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Chapter 2

TP53 germline mutation testing in 180 families suspected of Li-Fraumeni syndrome: mutation detection rate and relative frequency of cancers in different familial phenotypes

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Abstract
Li-Fraumeni syndrome (LFS) is a rare autosomal dominant cancer predisposition syndrome. Most families fulfilling the classical diagnostic criteria harbour *TP53* germline mutations. However, *TP53* germline mutations may also occur in less obvious phenotypes. As a result, different criteria are in use to decide which patients qualify for *TP53* mutation analysis, including the LFS, Li-Fraumeni-like (LFL) and Chompret criteria. We investigated which criteria for *TP53* mutation analysis resulted in the highest mutation detection rate and sensitivity in Dutch families. We describe the tumour spectrum in *TP53*-positive families and calculated tumour type-specific relative risks.
A total of 180 Dutch families referred for *TP53* mutation analysis were evaluated. Tumour phenotypes were verified by pathology reports or clinical records.
A *TP53* germline mutation was identified in 24 families. When the Chompret criteria were used 22/24 mutations were detected (sensitivity 92%, mutation detection rate 21%). In LFS and LFL families 18/24 mutations were found (sensitivity 75%). The two mutations detected outside the 'Chompret group' were found in a child with rhabdomyosarcoma and a young woman with breast cancer. In the mutation carriers, in addition to the classical LFS tumour types, also colon and pancreatic cancer were found significantly more often than in the general population.
We suggest *TP53* mutation testing for all families fulfilling the Chompret criteria. In addition, *TP53* mutation testing can be considered in the event of childhood sarcoma and breast cancer before 30 years. In addition to the risk for established LFS tumour types, *TP53*-positive individuals may also have an elevated risk for pancreatic and colon cancer.

Introduction

In 1969 Li and Fraumeni described a novel autosomal dominant cancer syndrome with a predisposition to bone and soft tissue sarcoma, breast cancer, brain tumour, adrenal cortical carcinoma and leukaemia [1]. LFS patients are at increased risk for multiple primary tumours [3]. Clinical criteria for classical Li-Fraumeni syndrome (LFS) [6] and Li-Fraumeni-like syndrome (LFL) have been established [7] whereby at least three family members were affected (see Table 1). Different LFL criteria were formulated by Eeles [110] who defined only two family members as being affected. In 1990 DNA analysis for LFS became available when germline mutations in the *TP53* gene were found in LFS kindreds [4]. All germline mutations that have been detected and published are collected in the IARC mutation database [35]. Currently 423 mutations have been described in 419 families (http://www-p53.iarc.fr/). In a study by Varley et al. *TP53* germline mutations were seen in approximately 75% of LFS and 40% of LFL families [8]. Because *TP53* germline mutations were also identified in families not fulfilling the LFS/LFL criteria due to their alternative tumour spectrum, age at diagnosis or sporadic occurrence of cancer, Chompret proposed different criteria for *TP53* germline mutation testing [9], which were updated in 2009 [10] (see Table 1). A *TP53* germline mutation was found in 29% and 35% of French and American families respectively who fulfilled the 2001 Chompret criteria [34, 111]. Table 1 summarizes the different criteria used to categorize families suspected of LFS. The classical LFS criteria [6], the LFL criteria according to Birch [7] and the revised Chompret criteria by Tinat et al. [10] are used for this article.

In *TP53* mutation carriers the tumour spectrum is wider than the classical tumour types used to recognize LFS (or LFL) defined in 1988 as breast cancer, sarcoma, brain tumour, adrenal cortical cancer and leukaemia [6]. Roughly, 20%-30% of the tumours in *TP53* mutation-positive families do not belong to the classical LFS tumour spectrum [5, 112, 113].
Besides the classical tumour spectrum, Birch et al. [5] found Wilms' tumour and phyllodes tumours to be strongly associated, pancreatic cancer moderately associated and neuroblastoma weakly associated in *TP53* mutation carriers.

In this study we evaluated the clinical spectrum of families undergoing *TP53* mutation analysis in the Netherlands, in order to help improve the guidelines specifying when *TP53* mutation analysis should be performed. We chose a probability of more than 10% to detect a germline mutation in order to be eligible for DNA analysis. We also examined specific tumour type relative cancer risks in the *TP53* mutation families. In addition, cancer risks for *TP53*-positive and *TP53*-negative LFL families were compared to identify tumour types, apart from the typical LFS tumours, that are more specifically associated with a *TP53* mutation.

