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Meeting Report
A report of the first international WT1 meeting, University of Manchester UK, 2008

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Abstract: On September 8th-9th 2008, scientists from Europe, North America and Japan gathered together at the University of Manchester (UK) at a meeting about all things *WT1*. The intent was to bring together recent advances in research focused on the Wilms' tumor suppressor gene *WT1* from different subject areas. The *WT1* gene has emerged as a key player in development and cancer in recent years. The subject areas ranged from developmental mouse genetics including kidney development, cancer cell biology, structural analysis and molecular processes and targets regulated by *WT1*. The meeting was jointly organized by Dr Stefan Roberts (University of Manchester, UK); Dr Michael Ladomery (University of the West of England, UK); and Prof. Nick Hastie (MRC Human Genetics Unit, UK). In this article we review the contents of the meeting, subdividing it into three broad and overlapping subject areas: new findings in the context of A) *WT1*'s role in development; B) *WT1*'s involvement in cancer; and C) the biochemistry of WT1 protein.

Key words: WT1, Wilms' tumor, oncogene, tumor suppressor, cancer, development

Introduction

The *WT1* gene is best known for its involvement in the childhood kidney cancer Wilms' tumor (nephroblastoma). The human *WT1* gene was cloned in 1990, associated with a deletion at 11p13 linked to WAGR syndrome (Wilms' tumor, aniridia, urogenital abnormalities and mental retardation). *WT1* is required for the formation of functional kidneys and gonads during embryonic development and is expressed throughout vertebrates. However, *WT1* is also necessary for the development of the spleen, heart, central nervous system and retina, and for male sex determination [1, 2]. *WT1* encodes a protein with four C2-H2 zinc fingers that belongs to the EGR family of transcription factors. The zinc fingers are multifunctional in that they bind both DNA and RNA. The *WT1* gene expresses at least 36 isoforms resulting from alternative splicing events, the use of alternative startcodons and an alternative first exon. *WT1* is thought to regulate cell proliferation, apoptosis, differentiation and cytoskeletal architecture. In the context of cancer, the involvement of *WT1* now goes beyond Wilms' tumor to include leukemia, melanoma, breast, prostate, and colorectal cancer among others. To add to an already complex picture, *WT1* acts as a tumor suppressor in some contexts and as an oncogene in others. Not surprisingly there are several unanswered questions about the role of *WT1* and its various protein isoforms in development and disease.

Increasing roles for the WT1 gene in development

Throughout the meeting, it was evident that the developmental roles of *WT1* go beyond its better known involvement in urogenital development – *WT1* is also implicated in development of the heart, spleen, retina, and central nervous systems. However the role of *WT1* during embryonic development is still best understood in the context of kidney formation. Danielle Badro from Andreas Schedl's group at

the INSERM in Nice, France, reported results of a microarray study to identify *Wt1*-dependent genes in the mouse during early kidney development. She reported that the screen yielded several genes with reported roles during kidney formation, including *uncx4.1*, *Wnt4*, *Pax8*, *Crym* (Crystallin mu protein), *Etv5* (Ets domain-containing variant gene 5) and *Rspo1* (R-spondin 1). The latter may be part of the *Wnt* signalling pathway and showed overlapping expression with *Wt1* in the metanephric mesenchyme of the kidney.

Sean Lee from the NIH at Bethesda, USA, reported of a different approach to isolate target genes of *WT1* in the context of kidney development. His group utilised an immortalised rat embryonic kidney cell line stably transfected with tetracycline inducible constructs controlling the expression of the *WT1* splice isoforms +KTS and –KTS [3]. The *WT1*(+KTS) isoform has been shown to be involved in RNA processing while the *WT1*(-KTS) variant acts as a transcriptional regulator [4]. The differential screening of two cell lines that express either *WT1*(-KTS) or *WT1*(+KTS) would reveal *WT1* target genes. Among the putative target genes identified was *WID* (WT1-induced Inhibitor of Dishevelled), also known as *IDAX*, which encodes a protein known to bind Dishevelled thus inhibiting Wnt signalling [5]. The Lee group confirmed a role for *WID* in *Wnt* signalling by co-expressing *WID* in HEK293 cells with a Wnt signalling reporter construct (based on the TOPFLASH system), which led to reduced signals, indicating that *WID* acts as a strong inhibitor of Wnt signalling. *WID* was expressed in overlapping domains with *Wt1* in renal vesicles and podocyte precursors in the developing kidneys, and inactivation of *WID* in mice by gene targeting resulted in reduced nephrons and renal tubules and abnormal kidney development.

