

The *MDM2* promoter polymorphism SNP309T→G and the risk of uterine leiomyosarcoma, colorectal cancer, and squamous cell carcinoma of the head and neck

P Alhopuro, S K Ylisaukko-oja, W J Koskinen, P Bono, J Arola, H J Järvinen, J-P Mecklin, T Atula, R Kontio, A A Mäkitie, S Suominen, I Leivo, P Vahteristo, L-M Aaltonen, L A Aaltonen

J Med Genet 2005;42:694–698. doi: 10.1136/jmg.2005.031260

See end of article for authors' affiliations

Correspondence to:
Dr L A Aaltonen,
Department of Medical
Genetics, Biomedicum
Helsinki, 00014 University
of Helsinki; lauri.
aaltonen@helsinki.fi

Revised version received
20 January 2005
Accepted for publication
15 February 2005

Background: MDM2 acts as a principal regulator of the tumour suppressor p53 by targeting its destruction through the ubiquitin pathway. A polymorphism in the MDM2 promoter (SNP309) was recently identified. SNP309 was shown to result, via Sp1, in higher levels of MDM2 RNA and protein, and subsequent attenuation of the p53 pathway. Furthermore, SNP309 was proposed to be associated with accelerated soft tissue sarcoma formation in both hereditary (Li-Fraumeni) and sporadic cases in humans.

Methods: We evaluated the possible contribution of SNP309 to three tumour types known to be linked with the MDM2/p53 pathway, using genomic sequencing or restriction fragment length polymorphism as screening methods. Three separate Finnish tumour materials (population based sets of 68 patients with early onset uterine leiomyosarcomas and 1042 patients with colorectal cancer, and a series of 162 patients with squamous cell carcinoma of the head and neck) and a set of 185 healthy Finnish controls were analysed for SNP309.

Results: Frequencies of SNP309 were similar in all four cohorts. In the colorectal cancer series, SNP309 was somewhat more frequent in women and in patients with microsatellite stable tumours. Female SNP309 carriers were diagnosed with colorectal cancer approximately 2.7 years earlier than those carrying the wild type gene. However, no statistically significant association of SNP309 with patients' age at disease onset or to any other clinicopathological parameter was found in these three tumour materials.

Conclusion: SNP309 had no significant contribution to tumour formation in our materials. Possible associations of SNP309 with microsatellite stable colorectal cancer and with earlier disease onset in female carriers need to be examined in subsequent studies.

The tumour suppressor p53 is a principal mediator of a number of cellular functions, including growth arrest, senescence, and apoptosis in response to DNA damage.¹ As such, p53 is the most frequently mutated gene in human tumours; alterations in the p53 gene are found in approximately 50% of all cancers.² MDM2 acts as a key regulator of p53 through an autoregulatory feedback loop. MDM2 is capable of binding p53 and regulating its ability as a transcriptional activator. MDM2 is also involved in the nuclear export of p53, and serves as an E3 ubiquitin ligase that promotes p53 destruction.^{1, 3} Additionally, MDM2 seems to interact with other cellular proteins that are important in cell cycle control, including pRb, E2F/DP1, and p19ARF, although some of these functions are less well characterised.⁴ Amplification or overexpression of MDM2 commonly occurs in human tumours. Tumour types displaying overexpression of MDM2 include soft tissue sarcomas, osteosarcomas, rhabdomyosarcomas, oral squamous cell, colorectal and breast carcinomas, and malignant melanomas.^{3, 5–7} Furthermore, MDM2 overexpression has been linked with the clinical behaviour of the tumours.⁶

Recently, a single nucleotide polymorphism in the MDM2 promoter, SNP309T→G (SNP309), was identified,⁸ and shown to result in overexpression of MDM2 RNA and protein and subsequent attenuation of the p53 pathway. It was further demonstrated that the heightened level of MDM2 was mediated by and dependent on transcription factor Sp1. Consequently, it was hypothesised that increased levels of MDM2 resulting from SNP309 could affect the p53 pathway in patients with germline mutations in one p53

allele (Li-Fraumeni syndrome) and have an impact on the tumour susceptibility of these individuals. To test this hypothesis, Bond *et al* studied a cohort of 88 patients with Li-Fraumeni syndrome, and found an association of the occurrence of SNP309 with earlier tumour onset, as well as with a phenotype of multiple primary cancers. In addition, in a material of 105 sporadic soft tissue sarcomas, of which 16 were leiomyosarcomas, SNP309 was found to be associated with an accelerated tumour formation.⁸

We report on our evaluation of SNP309 and its implication for disease onset in a population based set of early onset uterine leiomyosarcoma cases, and our analysis of the possible contribution of SNP309 to two other tumour types, colorectal cancer (CRC, 1042 cases) and squamous cell carcinoma of the head and neck (HNSCC, 162 cases), which are linked with the p53 pathway. Healthy blood donors served as controls.