Table 1. Criteria used for *TP53* germline mutation testing

Classical LFS criteria Li et al. [3]	- a proband with sarcoma diagnosed under the age of 45 years AND - a first-degree relative with any cancer under 45 years AND - another first- or second-degree relative with either cancer under 45 years or a sarcoma at any age
LFL criteria Birch et al. [4]	- a proband with any childhood cancer or sarcoma, brain tumour or adrenal cortical tumour under the age of 45 years AND - a first- or second degree relative with a typical LFS cancer at any age AND - a first- or second degree relative in the same lineage with any cancer under 60 years
LFL criteria Eeles et al. [5]	- two different tumours that are part of extended LFS in first- or second degree relatives at any age (sarcoma, breast cancer, brain tumour, leukaemia, adrenal cortical tumour, melanoma, prostate cancer and pancreatic cancer)
LFS Chompret criteria Chompret et al. [9]	- a proband affected by a narrow spectrum cancer (sarcomas, brain tumours, breast cancer and adrenal cortical carcinoma) before 36 years and at least one first or second degree relative affected by a narrow spectrum tumour (other then breast cancer if the proband is affected by breast cancer) before 46 years or multiple primary tumours OR - a proband with multiple primary tumours two of which belong to the narrow spectrum and the first of which occurred before 36 years OR - a proband with adrenal cortical carcinoma whatever the age of onset and family history
LFS Chompret criteria revised Tinat et al. [10]	- a proband with a tumour belonging to the LFS tumour spectrum (soft tissue sarcoma, osteosarcoma, brain tumours, pre-menopausal breast cancer, adrenal cortical carcinoma, leukaemia, lung bronchoalveolar cancer) before 46 years and at least one first or second degree relative with an LFS tumour (except breast cancer if the proband is affected by breast cancer) before 56 years or multiple primary tumours OR - a proband with multiple primary tumours (except multiple breast tumours), two of which belong to the LFS tumour spectrum and the first of which occurred before 46 years OR - a proband with adrenal cortical carcinoma or choroid plexus tumour, irrespective of the family history

Patients and methods

Patients

In the Netherlands, *TP53* mutation analysis was introduced in a clinical setting in 1995. The clinical use of *TP53* mutation testing, including exon sequencing and genomic analysis, is started after indication according to the LFS and LFL criteria and was influenced by the limited preventive strategies. In 2005 the second version of the Dutch national guidelines recommended *TP53* mutation testing for LFS, LFL, patients with multiple LFS-associated tumours and children with adrenal cortical carcinoma. In addition, *TP53* analysis should be considered for breast cancer under 30 years of age [114]. From 1995 till 2008, Dutch clinicians referred 180 families for counselling and *TP53* germline mutation testing predominantly because of the occurrence of cancer types possibly related to LFS. The families were classified into 4 groups: 1) families fulfilling the revised Chompret criteria [10], 2) classic LFS [6] (excluding the revised Chompret criteria), 3) LFL according to Birch [7] (excluding the revised Chompret criteria and LFS) and 4) other families considered to be suggestive of a germline *TP53* defect (LFS-suspected: two or more primary tumours at any age, two first degree relatives with a tumour at any age, of which at least one tumour is a typical LFS tumours (sarcoma, brain tumour, breast cancer, leukaemia and adrenal cortical cancer), early onset (before 21 years of age) sarcoma or brain tumours and breast cancer before 35 years of age (without detectable *BRCA1* or *BRCA2* mutation) (Table 2a). In addition, in Table 2b the total number of families fulfilling the LFS or LFL criteria regardless of Chompret criteria are summarized.

The sensitivity and specificity were calculated for the revised Chompret, LFS and LFL criteria. The sensitivity was calculated as the number of *TP53*-positive families meeting a classification divided by the total number of *TP53*-positive families. The specificity was calculated as the number of *TP53*-negative families not meeting the specific classification divided by the total number of *TP53*-negative families.

Family members of proven *TP53* mutation carriers were counselled and offered *TP53* mutation testing.

Molecular analysis

DNA analysis was performed in two laboratories, in Amsterdam (161 families) and Groningen (19 families). DNA was isolated from peripheral blood lymphocytes according to standard procedures. In Amsterdam mutation analysis of the *TP53* gene in the index patient, affected by cancer, was performed by sequence analysis of all coding exons (2-11) and the flanking intron-exon boundaries of these exons using standard procedures and multiplex ligation-dependent probe amplification (MLPA) to screen for large *TP53* deletions or duplications (*TP53* MLPA KIT P056 produced by MRC-Holland) [115]. In Groningen the *TP53* gene was analysed by denaturing gradient gel electrophoresis (DGGE) [116]. All possible candidate variants, identified as aberrant DGGE fragments, were confirmed with sequence analysis. Details on primers and PCR conditions are available upon request. To assess the possibly pathogenic status of a mutation the frequency of each identified *TP53* germline mutations was determined in a control group of 150 anonymous blood donors, using denaturing gradient gel electrophoresis (DGGE). All possible candidate aberrant fragments were confirmed with sequence analysis.

