Syndromes and constitutional chromosomal abnormalities associated with Wilms tumour

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Wilms tumour has been reported in association with over 50 different clinical conditions and several abnormal constitutional karyotypes. Conclusive evidence of an increased risk of Wilms tumour exists for only a minority of these conditions, including WT1 associated syndromes, familial Wilms tumour, and certain overgrowth conditions such as Beckwith-Wiedemann syndrome. In many reported conditions the rare co-occurrence of Wilms tumour is probably due to chance. However, for several conditions the available evidence cannot either confirm or exclude an increased risk, usually because of the rarity of the syndrome. In addition, emerging evidence suggests that an increased risk of Wilms tumour occurs only in a subset of individuals for some syndromes. The complex clinical and molecular heterogeneity of disorders associated with Wilms tumour, together with the apparent absence of functional links between most of the known predisposition genes, suggests that abrogation of a variety of pathways can promote Wilms tumorigenesis.

Multiple nephrogenic rests throughout the kidney are sometimes present and can be referred to as nephroblastomatosis.

The dramatic advances in the treatment of Wilms tumour are such that long term survival is now the norm: exceeding 90% for disease localised to the abdomen (stages 1–3), and over 70% in metastatic disease (stage 4). The treatment of Wilms tumour is determined both by stage and histological classification of the tumour, with treatment protocols varying between countries. Surgical resection is complemented in the majority of individuals by chemotherapy. Currently in the United Kingdom around 30% of individuals with Wilms tumour also receive radiotherapy.

A wide range of syndromes, congenital anomalies, and constitutional chromosomal abnormalities have been reported in association with Wilms tumour. Data from the British National Registry of Childhood Tumours showed that around 9% of individuals with Wilms tumour have a congenital anomaly, and a study of long term childhood cancer survivors revealed a syndrome diagnosis in 23 of 136 individuals (17%) with Wilms tumour. This is the highest proportion seen in any childhood malignancy.

The aim of this article is to document the syndromes, congenital abnormalities, and constitutional chromosomal aberrations reported to occur in association with Wilms tumour, and to review the evidence for an increased risk of Wilms tumour in these conditions. Accurate estimation of risk can be difficult in the absence of large prospective studies, which are rarely feasible in conditions reported in association with Wilms tumour, many of which are very rare. Where Wilms tumour is a diagnostic criterion for the condition, risk estimation is particularly difficult. It is probable that cases of a syndrome with Wilms tumour are more likely to be reported than cases without tumours, and that such reporter bias leads to an overestimate of the tumour risk. Because of this difficulty of accurate risk estimation we have generally given a qualitative risk estimate (for example, high, moderate, or low) rather than a precise figure.

For a comprehensive assessment of conditions reported in association with Wilms tumour, we undertook extensive searches for relevant articles using the PubMed, Online Mendelian

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Abbreviations: BWS, Beckwith-Wiedemann syndrome; IHH, isolated hypothalamic hypogonadotrophic hypogonadism; JH, isolated hypothyroidism; TSC, tuberous sclerosis complex; WAGR, Wilms-aniridia-genitourinary-mental retardation

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Inheritance in Man (OMIM), and the Winter-Baraitser dysmorphology databases (see electronic database section at the end of the paper). To facilitate searches we created a database of more than 8000 references with “Wilms tumour” or “nephroblastoma” in the title or abstract, which we downloaded from PubMed. We then searched this database for generic terms such as “syndrome” and “malformation”. We also reviewed the references of identified papers for additional relevant literature.

CONDITIONS WITH AN INCREASED RISK OF WILMS TUMOUR

The conditions in which there is conclusive evidence of an increased risk of Wilms tumour are shown in table 1. They can be broadly classified into five groups: WT1 associated syndromes caused by mutations or deletions of the WT1 gene; familial Wilms tumour; overgrowth conditions; tumour predisposition syndromes in which Wilms tumour is one of a number of benign or malignant tumours that can occur; and constitutional chromosomal disorders.

WT1 associated syndromes

The Wilms tumour 1 (WT1) gene is located at 11p13 and encodes a zinc finger transcription factor with a crucial role in renal and gonadal development. It consists of a C-terminal zinc finger DNA binding domain and an N-terminal transactivation domain, and occurs in multiple alternatively spliced isoforms.10 WT1 acts as a classic tumour suppressor gene and the wild type allele is somatically inactivated in tumours occurring in individuals with constitutional WT1 mutations or deletions. The median age of Wilms tumour diagnosis in such individuals is younger than in unselected series of Wilms tumour cases (~1 year in WT1 associated syndromes, 3 to 4 years in unselected Wilms tumour series) and tumours are more likely to be bilateral (38% in WT1 associated syndromes; 5% in unselected Wilms tumour series). The tumours also frequently contain intralobar nephrogenic rests and are often of stromal predominant histology.11

Constitutional WT1 defects are associated with a range of overlapping phenotypes characterised by various combinations of three cardinal features: Wilms tumour, genitourinary abnormalities, and renal dysfunction.