A role for *WT1* in kidney development was also reported in the zebrafish, by Frank Bollig from Christoph Englert's group, Jena, Germany. He described how inactivation of the two *WT1* orthologs in zebrafish, *wt1a* and *wt1b*, led to different phenotypes. Injection of a morpholino specific for *wt1a* resulted in oedema and kidney failure, caused by lack of glomeruli, while the *wt1b*-specific morpholino caused subtle oedema, and cyst formation in the kidney [6, 7]. The group also inactivated the zebrafish ortholog of *WID* by morpholino injection, which resulted in cyst formation in the kidney, resembling the *wt1b* loss-of-function phenotype. This finding suggests that *wt1b* inhibits *Wnt* signalling in the kidney, similar to the role of *WID* protein. In order to utilise the evolutionary distance between zebrafish and human to search for conserved regulatory elements of *WT1*, the group reported the generation of two transgene reporter constructs of about 30kb and 35kb size each, stretching between either *wt1a* or *wt1b* and the zebrafish orthologues of the nearest expressed genes in human, *CCDC73* and *GA17*. Gene duplication during evolution in zebrafish has led to the separation of wt1a with the *CCDC73* ortholog, while *wt1b* is close to the *GA17* orthologue. Transgenic zebrafish harbouring the *wt1b-ga17* constructs recapitulated expression of *wt1b* faithfully until 60 hours post-fertilization, when expression also started in the pancreas and intestine, where *ga17* is expressed [8].

Holger Scholz from the Charité – Universitätsmedizin in Berlin, Germany, described the involvement of *WT1* in cell signalling during haematopoiesis. *WT1*, expressed during haematopoiesis in progenitor cells, is important for the survival of several progenitor populations that give rise to blood cells. Erythropoietin (Epo) is required for embryonic haematopoiesis, and in CD117+ haematopoietic progenitor cells isolated from WT1(-exon 5/-KTS) fetal liver, both *Epo* and the Epo receptor gene (*EpoR*) were expressed at more than half of the normal level [9]. WT1-deficient fetal liver cells were less sensitive to recombinant Epo with respect to proliferation than WT1-positive cells. Furthermore, the erythroid colony forming capacity of WT1(-exon 5/-KTS) haematopoietic progenitor cells was reduced compared to that of wild-type cells. Their studies revealed that *WT1* is co-expressed with *EpoR* in CD117+ cells, and by *in vitro* binding and ChIP assays they showed that *WT1*(-KTS) binds to the EpoR promoter. Using a luciferase reporter assay in HEK293 and K562 erythroleukemia cells, Scholz and colleagues then demonstrated that *WT1*(-KTS) trans-activates the *EpoR* promoter. These findings indicate that the transcriptional activation of the *Epo* and *EpoR* genes by WT1(-KTS) are an important aspect of haematopoiesis.

Kim Moorwood, from the University of Bath, discussed two mouse models in which the Wt1 antisense transcript (*Wt1-as*) is disrupted. One

carries a transcriptional terminator sequence positioned to truncate *Wt1-as* (T-allele) and the other also has a deletion of a highly conserved element that is normally transcribed as part of *Wt1-as* (D-allele). Preliminary characterisation of these mice was presented, which showed that the animals had no obvious developmental anomalies or pathology in tissues where *Wt1* is known to have an important role. Body and organ weight analysis of seven month old animals revealed that female D-mice were significantly heavier than their wild-type siblings despite having similar major organ weights, and male D-mice had significantly lighter testes than their wild-type siblings. The underlying mechanisms causing this gain in weight are currently being analysed.

The complex involvement of WT1 in cancer

A common theme during the meeting was the complexity of *WT1* as both a tumor suppressor and oncogene depending on the context in which it is expressed. Despite having originally been associated with Wilms' tumor (nephroblastoma) and, over the years, with acute myeloid leukemia, *WT1* is now implicated in a growing list of cancers.