Cancer risk

To estimate the relative cancer risk in the *TP53* positive families a study cohort of tested and untested family members was selected with at least a 50% prior probability of being a carrier.

Pedigrees of all LFS-counselled families were available through the clinical genetic centres, including age at cancer diagnosis and tumour types. From the pedigrees of the *TP53* positive families, all mutation carriers and their first-degree relatives were included. In the *TP53* negative LFL (non LFS) families, patients who were tested for *TP53* germline mutations and their first-degree relatives were included. Subsequently, the obligate carriers (father or mother) with their siblings were selected from the pedigree and included. We chose not to adjust for ascertainment

bias because of the multiple case definitions of LFS and LFL. We present the results for the typical LFS tumours separately from the other tumours.

All cancers were coded according to the International Classification of Disease, revision 9. We attempted to confirm all cancer diagnoses by collecting clinical records and pathology reports. Follow-up started on 1 January 1960 (because reference data were available from that time onwards) or date of birth, whichever occurred later, and ended at the date of first cancer diagnosis, date of death or the date of last contact.

Since 36% of the birth dates were missing, we introduced unknown birth dates based on the known birth dates in each generation of the family and the pedigree structure. The dates of death were used for missing dates of diagnosis for individuals who died from cancer at a known site. In addition, when the dates of diagnosis of affected individuals who did not die from cancer were missing, site-specific mean ages at diagnosis of cancer in the general population were used, based on data of the Comprehensive Cancer Centre Amsterdam and the Netherlands Cancer Registries. Cancer risk for all *TP53* positive and *TP53* negative LFL (non LFS) family members was assessed with the standardized incidence ratio relative to the risk in the general population (relative risk; RR), which is the ratio of observed to expected cases in the cohort. The expected number of cases was calculated by multiplying person years at risk by the age, sex, calendar period, and site-specific cancer incidence rates in the general population, with the use of a computer program developed at the Netherlands Cancer Institute [117]. Incidence rates were obtained from the Eindhoven Cancer Registry up to 1990 and from the Netherlands Cancer Registry from 1990 onwards.

The comparison of RRs for *TP53*-negative and *TP53*-positive families was performed within the LFL group (excluding LFS families).

Results

Among the 180 patients analysed for *TP53* mutations, 24 *TP53*-positive families were diagnosed (detection rate 13%). One of the 24 mutations was a large *TP53* rearrangement, a deletion of exons 2-11. None of the identified *TP53* germline mutations was identified in a control group of 150 anonymous blood donors. The 180 families were subdivided into 4 groups as described in 'Patients and Methods'. In these subgroups, 22 out of 105 (21%) families fulfilling the revised Chompret criteria carried a *TP53* germline mutation (Table 2a), 8 out of 11 (73%) classical LFS families carried a *TP53* germline mutation (Table 2b), 10 out of 36 (28%) LFL families (Table 2b) and 2 out of 70 (2.9%) in the remaining LFS-suspected group (Table 2a). The two mutations in the non- revised Chompret/LFS/LFL group occured in a child with rhabdomyosarcoma at 4 years of age and a woman with breast cancer at 24 years of age.

The overlap in families fulfilling the revised Chompret, LFS and LFL criteria is shown in Figure 1. No mutation was found in the 5 families that fulfilled the LFS or LFL criteria but did not fulfil the revised Chompret criteria (Table 2a). The LFS family that did not fulfil the revised Chompret criteria showed one sarcoma, no other typical LFS tumours, the other tumours did develop at young ages. The LFL families that did not fulfil the Chompret criteria did have two typical LFS tumours, but one of the tumours did not occur before 56 years of age. On average 3.7 individuals were tested in the *TP53*-positive families, revealing 2.8 individuals as mutation carriers; in the *TP53*-negative families only the index patient was tested.

The sensitivity for the revised Chompret criteria was 92% (22/24 *TP53* mutation families), the specificity was 47% (73/156). Eighteen out of 24 *TP53* mutation families fulfilled the LFS or LFL criteria (sensitivity 75%). The specificity for the combined LFS/LFL criteria was 81% (127/156). The sensitivity and specificity for the LFS criteria was 33% (8/24) and 98% (153/156), for the LFL criteria (excluding LFS) 42% (10/24) and 83% (130/156), respectively.

Table 2.
Families classified according to familial phenotype.