WAGR syndrome

WAGR (Wilms-aniridia-genitourinary-mental retardation) syndrome (OMIM 194072) was the first WT1 associated condition to be characterised and is found in around 7–8/1000 individuals with Wilms tumour.12 It manifests with complete or partial aniridia, ambiguous external genitalia and cryptorchidism in males, and intellectual impairment. The risk of renal failure is high, affecting around 40% of individuals by the age of 20 years (median age of diagnosis 15 years).13 Heterozygous constitutional microdeletions at 11p13 encompassing both WT1 and PAH are responsible for WAGR, with the WT1 deletion causing the genitourinary features and Wilms tumour predisposition and deletion of PAH resulting in aniridia. Approximately 30% of individuals with aniridia carry microdeletions that encompass WT1, with the remainder usually harbouring smaller deletions or intragenic PAH mutations.14 These latter individuals are not at increased risk of Wilms tumour. Rare individuals with 11p13 microdeletions involving WT1 but excluding PAH have been reported and present with Wilms tumour or genitourinary abnormalities, or both, but without aniridia.15 16

Denys-Drash syndrome

Denys-Drash syndrome (OMIM 194080) classically describes the triad of Wilms tumour, nephropathy, and genitourinary abnormalities in males, which may be severe enough to result in pseudohypoaldosteronism.17 18 The nephropathy results from a characteristic mesangial sclerosis and typically presents with hypertension and proteinuria, usually progressing to renal failure and requiring renal replacement therapy before the age of 10 years.19 Genitourinary abnormalities in males are very common but are highly variable in severity, ranging from mild hypospadias to female external genitalia and streak gonads. While some XX individuals show gonadal dysgenesis, the majority have no gonadal abnormality and present with nephropathy or Wilms tumour. Most individuals with classic Denys-Drash syndrome harbour missense mutations affecting critical residues in the zinc finger domains that are implicated in DNA binding and are believed to act in a dominant negative fashion.20

Frasier syndrome

Frasier syndrome (OMIM 136680) describes the association of nephropathy with gonadal dysgenesis and gonadalablastoma.21 The nephropathy is typically a focal segmental glomerulosclerosis, which progresses to renal failure by the second or third decade.22 The genitourinary abnormalities in males are usually severe, and sex reversal in XY individuals is common. Frasier syndrome is caused by mutations in intron 9 that alter WT1 splicing and prevent the formation of WT1 isoforms that normally include a linker of three amino acids (KTS) between the third and fourth zinc fingers encoded by exons 9 and 10, respectively.23

Other WT1 associated phenotypes

WT1 mutations have also been reported in individuals with either one or two of the three cardinal features. Such individuals are more likely to harbour intragenic truncating WT1 mutations than missense mutations in the zinc finger domains. Several individuals with Wilms tumour in the absence of any other phenotypic abnormalities have been reported, but only around 2% of non-syndromic Wilms tumour patients carry germline WT1 mutations.24 Most are de novo, but rare families with a WT1 mutation/deletion resulting in more than one individual with Wilms tumour in the family are known.25 26

Table 1

<table>
<thead>
<tr>
<th>Conditions with an increased risk of Wilms tumour</th>
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<tr>
<td><strong>High risk (&gt;20%)</strong></td>
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<tr>
<td>• WT1 deletions (including WAGR syndrome)</td>
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<tr>
<td>• Truncating and pathogenic nonsense WT1 mutations (including Denys-Drash syndrome)</td>
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<tr>
<td>• Familial Wilms tumour</td>
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<td>• Perlman syndrome</td>
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<td>• Mosaic variegated aneuploidy</td>
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<tr>
<td>• Fanconi anemia D1/Biallelic BRCA2 mutations</td>
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<tr>
<td><strong>Moderate risk (5–20%)</strong></td>
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<tr>
<td>• WT1 intron 9 splice mutations (Frasier syndrome)</td>
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<tr>
<td>• Beckwith-Wiedemann syndrome caused by 11p15 uniparental disomy, isolated H19 hypermethylation, or of unknown cause</td>
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<tr>
<td>• Simpson-Golabi-Behm syndrome caused by GPC3 mutations/ deletions</td>
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<tr>
<td><strong>Low risk (&lt;5%)</strong></td>
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<tr>
<td>• Isolated hemihypertrophy*</td>
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<tr>
<td>• Bloom syndrome</td>
</tr>
<tr>
<td>• Li-Fraumeni syndrome/Li-Fraumeni-like syndrome</td>
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<tr>
<td>• Hereditary hyperparathyroidism-jaw tumour syndrome</td>
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<tr>
<td>• Multiexynanism</td>
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<tr>
<td>• Trisomy 18</td>
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<tr>
<td>• Trisomy 13</td>
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<tr>
<td>• 2q37 deletions</td>
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*Individuals with hemihypertrophy caused by 11p15 uniparental disomy or isolated H19 hypermethylation are at moderate risk of Wilms tumour. WAGR, Wilms-aniridia-genitourinary-mental.
The risk of Wilms tumour varies in different WT1 associated conditions. The Wilms tumour risk in individuals with microdeletions, missense mutations affecting zinc finger domains, or mutations that result in premature protein truncation is high—probably at least 50%.31,34 Missense mutations outside the zinc finger domains may be rare non-pathogenic polymorphisms, and caution should be exercised in their interpretation, particularly if they are not de novo. The risk of Wilms tumour in individuals with intron 9 splicing mutations is considerably lower than for other mutations; only four of 48 individuals reported with Frasier syndrome (8%) developed Wilms tumour.26–28 However, the risk of gonadal tumours is high in Frasier syndrome, whereas such tumours are rare in individuals with other classes of WT1 abnormality.