Kay Wagner from the University of Nice, France, presented evidence for a role of *WT1* in tumor angiogenesis and melanoma. He reported that in 95% of more than 100 analysed tumors, *WT1* was expressed in tumor endothelial cells, as revealed by immunofluorescence co-expression studies using *WT1* and endothelial markers. When *WT1* was inactivated by RNA interference in HUVEC cells, the capacity to form endothelial tubes in the angiogenesis assay was reduced and trans-well migration impaired. WT1 protein was also shown to co-express in tumor endothelial cells with the *Ets-1* transcription factor, a regulator of tumor angiogenesis. *WT1* downregulation resulted in loss of Ets-1 expression in an in vitro system, and WT1(-KTS) protein was found to bind and activate the *Ets-1* promoter in co-transfection, ChIP and EMSA experiments. Further indication for a regulation of *Ets-1* by *WT1 in vitro* came from RNAi experiments which resulted in the downregulation of known target genes of the *Ets-1* transcription factor [10]

In the second half of his presentation, Kay Wagner reported that WT1 protein, which is not normally expressed in skin keratinocytes and melanocytes, was expressed in over 80% of malignant melanoma cells - particularly the +17AA and +KTS isoforms. Expression analysis indicated that WT1 protein is co-expressed with Nestin and Zyxin, both shown to regulate melanoma cellular proliferation. By abolishing *WT1* function in melanoma cell lines using RNA interference, the group found that Nestin and Zyxin expression as well as cell proliferation were reduced. Taken together, these findings suggest that *WT1* is involved in tumor formation and progression through the regulation of angiogenesis and cellular proliferation [11].

Brigitte Royer-Pokora's group from the University of Düsseldorf, Germany, has investigated Wilms' tumor samples for mutations in *WT1* and *ß-Catenin* genes and found that all *WT1*-mutant tumors also have a *ß-Catenin* mutation, suggesting a link between *WT1* and *Wnt* signalling in tumor formation or progression. In contrast, only few tumors had mutations in *ß-Catenin* but no mutation in *WT1*. In a patient with a S50X germ line *WT1* truncation mutation, four independent tumors developed with different *ß-Catenin* mutations, suggesting a strong selection for activated *ß-Catenin* and/or *Wnt* signaling in *WT1*-mutant tumors. Western blot analyses from tumor extracts showed a high level of the WT1 protein in chemotherapy naive tumor samples, a lower amount in treated tumor samples and very low to negative expression in *WT1*-mutant tumors. All tumors also expressed ß-Catenin protein at a very high level. A new survey of the frequency of bilateral versus unilateral tumors showed that 80% of the patients with *WT1* truncation mutations that occur before amino acid codon 267 developed bilateral tumors whereas only 24% of those with a deletion of the entire gene had bilateral tumors. These data might indicate that a truncated *WT1*-mutant protein increases the risk for malignant transformation of kidney precursor cells and that an additional activation mutation of *ß-Catenin* is necessary for tumor formation.

Haruo Sugiyama and Yusuke Oji from Osaka University, Japan, described work that further broadens the involvement of *WT1* in cancer. WT1 protein is now routinely detected in tumors of the gastrointestinal tract, pancreatobiliary system, urinary and genital organs, breast, lung, bone and skin [12]. The WT1 signal in these tumors was at times strictly nuc-

lear, but sometimes cytoplasmic – and furthermore both diffuse and granular, consistent with *WT1*'s involvement in both transcriptional and posttranscriptional processes. *WT1* appeared to be overexpressed, consistent with an oncogenic as opposed to tumor suppressor role. Generally, all four main splice isoforms of WT1 are expressed in cancer; however they appear to have distinct functions in cell biology assays. The 17AA(-)/KTS(-) isoform induced small-sized cell shape, reduced cell-substratum adhesion, and enhanced cell migration and invasion in several cancer cell lines. These morphological changes were associated with aberrant expression of proteins that affect cytoskeletal architecture, including α-actinin and gelsolin [13].