2a
Number of families (n=180) presented for *TP53* mutation analysis divided in 4 groups of different familial phenotypes (LFS-Chompret revised, LFS-Li, LFL-Birch and LFS-suspected) including the *TP53*-positive results (n=24)

(Family) history		Number of families (180)	*TP53*-positive families (%)
LFS-Chompret revised	including 10 LFS and 32 LFL	105	22 (21)
LFS-Li (not fulfilling revised Chompret)		1	0
LFL-Birch (not fulfilling revised Chompret)		4	0
LFS-suspected		70	2 (2.9)
	At least 2 primary tumours	30	0
	2 first degree relatives with cancer (at least 1 typical LFS tumour)	19	0
	early onset sarcoma or brain tumour (<21 years)	9	1
	breast cancer before 35 years	12	1

LFS-Chompret revised = the 2009 revised Chompret criteria for Li-Fraumeni syndrome [10], LFS-Li = Li-Fraumeni syndrome according to Li et al [3], LFL-Birch = Li-Fraumeni-like syndrome according to Birch [4], LFS-suspected = LFS suspected families that do not fulfill the revised Chompret, LFS or LFL criteria

Table 2b.
Families fulfilling the LFS or LFL criteria

(Family) history	Number of families	*TP53*-positive families (%)
LFS	11	8 (73)
LFL*	36	10 (28)

LFS = Li-Fraumeni syndrome, LFL = Li-Fraumeni-like syndrome, * = excluding LFS

Tumour spectrum and age of onset

In 52 affected family members (out of 24 families) a germline *TP53* mutation was identified; the mutations, tumour types and ages of onset are given in Table 3. The affected mutation carriers developed their first tumour at a mean age of 34.2 years (first tumour-age: range 11 months-69 years). When one large family with relative late onset cancers [118] was excluded, the first tumour developed at a mean age of 28.2 years. Twenty two of the 52 mutation carriers developed at least two primary tumours (42.3%). The mean age of onset of all 77 tumours in *TP53* mutation carriers was 37.4 years (all tumours-age: range 11 months-71 years). The tumour type most frequently detected was breast cancer (21/77 tumours; 27%), followed by soft tissue sarcoma (13/77; 17%) and brain tumours (12/77; 16%; 8 astrocytoma/glioblastoma, a choroid plexus carcinoma, a malignant plexus papilloma, a medulloblastoma and a ependyoma). In total

31% of tumours (24/77) were not part of the typical LFS tumour spectrum (breast cancer, soft tissue sarcoma, osteosarcoma, brain tumours, adrenal cortical tumours and leukaemia). Most tumours were symptomatic and detected before the diagnosis LFS/LFL or LFS-suspected was made; two kidney tumours (both renal cell carcinoma) were detected through ultrasound screening. In the 156 *TP53* negative families, the index patient was the only patient tested for *TP53* mutations. The first tumour in these 156 index patients was diagnosed at a mean age of 32.7 years (range 0.5 – 65 years, data not shown). In total 53/156 index patients developed at least two primary tumours (34%). The mean age of diagnosis of all tumours (236) was 38.2 years. In this group too, the most frequently seen tumour type was breast cancer (89/236, 38%), followed by soft tissue sarcoma (31/236, 13%) and melanoma (22/236, 9.3%); 38% of the tumours diagnosed in the index patients were not typical LFS tumours.

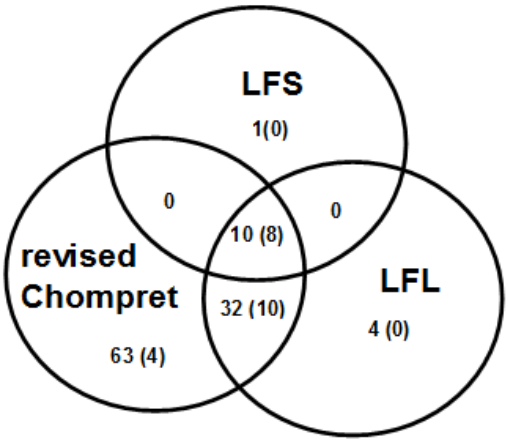
Cancer risk in TP53-positive families

Compared with the expected risks in the general population, the risks for colon, liver and pancreatic cancer were significantly increased in this *TP53*-positive group (RR 2.8, 18 and 7.3, respectively, Table 4a), in addition to those for the main LFS tumour types (RR ranging from 6.4 for breast cancer to 107 for bone cancer, Table 4). The overall relative cancer risk was increased four times (RR 4, 95% CI 3.3-4.8). On average 65% were confirmed by pathology reports (Table 4). Leukaemia was the only typical LFS cancer which showed a non-significantly elevated RR. Relative risks for all tumour types are shown in Table 4a.

Comparison of TP53-positive and TP53-negative LFL (non LFS) families

In the *TP53*-positive LFL families (overall cancer RR 6.4), the RRs for colon, liver and kidney cancer were significantly increased in addition to the RRs for the classical LFS tumour types (Table 4b). For the *TP53*-negative LFL families the risks for melanoma and lung and colon cancer were higher than in the general population (overall cancer RR 4.5, Table 4c).