**Familial Wilms tumour**

Only 1–2% of Wilms tumour cases cluster within families, but the underlying causes of these rare pedigrees are heterogeneous and complex. A minority of families with more than one individual with Wilms tumour are associated with syndromes described elsewhere in this review: WT1 mutations/deletions (four families),24,25 mosaic variegated aneuploidy syndrome (two families),31 biallelic BRCA2 mutations (one family),32 and 11p15 defects (one family).33 However, the underlying cause of most familial Wilms tumour is currently unknown.

An autosomal dominant Wilms tumour predisposition gene, FWT1, has been mapped to 17q21 but has not been identified.34–35 Wilms tumour in FWT1 linked families tends to be diagnosed at a later age and more advanced stage than sporadic Wilms tumour (median age at diagnosis six years). The penetrance of FWT1 mutations is only around 30% and the wild-type allele is not lost in tumours. These features suggest that FWT1 does not operate as a classical tumour suppressor gene.36 It has been proposed that there is a second familial Wilms tumour gene, FWT2, on 19q13. The evidence in favour of this locus is suggestive but not conclusive, as no single family with a LOD (log of odds) score >3 in excess of 3 has been identified. Although combining the LOD scores of five smaller families gave a LOD score >3 in the original paper, some of these families were also consistent with linkage at FWT1, and families unlinked at 19q13 were excluded from the analysis.37 Furthermore, several families not linked to WT1, FWT1, or FWT2 exist, indicating further genetic heterogeneity in familial Wilms tumour.38 As a consequence of this genetic heterogeneity, the penetrance, age distribution, and tumour histology observed in familial Wilms tumour pedigrees shows marked intrafamilial and interfamilial variation.

**Childhood overgrowth syndromes**

Childhood overgrowth syndromes are a heterogeneous, overlapping, and poorly defined collection of conditions. It is sometimes assumed that any condition involving overgrowth in childhood has an increased risk of malignancy. In part this may be because high birth weight has been identified as a possible risk factor for Wilms tumour in several main population based studies.39–44 However, the importance of birth weight as a risk factor outside the context of overgrowth disorders that predispose to Wilms tumour is unclear. Moreover, conclusive evidence of an increased risk of Wilms tumour has only been demonstrated in a minority of overgrowth conditions, and in some overgrowth conditions the incidence of this tumour has been shown to be very low.45 There is also no evidence that children with non-specific overgrowth have an increased tumour risk. Therefore, the Wilms tumour risk of overgrowth conditions should be evaluated on a syndrome specific rather than a collective basis.