A completely different approach to *WT1* and its expression in cancer and malignancies was reported by Hans Stauss, University College London, UK. *WT1* is strongly expressed in several tumors and haematological malignancies including chronic myelogenous and acute monocytic leukaemia. Strong expression of WT1 antigen in tumor cells can be exploited to eliminate malignant cells by employing allo-reactive T-cells. Hans Stauss' group had previously isolated *WT1*-specific cytotoxic T-cell lines from a patient; these cell lines specifically recognise a peptide derived from WT1 protein. Using *in vitro* and *in vivo* experiments with mouse models, WT1-reactive T-cells showed specificity towards *WT1*-expressing leukaemia cells by killing them, while non-leukaemia cells were not affected. Next, the group cloned the alpha and beta genes of the T-cell receptor from WT1-specific cytotoxic T cells, and inserted them into a retroviral vector. Retroviral gene transfer was used to generate *WT1*-specific T-cell receptor expression in human T-cells from healthy and leukaemia patient donors. Transduced T-cells showed WT1 specificity in their activity since *WT1* expressing human tumor cell lines were killed. Furthermore, their work revealed that the transduced *WT1*-specific T-cells were able to kill leukaemia cells derived from patients *in vitro*, and in an in vivo mouse model [14, 15]. These findings show promise for the development of a *WT1*-specific T-cell receptor therapy for patients with tumors or leukaemias that overexpress the *WT1* gene.

Epigenetic changes occur frequently in Wilms' tumor, especially the loss of imprinting (LOI) of IGF2/H19 at 11p15. Keith Brown from the University of Bristol, UK, presented data that identified two imprinted transcripts (WT1-AS and AWT1) from the *WT1* locus at 11p13, and showed LOI of these transcripts in some Wilms' tumors [16]. A higher level (83%) of 11p13 LOI than of 11p15 LOI (71%) was found in Wilms' tumors. There was no correlation between methylation levels at the 11p13 and 11p15 differentially methylated regions, or between allelic expression of WT1-AS/AWT1 and IGF2. Interestingly, retention of normal imprinting at 11p13 was associated with a small group of relatively late-onset, high-stage Wilms' tumors. An examination of genetic and epigenetic alterations in nephrogenic rests, which are premalignant Wilms' tumor precursors, showed that LOI at both 11p13 and 11p15 occurred before either 16q loss of heterozygosity (LOH) or 7p LOH. This suggests that these LOH events are very unlikely to be a cause of LOI but that LOH may act by potentiating the effects of overexpression of IGF2 and/or WT1-AS/AWT1 that result from LOI.

The biochemistry of WT1 and the search for its target genes

As well as a growing list of interacting proteins, the meeting highlighted the fact that the biochemical activities of WT1 protein are complicated by its ability to bind both RNA and DNA through the zinc finger domain. This suggests that WT1 can work at multiple levels in regulating gene expression: thus not only transcription, but potentially alternative splicing, nucleocytoplasmic traffic, mRNA translation and stability. To a large extent, the functional versatility of WT1 is achieved through its several splice isoforms - particularly the +KTS insertion after zinc finger three. Several questions remain to be answered, not least the identity of DNA and RNA *in vivo* targets of WT1 in the context of normal development and tumorigenesis.