Figure 1. Venn diagram showing the overlap of families fulfilling the revised Chompret criteria, LFS and LFL families



Number of families are given, in brackets are the mutation positive families (n=22).
Two *TP53* germline mutations are not included in the figure because they were found in patients that did not fulfil the criteria that are shown here.

Table 3. Clinical and molecular data on the 24 *TP53* germline mutation families.

exon/ intron	Base pair change	Protein effect	Fam-nr	criteria	Index case-age (age of death)	Family history: Tumour type-age (age of death)
4	c.374C>G	Thr125Arg#	1302	C-revised /LFL	Br-20 (25)	*B-30*/Br-43/Br-46 (46), *Br-?* (5), *Li-?* (28)
4	c.375G>A	Thr125Thr	1860	C-revised / LFL	B-40	Leu-35 (36), Br-24 (24), Br-5 (5), *B-41* (43)
5	c.422G>A	Cys141Tyr	1856	LFS-susp	B-24 (24)	*B-37* (37)
5	c.451C>T	Pro151Ser	6569	C-revised /LFL	Br-24	*STS-5* (?), *ACC-52* (?)
5	c.473G>A	Arg158His	93	C-revised /LFL	Pa-49 (50)	B-34/B-50 (53), STS-36/Lu-36 (38), *Bl-61* (61)
5	c.473G>A	Arg158His	706	C-revised /LFS	LMS-44	St-41/B-43, ChS-30 (35), *Br-16* (17), Schw-58, Scc-25
Intr 5	560-1G>A	IVS5-1G>A	1141	C-revised /LFS	LMS-36/ La-48 (49)	OS-22 (23), Pa-52 (52), *LS-2* (2), Br-41 (42), RMS-11 (12), Lu-51 (52)
6	c.637C>T	Arg213stop	1308	C-revised /LFS	B-27/Pa-45 (47)	*STS-38/Pa-41* (41), *Ly-9* (10), *Br-2* (?)
6	c.638G>A	Arg213Gln	934	C-revised /LFL	B-42	Ki-48/Th-52 (52), *Br-?* (5), Mes-55 (55), *C-26* (27), Mel-46, B-68/ C-71 (?), O-59 (62), Br-28 (32), *B-42* (47), St-71 (?), *C-?* (47), Lu-55/St-59 (?), B-69/Ki-71, Ki-53
6	c.641A>G	His214Arg#	108	C-revised /LFL	B-35/Br-40/ ACC-41 (41)	B-30/O-30 (33), Leu-36 (37), *B-39*/Lu-56 (56)
6	c.665C>T	Pro222Leu#	3838	LFS-susp	RMS-4	*Ca-?* (68)
7	c.695T>C	Ile232Thr#	3070	C-revised /LFL	RMS-54	*B-37* (37), *Br-?* (28), *Lu-?* (22)
7	c.733G>A	Gly245Ser	3843	C-revised /LFL	B-28 (?)	B-34 (35), *Li-10*, *Bl-40*/*Lu-50* (52)
7	c.733G>A	Gly245Ser	3901	C-revised /LFL	Br-27/Oes-37 (37)	B-28, B-34 (38), Ce-43, B-44
7	c.742C>T	Arg248Trp	1375	C-revised /LFS	OS-13/B-26	B-39 (41), *B-?* (28)
7	c.742C>T	Arg248Trp	324	C-revised /LFL	B-32/LMS-42	RMS-2/OS-18 (?), *Ca-?* (40)
8	c.794T>C	Leu265Pro	3075	C-revised /LFS	RMS-2/OS-16 (?)	RMS-2 (3), Br-7/Oes-44 (45), B-40
8	c.818G>A	Arg273His	4057	C-revised	Br-0	*OS-33* (39)
8	c.916C>T	Arg306stop	816	C-revised /LFS	B-34/RMS-48	*RMS-14* (?), *RMS-?* (29)
8	c.916C>T	Arg306stop	16	C-revised	RMS-4/B-22 (?)	*father Pr-?, mother B-?*
Intr 9	c.994-1 G>T	IVS9-1G>T#	3603	C-revised /LFS	C-28/STS-37/Br-51	*B-34*/*Br-36* (41), *Lu-61* (61), *Ca-?* (35), *Ca-?* (35)
10	c.1027G>T	Glu343stop#*	5838	C-revised	ACC-5	
10	c.1031T>C	Leu344Pro	37	C-revised /LFS	B-32/B-33/ Scc-34	OS-18 (20), *Lu-55* (57), *OS-?* (40), *OS-?* (40), *B-?* (?), *OS-?* (?), *Br-?* (?)
2-11	c.1-?_1182 +?del	Del exon 2-11	2556	C-revised	ChS-13/LMS-45 /C-48/OS-49 (?)	*B-29* (29), *C-69*