**Beckwith-Wiedemann syndrome**

Beckwith-Wiedemann syndrome (BWS; OMIM 130650) is an overgrowth disorder with a prevalence of around 1 in 14 000.46 In addition to prenatal and postnatal overgrowth, characteristic clinical findings include macroGLOSSIA, anterior abdominal wall defects, ear creases and pits, neonatal hypoglycaemia, and hemihypertrophy. Non-malignant abnormalities of the renal tract include nephromegaly, multiple renal cysts, medullary sponge kidney, medullary dysplasia, hydroureter, and renal stone disease.47 The overall risk of childhood malignancy in BWS has been estimated to be 4–21%. Wilms tumour is the most frequently reported tumour, affecting 1–8% of individuals.48–50 Bilateral Wilms tumour (17%) and nephroblastoma (7%) are increased in BWS, and occur at increased frequency compared with unselected series of Wilms tumour patients (5% and 15%, respectively).49,50 BWS is caused by dysregulation of imprinted genes at chromosome 11p15 that control prenatal and childhood growth. Various genetic and epigenetic abnormalities at 11p15 have been demonstrated in BWS. In this review, these are beyond the scope of this article and the reader is referred to recent reviews.51 Isolated hypomethylation of a differentially methylated region, known as KvDMR1, is the commonest cause of BWS, found in around 50% of cases. Mosaic paternal uniparental disomy of 11p15 is present in around 20% of individuals and is particularly associated with hemihypertrophy. Isolated hypermethylation of the H19 differentially methylated region and mutations in the growth suppressor, CDKN1C, each occur in about 5% of cases. CDKN1C mutations can result in fetal BWS if the mutations are maternally transmitted. Chromosomal aberrations affecting 11p15 including translocations, inversions, duplications, and rarely ring chromosomes, and microdeletions are found in a small number of individuals (1–2%). These are reviewed elsewhere and are not individually documented here.45 The cause of BWS is unknown in about 20% of cases.

Several studies have evaluated tumour risk in the epigenetic subgroups of BWS, although the risk is somewhat difficult to quantify because some studies preferentially include cases with tumours while others do not report tumour types.52–56 Overall, current data suggest the risk of Wilms tumour is appreciably increased with defects that result in an absolute increase of growth promoters (such as isolated hypomethylation at KvDMR1), but is either not increased or only modestly increased with defects that solely result in decrease in growth suppressors (such as isolated hypermethylation of KvDMR1 or CDKN1C mutation).45 The 20% of individuals without an identified underlying cause are at increased risk of Wilms tumour. Importantly, the largest group of individuals with BWS—those with isolated loss of methylation at KvDMR1—do not appear to be at increased risk of Wilms tumour.51–53 11p15 epigenotyping in BWS therefore not only provides molecular confirmation of the diagnosis in many individuals, but also facilitates identification of the subset of individuals with BWS who are at increased risk of Wilms tumour.

**Simpson-Golabi-Behmel syndrome**

Simpson-Golabi-Behmel syndrome (OMIM 312870) is an X linked overgrowth disorder associated with coarse facial features, skeletal and cardiac abnormalities, accessory nipples, and intellectual impairment in some individuals. Renal dysplasia or nephromegaly is reported in around 30% of cases and hydroureter and hydronephrosis are also described.62 Mutations or deletions of Glypican-3 (GPC3) at Xq26 cause Simpson-Golabi-Behmel syndrome and are found in about 70% of affected individuals.44 The cause in the remainder is unknown, although one family with a more severe phenotype
(but no cases of Wilms tumour) was linked to Xp22.46 GPC3 is a cell surface heparan sulphate proteoglycan that modulates the effects of several growth factors and interacts with the Wnt pathway.46–47 Although it was initially proposed that GPC3 could directly interact with insulin-like growth factor 2 (IGF2), thus providing a functional link between the phenotypically overlapping conditions of BWS and Simpson-Golabi-Behmel syndrome,48 there is no current evidence linking GPC3 with the IGF2 pathway.49 Of the 35 patients with GPC3 mutations reported, three (9%) developed Wilms tumour.44,64,65 Other embryonal tumours can also rarely occur. There is no evidence to suggest an increased risk of Wilms tumour in female GPC3 mutation/deletion carriers or in individuals with a clinical diagnosis of Simpson-Golabi-Behmel syndrome but without GPC3 mutations.

Isolated hemihypertrophy
Isolated hemihypertrophy (OMIM 235000; also referred to as isolated hemihyperplasia) is a poorly defined term referring to asymmetrical overgrowth that results in one region of the body being larger than its counterpart on the other side. Hemihypertrophy is associated with various genetic syndromes (including Beckwith-Wiedemann, proteus, Klippel-Trenaunay-Weber, and cutis-marmorata-telangiectatica-congenita) but the majority of individuals present without signs of another genetic condition and are said to have isolated (or idiopathic) hemihypertrophy (IHH). Estimates of the prevalence of IHH vary from 1 in 13,000 to 1 in 86,000.72–74 However, the distinction of IHH from normal variation in limb width/length is unclear and there is no consensus on diagnostic criteria. This is exemplified by data showing that the hemihypertrophy was so subtle in more than 50% of individuals reported with tumours in association with IHH that it was only diagnosed at tumour diagnosis or later.75–76 Lack of clarity about diagnostic criteria together with a predilection to describe any degree of asymmetry in children with tumours as “hemihypertrophy” makes the true frequency of IHH or the proportion of individuals that develop tumours very difficult to estimate.