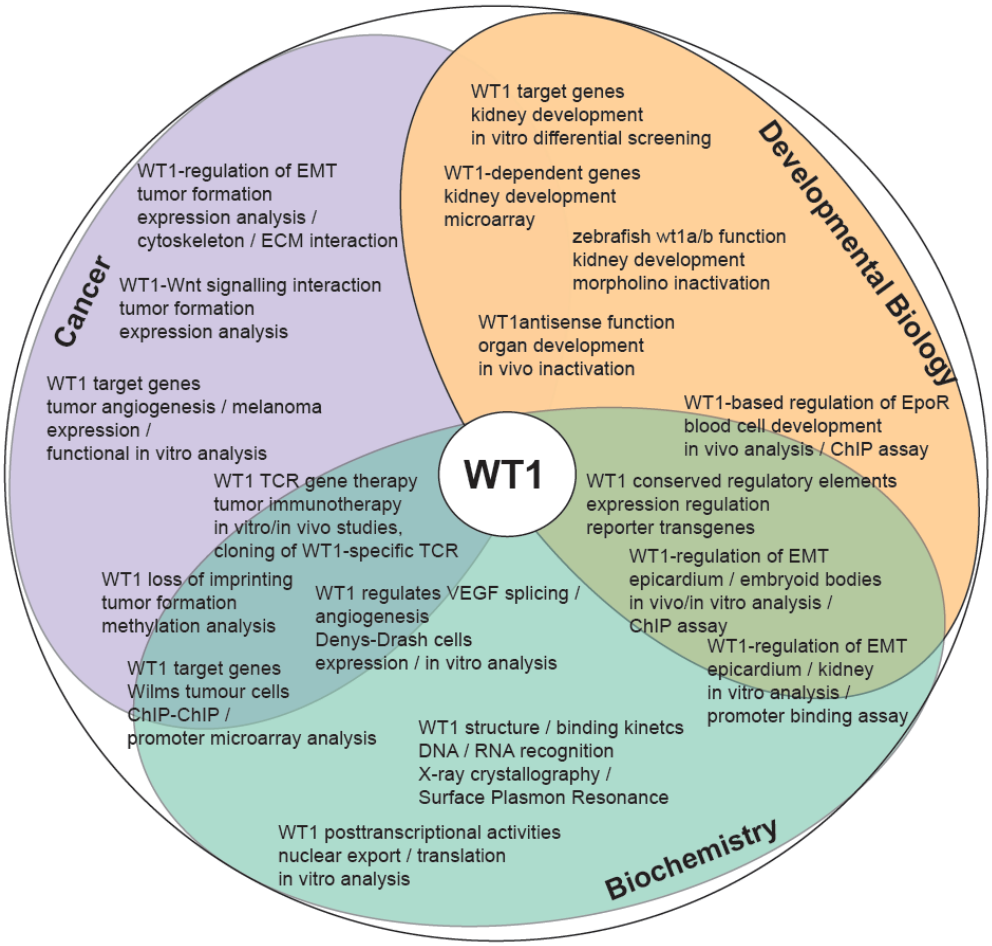
Jonathan Licht from Northwestern University in Chicago, USA, gave a talk that described a whole genome screen for WT1 targets [17]. To date, only a limited number of verified direct transcriptional targets of WT1 have been published. The group started with cell lines engineered to overexpress *WT1* and correlated changes in gene expression with genes differentially expressed in Wilms' tumors that are either mutant or wild type for WT1. This approach identified target genes such as *Spry1*, *MKP3* and *IFI16*. WT1-mediated activation of

Spry1 and *MKP3*, negative regulators of ERK signaling, is consistent with the role of WT1 as tumor suppressor. In contrast, the activation of *WT1* expression in the Wilms' tumor cell line IFI16 promoted cell growth, indicating a context-dependent oncogenic activity of *WT1*. Next the group performed a genome-wide screen for direct WT1 targets using a combination of ChIP on chip (chromatin immunoprecipitation combined with microarray analysis). In general, promoter regions bound by WT1 were as expected, G-rich and overlapped with sites for other transcription factors such as Sp1, EGR1 and KLF6. Around two hundred potential *WT1* gene targets were defined and grouped into functional categories: genes involved in MAPK signalling, the Wnt pathway, focal adhesion, actin cytoskeleton, ECM-receptor interaction, and interestingly, axonal guidance and long-term potentiation. The ability of *WT1* to affect Wnt signalling was further demonstrated by co-injection of *WT1* with *Wnt8* in Xenopus laevis embryos. While *Wnt8* caused a duplication of the head of the frog embryo, *WT1* efficiently suppressed this activity.

WT1 has been proposed to be a regulator of EMT (epithelial-mesenchymal transition) for many years, but conclusive evidence has now emerged from Nick Hastie's laboratory, at the MRC Human Genetics Unit, Edinburgh. Ofelia Martinez-Estrada presented data that explains how WT1 regulates epithelial-mesenchymal transition (EMT) in studies performed in epicardial cells and in embryoid bodies. She showed how Snail, the master regulator of EMT, was downregulated in WT1(-17AA/-KTS) epicardium compared with controls, while E-cadherin, normally suppressed by Snail, was upregulated in these epithelial epicardial cells. This observation led her to hypothesize that WT1 protein was required for the transition of epithelial epicardial cells to a mesenchymal phenotype, as epicardial cells undergo EMT during embryogenesis to give rise to cells of the coronary vessels and cardiomyocytes. WT1 was found to bind directly to the *Snail* promoter by ChIP assay, and further evidence suggested that WT1 acts also as a direct repressor of E-cadherin. Using embryoid bodies (EBs) generated from WT1(-17AA/-KTS) ES cells, she confirmed the observations made in epicardial cells, since WT1 mutant EBs lacked mesenchymal cells, suggesting that WT1 is an important regulator of EMT during embryonic development.

