</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Heyl</td>
<td></td>
<td>A</td>
<td>Transcription factor/Notch signalling</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Cxcc5</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Lsp1</td>
<td></td>
<td>A</td>
<td>F-actin binding</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Pbx2</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Pldc2</td>
<td></td>
<td>A</td>
<td>Plexin domain-containing protein</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Rps6ka3</td>
<td></td>
<td>A</td>
<td>Protein kinase</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Scx</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Sox11</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Hartwig et al., 2010</td>
</tr>
<tr>
<td>Gas1</td>
<td></td>
<td>A</td>
<td>FGF signalling</td>
<td>Kann et al., 2015b</td>
</tr>
<tr>
<td>Wnt4</td>
<td></td>
<td>A</td>
<td>Signalling via NFAT</td>
<td>Sim et al., 2002; Essafi et al., 2011</td>
</tr>
<tr>
<td>Podxl</td>
<td>Podocytes</td>
<td>A</td>
<td>Anti-adhesive membrane protein</td>
<td>Palmer et al., 2001</td>
</tr>
<tr>
<td>Nphrin (Nphs1)</td>
<td></td>
<td>A</td>
<td>Renal filtration barrier</td>
<td>Wagner et al., 2004; Guo et al., 2004</td>
</tr>
<tr>
<td>Mag2</td>
<td></td>
<td>A</td>
<td>Assembly of slit diaphragm</td>
<td>Dong et al., 2015; Lefebvre et al., 2015; Kann et al., 2015a</td>
</tr>
<tr>
<td>Nphs2</td>
<td></td>
<td>A</td>
<td>Component of slit diaphragm</td>
<td>Dong et al., 2015; Lefebvre et al., 2015; Kann et al., 2015a</td>
</tr>
<tr>
<td>Mafb</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Dong et al., 2015</td>
</tr>
<tr>
<td>Scl</td>
<td></td>
<td>A</td>
<td>In skin cornified envelope</td>
<td>Ratelade et al., 2010</td>
</tr>
<tr>
<td>Sulf1</td>
<td></td>
<td>A</td>
<td>Sulfatase</td>
<td>Ratelade et al., 2010; Schumacher et al., 2011</td>
</tr>
<tr>
<td>Snai1</td>
<td>Epicardium/embryoid bodies</td>
<td>A</td>
<td>Activates EMT</td>
<td>Martínez-Estrada et al., 2010</td>
</tr>
<tr>
<td>E-cadherin (Cdh1)</td>
<td>Epicardium</td>
<td>R</td>
<td>Epithelial cell adhesion</td>
<td>Martínez-Estrada et al., 2010</td>
</tr>
<tr>
<td>Wnt4</td>
<td></td>
<td>R</td>
<td>Signalling</td>
<td>Essafi et al., 2011</td>
</tr>
<tr>
<td>Raldh2 (Aldh1a2)</td>
<td></td>
<td>R</td>
<td>Retinoic acid synthesis</td>
<td>Guadix et al., 2011</td>
</tr>
<tr>
<td>Cxcl10</td>
<td></td>
<td>R</td>
<td>Chemokine</td>
<td>Velecela et al., 2013</td>
</tr>
<tr>
<td>Ccl5</td>
<td></td>
<td>R</td>
<td>Chemokine</td>
<td>Velecela et al., 2013</td>
</tr>
<tr>
<td>Sfl</td>
<td>Adrenal-gonadal primordium</td>
<td>A</td>
<td>Transcription factor</td>
<td>Wilhelm and Englert, 2002</td>
</tr>
<tr>
<td>Gli1</td>
<td>Developing adrenal gland</td>
<td>A</td>
<td>Transcription factor in SHH pathway</td>
<td>Bandiera et al., 2013</td>
</tr>
<tr>
<td>Tcf21</td>
<td></td>
<td>A</td>
<td>Transcription factor</td>
<td>Bandiera et al., 2013</td>
</tr>
<tr>
<td>Scy</td>
<td>Developing male gonad</td>
<td>A</td>
<td>Transcription factor</td>
<td>Miyamoto et al., 2008</td>
</tr>
<tr>
<td>Lef1</td>
<td>Posterior taste field</td>
<td>A</td>
<td>Transcription factor</td>
<td>Gao et al., 2014</td>
</tr>
<tr>
<td>Ptc1</td>
<td></td>
<td>A</td>
<td>Receptor for SHH</td>
<td>Gao et al., 2014</td>
</tr>
<tr>
<td>Bmp4</td>
<td></td>
<td>A</td>
<td>Signalling via SMADS</td>
<td>Gao et al., 2014</td>
</tr>
</tbody>
</table>

In all cases, WT1 has been shown to interact with these genes in the appropriate tissue by ChIP, whether in the primary paper listed or in a subsequent publication. In all cases, WT1 mutation or overexpression leads to a change in the expression of the target gene in the appropriate tissue.

state. Conversely, deletion of Wt1 in the epicardium switches the chromatin between these two CTCF sites from a repressed to an active conformation and this is associated with activation of Wnt4 expression. This switching of states is referred to as ‘chromatin flip-flop’ (Essafi et al., 2011). It has been proposed that WT1 activates the Wnt4 domain in the kidney mesenchyme to allow access of other transcriptional activators of Wnt4, including β-catenin and SIX2, whereas in the epicardium WT1 keeps the locus in a silent state, preventing access of Wnt4 activators.

Effects through RNA binding and post-transcriptional regulation

The first indication that WT1 might also function post-transcriptionally came with the observation that the +KTS isoform specifically localises and interacts with splice factors in kidney cells (Larsson et al., 1995). It was subsequently revealed that WT1 can be incorporated into functional spliceosomes in cell-free systems (Davies et al., 1998). These observations were soon followed up by experiments showing that both major WT1 isoforms, but not EGR1, can bind RNA derived from exon 2 of Igf2, the +KTS isoform showing higher affinity (Caricasole et al., 1996). The RNA interaction occurred through the zinc fingers and required the atypical first zinc finger. Subsequently, it was shown that both zinc finger 1 and the KTS insertion are important for WT1-RNA interactions in Xenopus oocytes (Ladomery et al., 2003). Using systematic evolution of ligands by exponential enrichment (SELEX), three high-affinity RNA-binding motifs have been identified for the WT1-KTS isoform (Bardeesy and Pelletier, 1998), and structural studies have shown that both the sequence and secondary structure of RNA determine binding specificity and affinity for WT1 (Zhai et al., 2001). It has also been demonstrated that, although the majority of WT1 is in the nucleus, some is present in the cytoplasm, located on actively translating polysomes, with all isoforms shuttling between the nucleus and cytoplasm (Niksic et al., 2004). Furthermore, WT1, specifically the +KTS isoform, was shown to recruit a viral RNA segment to polysomes (Bor et al., 2006). Additional circumstantial evidence for post-transcriptional functions comes from reports that WT1 interacts with RNA-binding proteins, often in an isoform-dependent manner. These include the splice factors U2AF65 (U2AF2) (Davies et al., 1998) and RBM4 (Markus et al., 2006), HNRPU (HNRNPUL) (Spraggon et al., 2007) and the Wilms’ tumour associated protein WTAP (Little et al., 2000). The latter protein is very topical as it is an