A prospective study of 168 patients with IHH reported 10 tumours in nine individuals, of whom five (3%) had Wilms tumour, suggesting that the risk of Wilms tumour is modestly increased.77 Notably, tumours occur at equal frequency in the larger and smaller kidney in asymmetrical individuals. Abnormalities within the IHH region at 11p15 that are known to cause BWS (see above) have been reported in 20–35% of those with hemihypertrophy in two small series of cases of hemihypertrophy and childhood tumours (five of 14 and three of 15, respectively)78 and in another series of individuals without tumours (eight of 27).79 It would be anticipated that such individuals would carry similar risks of Wilms tumour as those with BWS because they have the same epigenetic defect. It is unclear whether IHH patients without 11p15 defects are at increased risk of Wilms tumour. There have been isolated reports of individuals with karyotypic abnormalities such as trisomy 8 mosaicism and diploid-triploid mosaicism in IHH.80 However, the cause of the majority of cases is unknown.

Perlman syndrome
Perlman syndrome (OMIM 267000) is an autosomal recessive condition characterised by prenatal overgrowth with polyhydramnios, viscerocele, facial dysmorphism, developmental delay, cryptorchidism, renal dysplasia, Wilms tumour, and high mortality in infancy.81 The cause is unknown, although a GPC3 mutation was identified in one family, emphasising the clinical overlap with Simpson-Golabi-Behmel syndrome.82 Seven of the 21 cases reported (33%) developed Wilms tumour83–89 and nephroblastomatosis or renal hamartomas, or both, have been identified in all but one of the infants born at term.90 Of the eight individuals who survived beyond 28 days, five developed Wilms tumour. No other tumours have been reported.

Tumour predisposition syndromes
Constitutional mutations in at least 70 genes are known to confer susceptibility to benign or malignant tumours,91 but only a small minority is associated with an increased risk of Wilms tumour. In addition, the occurrence of familial clustering of Wilms tumour with other malignancies (such as neuroblastoma) that cannot be accounted for by mutations in known genes suggests the existence of as yet uncharacterised tumour predisposition syndromes which increase the risk of Wilms tumour (Rahman N, unpublished data).

Mosaic variegated aneuploidy
Mosaic variegated aneuploidy (OMIM 257300) is an autosomal recessive disorder characterised by constitutional mosaicism for losses and gains of whole chromosomes. Biallelic mutations in BUB1B—which encodes BUB1, a component of the mitotic spindle checkpoint—cause around 15% of cases (Hanks et al.92 and Rahman N, unpublished data). Clinical features are variable and include microcephaly, growth retardation, developmental delay, cataracts, and congenital heart defects. Childhood cancers—including Wilms tumour, rhabdomyosarcoma and haematological malignancies—have been reported in a number of patients. Wilms tumour is the most commonly reported cancer, present in 10 of 40 published cases (25%).93–96

Biallelic BRCA2 mutations/Fanconi anaemia D1
Fanconi anaemia is an autosomal recessive condition characterised by short stature, radial ray defects, abnormal skin pigmentation, and bone marrow failure. Myelodysplastic syndrome and acute myeloid leukaemia often occur in childhood and there is an increased risk of solid tumours in those who survive to adulthood.97 Cells from individuals with Fanconi anaemia show increased chromosome breakage when exposed to DNA cross linking agents. At least 12 complementation groups have been defined and 11 genes identified.97–98 BRCA2 encodes a protein involved in repair of double strand DNA breaks.99 Heterozygous (monoallelic) constitutional mutations in BRCA2 predispose to breast and ovarian cancers in adulthood, but not to childhood cancers. Biallelic BRCA2 mutations cause Fanconi anaemia subgroup D1 (OMIM 605724). Affected children are less likely to have skeletal abnormalities and their cells often show spontaneous chromosome breaks, in contrast to other subgroups. The cancer spectrum is also distinctive with a high risk of childhood solid tumours, particularly Wilms tumour and brain tumours.32,100 Five of the 24 reported cases (21%) developed Wilms tumour.32,101–102 The risk of Wilms tumour in other Fanconi anaemia subgroups does not appear to be increased.

Bloom syndrome
Bloom syndrome (OMIM 210900) is an autosomal recessive chromosomal instability disorder characterised by short stature, sun sensitive telangiectatic erythematous skin lesions, areas of hyperpigmented and hypopigmented skin, immunodeficiency, and a characteristic facial appearance. It is caused by biallelic mutations in BLM,103 which encodes a DNA helicase important in protection against aberrant recombination between sister chromatids and homologous chromosomes. Bloom syndrome is associated with a range of malignancies and around 50% of cases develop cancer.104 Fewer than 200 individuals with Bloom syndrome have been reported, six (7%) of whom developed Wilms tumour, suggesting that the risk of this tumour is low.105–107
Li-Fraumeni syndrome