Ofelia Martinez-Estrada's presentation was complemented by her group colleague Abdelkader Essafi's talk that described *WT1* as a molecular switch controlling epithelial-mesenchymal balance in a tissue-context dependent manner. Abdelkader approached the role of *WT1* during the transition between epithelium and mesenchyme from a molecular point of view. He highlighted how during nephron development WT1 regulated the Wnt pathway via Wnt4, which led to formation of an epithelium from metanephric mesenchyme (MM). The opposite effect was induced by WT1 in the epicardium or in ES cells, where Snail expression was maintained by WT1 to allow epithelial cells to become mesenchymal. Importantly, *WT1* interacted with promoters of both *Snail* and *Wnt4* in MM and epicardium. However, WT1 binding to Snail in the MM, and to *Wnt4* promoters in the epicardium, resulted in the inactivation of both genes in the respective tissues.

Elianna Amin from Michael Ladomery's group from the University of the West of England, Bristol, presented data that links WT1 to the alternative splicing of Vascular Endothelial Growth Factor (VEGF-A, or VEGF). VEGF is the most potent mediator of physiological and pathological angiogenesis. Over five years ago, a novel splice isoform of VEGF was discovered that arises from an alternative 3' splice site in exon 8. The new isoform is termed VEGFxxxb, where xxx refers to the number of amino acids in given VEGF isoforms. This novel VEGF isoform is, strikingly, anti-angiogenic and downregulated in all solid tumors tested. Its alternative splicing is influenced by growth factors and by the proto-oncogene splice factor ASF/SF2 [18]. Glomerular podocytes normally express similar amounts of pro- and anti-angiogenic VEGF. In human podocytes derived from Denys-Drash Syndrome patients with a WT1 mutation (R366C), anti-angiogenic VEGF was severely downregulated, but its expression was rescued with wildtype WT1(+17AA,-KTS). Elianna Amin showed that the expression of the splice factor kinase gene *SRPK1* was transcriptionally repressed by WT1. One of the best studied substrates of SRPK1 is, in fact, the oncogenic splice factor ASF/SF2. Cytoplasmic phosphorylation of ASF/SF2 by SRPK1 caused ASF/SF2 to accumulate in the nucleus, where it promoted the expression of pro-angiogenic VEGF. ASF/SF2 localisation was also found to be altered in DDS podocyte cell



Figue. 1. Themes covered in the 2008 International WT1 Meeting held at the University of Manchester. Three broad and overlapping areas of WT1 biology were covered: the role of WT1 in development, WT1 in cancer, WT1 biochemistry and the continuing search for its target genes. The wide spectrum of topics illustrates the increasing functional complexity of the WT1 gene, setting the scene for much future research.

lines and patient samples. These findings have broad implications: by regulating *SRPK1* expression, and thus the phosphorylation and activity of splice factors, WT1 is likely to affect the alternative splicing of several genes involved in development and tumorigenesis.

Raymond Yengo, in Marjolein Thunnissen's lab from the University of Lund, Sweden, presented results from *in vitro* binding assays that shed further light on the ability of WT1 to bind both DNA and RNA. These *in vitro* binding assays were based on the purified zinc-finger domain [19]. A close look at the sequences of the four zinc fingers that constitute the DNA recognition domain of WT1 revealed a significant dissimilarity between zinc finger 1 and the other three zinc fingers. The work presented was aimed at elucidating the effect of the KTS insert on DNA binding and the significance of zinc finger 1 in the context of DNA recognition. Using a combination of Surface Plasmon Resonance and X-ray Crystallography Raymond showed that given a particular DNA recognition sequence, the KTS insert did not significantly affect the DNA binding affinity of WT1 and zinc finger 1 contributed only minimally to DNA recognition. The group also examined the binding kinetics of WT1 zinc fingers to an RNA ligand derived from a native RNA sequence, ACT34, previously identified in a yeast three hybrid screen of RNA that co-immunoprecipitated with WT1 [20]. WT1 bound to a stemloop structure in the RNA, with

contributions by all four of its zinc fingers. However, both zinc finger one and the KTS insertion appeared to regulate the interaction kinetics with the RNA ligand.