Fam-nr=family number, LFL= Li-Fraumeni-like syndrome criteria according to Birch, C-revised= Chompret criteria revised in 2009, LFS=classical Li-Fraumeni syndrome criteria, LFS-susp=suspected for LFS but not fulfilling LFS/LFL/revised Chompret criteria

ACC=adrenal cortical carcinoma, B=breast cancer, Bl=bladder cancer, Br=brain tumour, C=colorectal cancer, Ca=cancer unspecified, Ce=cervical cancer, ChS=chondrosarcoma, Ki=kidney cancer, La=laryngeal carcinoma, Leu=leukaemia, Li=liver cancer, LMS=leiomyosarcoma, LS=lymphosarcoma, Lu=lung cancer, Ly=lymphoma, Mel=melanoma, Mes=mesothelioma, O=ovarian cancer, Oes=oesophageal cancer, OS=osteosarcoma, Pa=pancreatic cancer, Pr=prostate cancer, RMS=rhabdomyosarcoma, Schw=schwannoma, Scc=squamous cell carcinoma, St=stomach cancer, STS=soft tissue sarcoma, Th=thyroid cancer, -?=age of diagnosis unknown, (?)=age of death unknown, Intr=intron, #=not included in IARC database, *=de novo mutation. *In italics*= tumours of patients for which the date of birth or diagnosis are unknown.

Discussion

Should *TP53* germline mutation testing only be performed in LFS or LFL families, or do other families or sporadic cases need to be included as well? In the Netherlands, the general advice in 2001 was to be cautious about offering *TP53* mutation testing because present preventive strategies are limited [119]; in 2005 *TP53* mutation testing was recommended for LFS families, LFL families, patients with multiple LFS-associated tumours, children with adrenal cortical carcinoma and possibly for those with breast cancer under 30 years of age [114].

We tried to determine which familial phenotypes carried a *TP53* germline mutation. In 180 Dutch families, the highest proportion with *TP53* mutations is found in classical LFS families (8/11, 73%). The revised Chompret criteria achieved the highest sensitivity (92%) with a mutation detection rate of 21%.

Six *TP53*-positive families did not fulfil the LFS or LFL criteria (Table 2). Four of these six *TP53*-positive families did fulfil the revised Chompret criteria; of these four, two mutations were detected in patients with at least two typical LFS tumours, one in a child with a choroid plexus carcinoma and one in a child with an adrenal cortical carcinoma. In addition, for the *TP53*-positive LFS-suspected cases, the family of the child with a rhabdomyosarcoma at 4 years of age and the family of the patient with breast cancer at 24 years of age did not fulfil the revised Chompret criteria. However, five years after detecting the *TP53* germline mutation in the patient who developed breast cancer at 24 years of age, the mother of the patient developed a sarcoma at 61 years of age and turned out to be a carrier of the *TP53* germline mutation as well.

Many authors have investigated the prevalence of *TP53* germline mutations in patients with typical LFS tumours without a striking family history. Patients with sporadic childhood soft tissue sarcomata (STS) carry a *TP53* germline mutation in 6.6-9% of cases, although some of these cases turn out to be familial [64, 72]. In the Dutch families described here, only 7 patients with STS were included and one *TP53* germline mutation was found (14%). In breast cancer under 30 years of age, *TP53* germline mutations were found in 3.3% of sporadic cases, and 9% (2/22) of familial cases [62]. In three large study cohorts of breast cancer, 0.8% (4/499) carried a *TP53* germline mutation, all 4 mutation carriers showed a family history of cancer [59-61]. In our cohort of 12 patients with breast cancer under 35 years of age, one *TP53* germline mutation was found (8%). Breast cancer at young age was not included in the 2009 revised Chompret criteria because they concluded that the mutation detection rate for patients with early onset breast cancer without a family history of cancer or multiple primary tumours was less than 5% [10]. Ginsburg et al. did not find any *TP53* mutations in 95 sporadic breast cancer cases under 30 years of age [120]. Testing adrenal cortical carcinoma patients for germline *TP53* mutations revealed a 50 to 97% chance of finding a mutation [37, 39, 40, 54]. The only sporadic adrenal cortical carcinoma in our cohort carried a de novo *TP53* germline mutation. Garber et al. [71] mentioned the association of choroid plexus carcinoma with LFS or with *TP53* germline mutations; this was confirmed by Krutilkova et al. [70]. Gonzalez et al. [34] also reported a strong link between individuals with a CPC and germline *TP53* mutations. All eight patients in their series with CPC referred for sequencing of the *TP53* gene were found to carry a *TP53* germline mutation. In our cohort two patients who developed childhood choroid plexus carcinoma were included; one of them carried a germline *TP53* mutation.