Li-Fraumeni syndrome (OMIM 151623) is an autosomal dominant tumour predisposition syndrome characterised by a high incidence of a range of tumours, notably breast cancer, sarcomas, adrenocortical cancer, and brain tumours.184 Heterozygous germline mutations in TP53—a gene with a crucial role in the induction of cell cycle arrest, apoptosis, and DNA repair in response to a variety of stimuli—are identifiable in around 70% of families with classical Li-Fraumeni syndrome.185–188 Wilms tumour is not one of the cardinal tumours included in the diagnostic criteria for this syndrome, but has been reported in at least six families harbouring TP53 mutations, and in several mutation negative families which fulfil the Li-Fraumeni syndrome and Li-Fraumeni-like diagnostic criteria.111–118 Five of the six TP53 mutations reported in association with Wilms tumour affect splicing. Such mutations account for only 4% of all reported germline TP53 mutations.176 This suggests that the risk of Wilms tumour in Li-Fraumeni syndrome may be influenced by the type of TP53 mutation. However, the Wilms tumour risk overall appears to be low, both in families with an identified TP53 mutation and in those with either classic Li-Fraumeni or a Li-Fraumeni-like phenotype in which TP53 mutations have not been found.

Hereditary hyperparathyroidism-jaw tumour syndrome

Hereditary hyperparathyroidism-jaw tumour syndrome (OMIM 145001) is an autosomal dominant condition characterised by fibro-osseous lesions of the maxilla and mandible and parathyroid tumours.119 Heterozygous inactivating mutations in the HRPT2 gene are causative.120 Preliminary evidence suggests that HRPT2 plays a role in transcriptional elongation and RNA processing.121 More than 100 affected individuals from around 40 families have been reported. A variety of renal abnormalities occur including renal cysts, benign mixed epithelial-stromal tumours, renal cortical adenomas, and papillary renal cell carcinomas.122–125 Wilms tumour has been reported in three individuals (<3%), one of whom apparently developed bilateral Wilms tumour at the exceptionally late age of 53 years.122,126

Mulibrey nanism

Mulibrey nanism (muscle-liver-brain-eye nanism; OMIM 253250) is an autosomal recessive disease with a phenotype that includes short stature, a distinctive facial appearance, yellowish dots in the peripheral retina, hepatomegaly, hepatic hamartomas, and ovarian fibrothecomas.127–129 Mutations in TRIM37, a member of the tripartite motif subfamily of zinc finger proteins, are causative.130 TRIM37 has been shown to have ubiquitin E3 ligase activity, although its substrates have not been identified.130 At least 110 individuals with mulibrey nanism have been reported, three of whom (<3%) developed Wilms tumour.127,131,132

Constitutional chromosomal abnormalities

In addition to karyotypic abnormalities affecting 11p13 and 11p15, at least three other constitutional chromosomal abnormalities are associated with an increased risk of Wilms tumour.

Trisomy 18

Trisomy 18 (Edwards syndrome) occurs in about 1 in 3000 live births and usually results in multiple congenital malformations.131 Over 90% of affected individuals die within the first year of life. Renal abnormalities, particularly horseshoe kidney, are common, occurring in more than half the cases.132 There have been 12 reports of Wilms tumour in individuals with trisomy 18.133–135 Furthermore, periblar nephrogenic rests or nephroblastomatosis, or both, have been reported in a number of cases in the absence of Wilms tumour.134 Of interest, the median age at diagnosis of Wilms tumour in trisomy 18 (five years) is greater than in sporadic Wilms tumour. Given the high early mortality of trisomy 18, the risk of Wilms tumour to long term survivors is clearly increased.

Trisomy 13

Trisomy 13 (Patau syndrome) occurs in around 1 in 10 000 live births and is associated with multiple congenital malformations including renal tract abnormalities.135 Neonatal and infant mortality is very high, with a median survival of one week.136 Two cases with Wilms tumour have been reported, one of which occurred within a horseshoe kidney.137,138 Given the very high early mortality in trisomy 13, the risk to those surviving the neonatal period is likely to be increased.

2q37 deletion

Three individuals with Wilms tumour in association with constitutional terminal deletions of chromosome 2q have been reported. Two had isolated deletions of 2q37 with the proximal breakpoint at 2q37.1.139,140 The third had a paternally inherited unbalanced chromosomal translocation that resulted in monosomy 2q37 and trisomy 15q22-qter.141 All three children had congenital gonadal/urogenital abnormalities. At least 66 individuals have been reported with isolated terminal deletions of chromosome 2q. The most frequently reported breakpoint is 2q37.3 and only 15 cases have been reported with a breakpoint at 2q37.1.142 Seven of the 66 cases (11%) with terminal 2q deletions are reported to have gonadal/urogenital abnormalities, including four of 15 (27%) with a breakpoint at 2q37.1. The overall risk of Wilms tumour in individuals with a 2q37 deletion may be as high as 3% (two of 66). However, it is possible that the risk is primarily to individuals with deletions extending to 2q37.1, who may therefore be at higher risk.