Marie-Louise Hammarskjold's group from the University of Virginia, USA, is interested in elucidating the nature of the posttranscriptional activities of WT1 protein. It has been known for several years that WT1 interacts with splice factors (notably U2AF65 and WTAP) and that its zinc fingers bind to RNA. Marie-Louise presented evidence that WT1 might also affect nuclear export and translation. Various WT1 isoforms were tested for constitutive transport elements that are able to drive the export and translation of an HIV construct that possesses a retained intron [21]. WT1(+KTS), the isoform least able to bind DNA, was shown to promote export and polyribosomal association of the RNA. The interaction of WT1 with splice factors and RNA has been documented for several years; however this is the first evidence of a specific posttranscriptional activity regulated by WT1. The integration of WT1's transcriptional and posttranscriptional activities remains an open question to be addressed in future research.

Conclusion and future meetings

In conclusion, this multidisciplinary meeting on the *WT1* gene offered scientists from various fields working on different aspects of the WT1 protein, an excellent opportunity to exchange results and discuss findings. Several presentations provided further evidence for posttranscriptional activities for WT1, including splicing, nuclear export and translation, while the majority of the research presented was focussed on the role of WT1 as a transcriptional regulator in various healthy and cancerous tissues (**Figure 1**). Growing evidence reveals that WT1 interacts with the Wnt signalling pathway in a range of tissues, thus influencing normal development and tumor growth. In addition, progress has been made in understanding the regulation of *WT1* expression, WT1 protein structure and WT1 binding kinetics were also presented.

Due to space limitations, not all presentations could be discussed, and we apologise to any colleagues whose work was omitted. In particular, as well as the talks described in this review, fifteen posters were also presented at the meeting. The participants discussed plans for future meetings, and it was decided that meetings would take place every two years. Christoph Englert offered to organise the next meeting in Germany in late Summer 2011. It is hoped that the next meeting will benefit from even wider participation.

List of Participants

Participants in 2008 included**:** Joanna Allardyce, Liverpool, UK; Elianna Amin, Bristol, UK; Danielle Badro, Nice, France; Frank Bollig, Jena, Germany; Anja Bondke, Berlin, Germany; Keith Brown, Bristol, UK; Maike Busch, Düsseldorf, Germany; Hayley Campbell, Manchester, UK; You-Ying Chau, Edinburgh, UK; Tatiana Dudnakova, Edinburgh, UK; Christoph Englert, Jena, Germany; Abdelkader Essafi, Edinburgh, UK; Sarah Goodfellow, Manchester, UK; Juan Antonio Guadix, Edinburgh, UK; Salaheldin Hamed, Briston, UK; Marie-Louise Hammarskjold, Charlottesville, USA; Jörg Hartkamp, Manchester, UK; Nicholas Hastie, Edinburgh, UK; Peter Hohenstein, Edinburgh, UK; Karin Kirschner, Berlin, Germany; Michael Ladomery, Bristol, UK; Sean Lee, Bethesda, USA; Yifan Le, Bristol, UK; Jonathan Licht, Chicago, USA; Karim Malik, Bristol, UK; Ofelia Martinez-Estrada, Edinburgh, UK; Thuluz Meza Menchaca, Bath, UK; Colin Miles, Newcastle, UK; Kim Moorwood, Bath, UK; Haruo Oji, Osaka, Japan; Yoshihiro Oka, Osaka, Japan; Derya Ozemir, Edinburgh, UK; Stefan Roberts, Manchester, UK; Brigitte Royer-Pokora, Düsseldorf, Germany; Moin Saleem, Bristol, UK; Susann Schiebel, Berlin, Germany; Holger Scholz, Berlin, Germany; Ralph Sierig, Jena, Germany; Lee Spraggon, Newcastle, UK; Hans Stauss, London, UK; Andreas Steege, Berlin, Germany; Haruo Sugiyama, Osaka, Japan; Marjolein Thunnissen, Lund, Sweden; Kay Wagner, Nice, France; Andrew Ward, Bath, UK; Bettina Wilm, Liverpool, UK; Raymond Yengo, Lund, Sweden.

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