In the family subtype group 'two first degree relatives with a tumour at any age' and the family subtype group 'at least two primary tumours at any age' (Table 2) no germline *TP53* mutations were detected in 19 and 30 index patients, respectively. Therefore, we concluded that it is not advisable to perform *TP53* germline mutation analysis for families with two cancer affected first degree relatives, when only one of these tumours is typical for LFS and, not for individuals with two or more primary tumours, when their families do not fulfil the revised Chompret criteria.

Our series does of course have some ascertainment bias, because only families who were referred to a clinical genetics centre and were offered and had chosen for *TP53* mutation testing

were included. The number of families who did not seek, had not been offered or had refused genetic counselling and *TP53* mutation testing was not known.

The second part of our study dealt with assessment of the relative risk of developing cancer based on our survey of different tumour types and ages of onset in LFS/LFL families, with or without *TP53* germline mutation, compared to the general population.

In all *TP53*-positive families, in addition to the main LFS tumour types the relative risks for colon, pancreatic and liver cancer were significantly increased. This means that *TP53* mutation carriers might exhibit higher risks for these tumour types (Table 4a). Pancreatic cancer as an LFS component tumour has been mentioned before [5], but is not part of either the Chompret or Dutch recommendations for *TP53* mutation testing. Liver cancer occurred twice in our study sample, one was confirmed by pathology report, the other might very well have been a metastatic disease.

Focussing on the *TP53*-positive LFL families only (n=10, table 4b), in addition to the classical LFS tumour types, the relative risks for colon, liver and kidney cancer were significantly increased. In the *TP53*-negative LFL families (n=26, table 4c) the relative risks for melanoma and lung and colon cancer were significantly increased. So the occurrence of melanoma and lung cancer in LFL families might not be a very good predictor at present for finding a *TP53* germline mutation.

In conclusion, we recommend *TP53* germline DNA analysis for all families that fulfil the revised Chompret criteria because it has the highest sensitivity for finding a *TP53* germline mutation and a mutation detection rate above 20%. In addition, *TP53* germline DNA analysis could be considered in childhood sarcomata and breast cancer before the age of 30 years (without detectable *BRCA1* or *BRCA2* mutation). Pancreatic and colon cancer might be LFS-component tumours because of their increased relative risks in *TP53* mutation carriers.

Table 4. Tumour type-specific cancer risks in *TP53* mutation families, *TP53*-positive LFL families and *TP53*-negative LFL families.

Table 4a. Cancer risks for *TP53* mutation families.

ICD code	Location	Obs	Exp	RR	95% CI	P value	Pa n (%)	No of fam
-	All	106	26	4	3.3-4.8	**0.000**	69 (65)	24
	Typical LFS tumours							
170	Bones	9	0.08	107	49-203	**0.000**	5 (56)	6
171	Connective tissues	14	0.23	61	33-102	**0.000**	10 (71)	11
174	Breast	28	4.4	6.4	4.3-9.3	**0.000**	22 (79)	16
191	Brain	13	0.37	35	19-60	**0.000**	9 (69)	10
194	Adrenal cortical	2	*				1 (50)	2
205	Leukaemia	2	0.6	3.2	0.4-12	0.258	2 (100)	2
	Other tumours							
153	Colon	6	2.2	2.8	1-6	**0.049**	3 (50)	3
155	Liver	2	0.1	18	2.1-64	**0.017**	1 (50)	2
157	Pancreas	4	0.54	7.3	2-19	**0.006**	3 (75)	4
	Other tumours	20	11	1.8	1.1-2.8			
	Stomach	3	1.1	2.6	0.5-7.7	0.215	2 (67)	3
	Lung	6	3.9	1.5	0.6-3.4	0.398	2 (33)	5
	Pleura/Meso-thelium	1	0.1	9.6	0.2-53	0.21	1 (100)	1
	Melanoma	1	0.7	1.4	0.03-7.6	1.000	1 (100)	1
	Cervix uteri	1	0.4	2.6	0.07-15	0.622	1 (100)	1
	Ovarium	1	0.6	1.6	0.04-8.7	0.933	1 (100)	1
	Prostate	1	1.9	0.5	0.01-3	0.896	0	1
	Bladder	1	0.9	1.1	0.03-6.1	1.000	0	1
	Kidney	3	0.7	4.4	0.9-13	0.067	3 (100)	2
	Other/unspe-cified parts of nervous system	1	0.03	39	1-218	0.075	1 (100) (schwan-noma)	1
	Non Hodgkin Lymphoma	1	0.8	1.3	0.03-7.1	1.000	1 (100)	1
	(Unknown	6)						

See methods section for estimating RR. ICD code = International Classification of Disease code, Obs = observed, Exp = expected, RR = relative risk, CI = confidence interval, Pa = confirmed by pathology report or clinical records, No of fam = number of families in which the specific tumour type occurred.