CONDITIONS IN WHICH AN INCREASED RISK OF WILMS TUMOUR IS UNCERTAIN OR UNLIKELY

In a large number of the conditions reported in association with Wilms tumour an increased risk of this tumour is uncertain or unlikely (table 2). For relatively common conditions in which only a few cases of Wilms tumour have been reported it is likely that the occurrence of the tumour is coincidental and that the conditions are not associated with an increased risk. For example, fragile X syndrome, Marfan syndrome, and tuberous sclerosis are all relatively common conditions in which only a single individual with Wilms tumour has been reported, while it has been reported in two cases of Down syndrome.143–148 Wilms tumour has been reported in seven individuals with neurofibromatosis type 1.149 However, neurofibromatosis type 1 occurs in around 1 in 3000 of the general population, and several large population based,150 cohort,151,152 and cancer registry studies153 have found no evidence of an increased risk for this tumour. For other conditions a small increased risk cannot be excluded on the basis of available data, but the absolute risk of Wilms tumour is very small. For example, Sotos syndrome—an overgrowth disorder caused by haploinsufficiency of NSD1—was reported to be associated with Wilms tumour and other cancers, based on cases with a clinical diagnosis of the syndrome, which can be difficult for those without experience of the condition.160 The advent of molecular diagnosis has shown that the incidence of Wilms tumour in individuals with NSD1 abnormalities is very low.161 Similarly, four individuals with Turner syndrome were found among an American series of 5854 cases with Wilms tumour, two of which occurred in a horseshoe kidney.162 No case of Wilms tumour was identified in a British series of 400...
individuals with Turner syndrome,182 and only a single Wilms tumour was reported among a Danish series of 597 individuals with Turner syndrome.183 These data suggest that the risk of Wilms tumour in Turner syndrome is close to the population risk.

In the case of rarer conditions reported in association with Wilms tumour (table 2), and the many published individuals with this tumour whose phenotypes are not readily classifiable,8 9 193 194 it is difficult to clarify whether reports represent coincidental findings or reflect an increased risk of Wilms tumour,204 which may be implicated in the occurrence of Wilms tumour in these individuals.

Various congenital abnormalities have been suggested to be associated with an increased risk of Wilms tumour outside the context of syndromes and constitutional chromosomal abnormalities.210–213 While an increased risk can rarely be excluded on the basis of available data it is clear that the magnitude of any increased risk can only be small. For example, horseshoe kidney was found in 35 of 8617 American Wilms tumour patients (0.41%) (excluding cases with chromosomal abnormalities), compared with a population incidence of around 1 in 400 (0.25%).214 This suggests that the function of a Wilms tumour predisposition gene. For example, two distinct but overlapping abnormalities of chromosome 15q have been reported in individuals with Wilms tumour.198 202 Both result in an increased number of copies of IGFIR, which may be implicated in the occurrence of Wilms tumour in these individuals.

Table 2 Phenotypes reported in association with Wilms tumour in which an increased risk is uncertain or unlikely

<table>
<thead>
<tr>
<th>Disorder</th>
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<th>No of cases (families)</th>
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<td>Loss of SNRPN methylation; no evidence of 15q11 deletion or UPD</td>
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<td>Angelman syndrome</td>
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<tr>
<td>Cleidocranial dysostosis</td>
<td>119600</td>
<td>1</td>
<td>Two cases have also been reported with nephrogenic rests 152 153</td>
<td>152</td>
</tr>
<tr>
<td>Cornelia de Lange syndrome</td>
<td>122470</td>
<td>1</td>
<td>Presacral ectopic Wilms tumour</td>
<td>154</td>
</tr>
<tr>
<td>Curroirana syndrome</td>
<td>176450</td>
<td>1</td>
<td></td>
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</tr>
<tr>
<td>Down syndrome</td>
<td>190685</td>
<td>2 (2)</td>
<td></td>
<td>155, 156</td>
</tr>
<tr>
<td>Epidermal naevus syndromes</td>
<td>–</td>
<td>3 (3)</td>
<td></td>
<td>157–159</td>
</tr>
<tr>
<td>Fragile-X syndrome</td>
<td>309550</td>
<td>1</td>
<td></td>
<td>160</td>
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<tr>
<td>Greig cephalopolysyndactyly syndrome</td>
<td>175700</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hoy-Wells syndrome</td>
<td>106260</td>
<td>1</td>
<td>Bilateral Wilms tumour; familial reticulate pigmentation of skin also present</td>
<td>161</td>
</tr>
<tr>
<td>Holoprosencephaly and neuronal migration defects</td>
<td>–</td>
<td>1</td>
<td></td>
<td></td>
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<tr>
<td>Hyperprolinemia type 1</td>
<td>239500</td>
<td>1</td>
<td>Renal abnormalities present in three generations of the family</td>
<td>162</td>
</tr>
<tr>
<td>Imperforate anus with rectourethral fistula</td>
<td>–</td>
<td>1</td>
<td></td>
<td>163</td>
</tr>
<tr>
<td>Incontinence pigmendi</td>
<td>308300</td>
<td>2 (2)</td>
<td></td>
<td>164, 165, 166</td>
</tr>
<tr>
<td>Juvenile polyposis syndrome</td>
<td>174900</td>
<td>1</td>
<td>BMPRIA splice-site mutation; colonic carcinoma, adrenal hamartoma, Ebstien anomaly</td>
<td>167</td>
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<tr>
<td>Klippel-Trenaunay syndrome</td>
<td>149000</td>
<td>1</td>
<td>Bilateral nephroblastomatosis also reported in one case</td>
<td>168, 169</td>
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<tr>
<td>Macrocephaly-cuts marmorata telangiectatica congenita</td>
<td>602501</td>
<td>1</td>
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<tr>
<td>Marfan syndrome</td>
<td>154700</td>
<td>1</td>
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<td>171</td>
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<tr>
<td>Marshall-Smith syndrome</td>
<td>602535</td>
<td>1</td>
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<td>172</td>
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<tr>
<td>Moebius syndrome</td>
<td>157900</td>
<td>1</td>
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<td>173</td>
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<tr>
<td>Monopodal syrenomelia</td>
<td>–</td>
<td>1</td>
<td></td>
<td>174</td>
</tr>
<tr>
<td>Neuralabromatosis type 1</td>
<td>162200</td>
<td>7 (7)</td>
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<td>175</td>
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<tr>
<td>Noonan syndrome</td>
<td>163990</td>
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<td>176</td>
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<tr>
<td>Osteogisis imperfecta</td>
<td>–</td>
<td>1</td>
<td>Molecular defect not defined; hemihypertrophy</td>
<td>177</td>
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<tr>
<td>Peters anomaly</td>
<td>604229</td>
<td>1</td>
<td></td>
<td>178</td>
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<tr>
<td>Pierre Robin sequence</td>
<td>261800</td>
<td>1</td>
<td>Developmental delay</td>
<td>179</td>
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<tr>
<td>Poland anomaly</td>
<td>173800</td>
<td>1</td>
<td>Ipsilateral shortening of lower limb</td>
<td>180</td>
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<tr>
<td>Polycystic kidneys, ichthyosis, and ear malformations</td>
<td>–</td>
<td>1</td>
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<td>181</td>
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<tr>
<td>Prader-Willi syndrome</td>
<td>176270</td>
<td>1</td>
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<td>182</td>
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<td>Russell-Silver syndrome</td>
<td>180860</td>
<td>1</td>
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<td>183</td>
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<tr>
<td>Tuberous sclerosis</td>
<td>191100</td>
<td>1</td>
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<td>184</td>
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<tr>
<td>Turner syndrome</td>
<td>–</td>
<td>6 (6)</td>
<td></td>
<td>185</td>
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<tr>
<td>VATER association</td>
<td>192350</td>
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CONCLUSIONS
This review provides clear evidence of an increased risk of Wilms tumour in a broad range of syndromes and chromosomal disorders (table 1). The clinical heterogeneity of these disorders is matched by the functional diversity of their causative genes. The absence of any known functional interaction between most of these genes demonstrates the diversity of molecular pathways by which Wilms tumorigenesis occurs.

Emerging evidence continues to modify the spectrum of conditions associated with predisposition to Wilms tumour and to refine the level of risk. Of particular interest is the recent evidence that different mechanisms of epigenetic dysregulation can have a substantial impact on the risk of Wilms tumour. The continued clarification of the phenotypic groups and subgroups predisposed to Wilms tumour will foster further insights into the molecular basis of these conditions and Wilms tumorigenesis, and will facilitate the diagnosis of underlying disorders in children with Wilms tumour. In addition, it provides a basis for the management and counselling of a child with a possible Wilms tumour predisposition syndrome. While the methods and inclusion criteria for Wilms tumour screening are contentious and beyond the scope of this review, the inclusion of any patient group must be considered in the context of their level of risk.218

ELECTRONIC DATABASES USED TO IDENTIFY CONDITIONS REPORTED IN ASSOCIATION WITH WILMS TUMOUR

Syndromes associated with Wilms tumour


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Syndromes associated with Wilms tumour


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Syndromes and constitutional chromosomal abnormalities associated with Wilms tumour

R H Scott, C A Stiller, L Walker and N Rahman

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