* no data were available on occurrence in the general population

Table 4b. Cancer risks for *TP53*-positive LFL families.

ICD code	Location	Obs	Exp	RR	95% CI	P value	Pa n (%)	No of fam
-	All	55	8.6	6.4	4.8-8.3	**0.000**	38 (69)	10
	Typical LFS tumours							
170	Bones	-						
171	Connective tissues	4	0.1	41	11-104	**0.000**	2 (50)	4
174	Breast	20	2	10	6.1-16	**0.000**	16 (80)	9
191	Brain	9	0.16	57	26-108	**0.000**	6 (67)	6
194	Adrenal Cortical	1	*				0	1
205	Leukaemia	2	0.23	8.7	1.1-31	0.052	2 (100)	2
	Other tumours							
153	Colon	4	0.7	5.6	1.5-14	**0.014**	2 (50)	1
155	Liver	2	0.04	57	6.9-205	**0.004**	1 (50)	2
189	Kidney	2	0.2	9.6	1.2-35	**0.045**	2 (100)	1
	Other tumours	11	2.6	4.3	2.5-8.1		9 (69)	
	Stomach	1	0.33	3.0	0.1-17	0.555	1 (100)	1
	Pancreas	1	0.17	5.8	0.2-32	0.321	1 (100)	1
	Lung	3	0.8	3.7	0.8-11	0.103	1 (33)	2
	Pleura/ Mesothelium	1	0.02	42	1.1-232	0.072	1 (100)	1
	Melanoma	1	0.33	3	0.1-17	0.558	1 (100)	1
	Cervix uteri	1	0.2	5.4	0.1-30	0.339	1 (100)	1
	Ovarium	1	0.3	3.4	0.1-19	0.503	1 (100)	1
	Prostate	1	0.2	4.9	0.1-27	0.369	0	1
	Bladder	1	0.2	5	0.1-28	0.364	0	1

See methods section for estimating RR. ICD code = International Classification of Disease code, Obs = observed, Exp = expected, RR = relative risk, CI = confidence interval, Pa = confirmed by pathology report or clinical records, No of fam = number of families in which the specific tumor type occurred

* no data were available on occurrence in the general population

Table 4c. Cancer risks for *TP53*-negative LFL families.

ICD code	Location	Obs	Exp	RR	95% CI	P value	Pa n (%)	No of fam
-	All	112	25	4.5	3.7-5.4	**0.000**	63 (56)	26
	Typical LFS tumours							
170	Bones	4	0.07	60	16-154	**0.000**	2 (50)	3
171	Connective tissues	12	0.21	58	30-102	**0.000**	10 (83)	11
174	Breast	35	3.41	10	7.1-14.3	**0.000**	25 (71)	24
191	Brain	11	0.34	33	16-58	**0.000**	6 (55)	7
194	Adrenal cortical	1	*				1 (100)	1
205	Leukaemia	4	0.55	7.3	2-19	**0.006**	1 (25)	4
	Other tumours							
153	Colon	6	2	3.1	1.1-6.7	**0.032**	5 (83)	4
162	Lung	10	4.5	2.3	1.1-4.1	**0.033**	2 (20)	8
172	Melanoma	8	0.7	12	5.3-24	**0.000**	5 (63)	7
	Other tumours	17	7	2.4	1.4-3.9		8 (47)	
	Salivary gland	1	0.05	20	0.5-109	0.12	1 (100)	1
	pharynx	1	0.16	6.4	0.2-36	0.292	1 (100)	1
	Stomach	4	1.15	3.5	1-9	0.06	2 (50)	2
	Pancreas	1	0.51	2	0.1-11	0.786	0	1
	Cervix uteri	1	0.31	3.3	0.1-18	0.52	0	1
	Uterus	1	0.46	2.2	0.1-12	0.732	0	1
	Prostate	2	2.07	1	0.1-3.5	1.000	2 (100)	2
	Bladder	1	0.98	1.0	0.0-5.7	1.000	0	1
	Kidney	1	0.69	1.5	0.0-8.1	0.983	0	1
	Thyroid	1	0.14	7.3	0.2-40	0.264	1 (100)	1
	Non Hodgkin Lymphoma	3	0.44	4.6	0.6-17	0.146	1 (33)	3
	(unknown	4)						

See methods section for estimating RR. ICD code = International Classification of Disease code, Obs = observed, Exp = expected, RR = relative risk, CI = confidence interval, Pa = confirmed by pathology report or clinical records, No of fam = number of families in which the specific tumor type occurred

* no data were available on occurrence in the general population

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