METHODS

Patients

Samples from population based series of patients with early onset uterine leiomyosarcoma were analysed for SNP309. This unique material consists of tumour specimens from 68 Finnish patients diagnosed with histologically verified uterine leiomyosarcomas at ≤45 years of age. The paraffin embedded samples for this material were collected from cases

Abbreviations: CRC, colorectal cancer; HNSCC, squamous cell carcinoma of the head and neck; RFLP, restriction fragment length polymorphism

Table 1 Frequencies of MDM2 SNP309 in controls and cancer patients

Cohorts and subgroups	No. of individuals	No. of individuals according to SNP309 genotype (%)			Pearson χ^2 *
		Wild type	Heterozygote	Homozygote	
Healthy controls	185	56 (31)	98 (53)	31 (16)	
EO leiomyosarcomas	68	21 (31)	36 (53)	11 (16)	0.99†
Age <41 years	33	9 (27)	20 (61)	4 (12)	0.44
Age >41 years	35	12 (34)	16 (46)	7 (20)	
Familial cancer	38	11 (29)	19 (50)	8 (21)	0.47
No familial cancer	30	10 (33)	17 (57)	3 (10)	
Local tumour	49	14 (29)	28 (57)	7 (14)	0.21
Diffused tumour	5	2 (40)	1 (20)	2 (40)	
CRC	969	334 (34)	465 (48)	170 (18)	0.44†
Microsatellite stable	849	294 (34.5)	397 (47)	158 (18.5)	0.04
Microsatellite unstable	120	40 (33)	68 (57)	12 (10)	
Female	481	147 (31)	239 (50)	95 (20)	0.02
Male	488	187 (38)	226 (46)	75 (15)	
Multiple cancer	124	42 (34)	52 (42)	30 (24)	0.10
A single CRC, no other Malignancies	845	292 (34.5)	413 (49)	140 (16.5)	
Dukes A-B	572	185 (32)	282 (49)	105 (18)	0.24
Dukes C-D	391	147 (38)	180 (46)	64 (16)	
Grade 1	192	69 (36)	97 (50.5)	26 (13.5)	0.40
Grade 2	677	225 (33)	326 (48)	126 (19)	
Grade 3-4	80	32 (40)	34 (42.5)	14 (17.5)	
Familial CRC	835	282 (34)	401 (48)	152 (18)	0.31
No familial CRC	134	52 (39)	64 (48)	18 (13)	
Familial cancer	436	146 (33)	209 (48)	81 (19)	0.70
No familial cancer	533	188 (35)	256 (48)	89 (17)	
SCCHN	157	58 (37)	75 (48)	24 (15)	0.47†
Age ≤61 years	84	32 (38)	42 (50)	10 (12)	0.45
Age >61 years	73	26 (36)	33 (45)	14 (19)	
Recurrent SCCHN	122	44 (36)	60 (49)	18 (15)	0.88
No recurrence	32	13 (41)	15 (47)	4 (12)	
T1 tumours	68	28 (41)	31 (46)	9 (13)	0.6
T≥2 tumours	89	30 (34)	44 (49)	15 (17)	
NO tumours	108	43 (40)	46 (42.5)	19 (17.5)	0.14
N+ tumours	49	15 (31)	29 (49)	5 (10)	

*Subgroup versus subgroup; †group versus healthy controls. EO, early onset.

diagnosed in Finland between the years 1984 and 2002 based on the Finnish cancer registry data. During this time, 80 uterine leiomyosarcomas had been diagnosed in the specified age group, thus our material represents 85% of the diagnosed cases in Finland. Twelve cases could not be analysed because no paraffin embedded tissue was available.

Population based material from 1042 Finnish colorectal cancer patients was screened for MDM2 SNP309. This well documented material has been described in more detail in previous works.^{9, 10}

The HNSCC material (n = 162) was from patients with HNSCC who were treated at the Department of Otorhinolaryngology Head and Neck Surgery at Helsinki University Central Hospital between 1997 and 2003 and who had given their blood sample to the tumour bank. Patients' median age at diagnosis was 62 years (range 26–89 years). The most common tumour sites were larynx (61/162), tongue (34/162), tonsils (24/162) hypopharynx (8/162), and base of the mouth (8/162).

In total, 185 healthy blood donors served as controls in the study. DNA extractions were performed using standard methods.

Sequencing

Genotyping of the uterine leiomyosarcoma cases and the healthy controls was performed by genomic sequencing. PCR primers used in the reactions were as follows: 5'-GTTTGTGTTGACTGGGCTA-3' and 5'-CTGCGATCATCCGGACCT-3'. PCR was performed in 25 µl volumes containing 50 ng genomic DNA, 1× PCR buffer (Applied Biosystems, Foster City, CA, USA), 200 µmol/l each dNTP (Finnzymes, Espoo,

Finland) 0.25 µmol/l both primers, and 1.25 U AmpliTaq Gold DNA polymerase. PCR products were purified using ExoSAP-IT PCR purification kit (USB Corporation, Cleveland, OH, USA), and sequenced using AB 3100 and 3730 BD3.1 sequencing chemistry and 5.1 sequencing analysis software (Applied Biosystems).

Restriction fragment length polymorphism

An RFLP method was used in the genotyping of the CRC and HNSCC samples. PCR was performed as described by Bond *et al.*⁸ Digestion was performed in 50 µl reaction volume using *Msp*AI restriction endonuclease (New England Biolabs, Beverly, MA, USA) according to manufacturer's instructions. Restriction fragments were visualised in 4% agarose gel electrophoresis.

Statistical methods

Possible statistical differences in continuous variables were tested by one way analysis of variance (SPSS version 12.0 for Windows) and in dichotomous variables by Pearson's χ^2 test. A p value <0.05 was considered significant. In the CRC material, the effect of multiple testing was corrected using Bonferroni adjustment, and p<0.005 was considered significant.

RESULTS

Healthy controls

In a cohort of 185 healthy controls, 56 individuals (30%) were wild type (TT), 98 (53%) heterozygous (TG), and 31 (17%) homozygous (GG) for SNP309 (table 1).

Table 2 Mean ages at diagnosis according to SNP309 status in cancer cohorts

Cohorts and subgroups	No. of individuals	Mean age at diagnosis (years)		Pearson χ^2 *
		WT	SNP309	
Leiomyosarcoma	68	40.9 (n = 21)	39.3 (n = 47)	0.24
CRC	969	68.1 (n = 334)	67.0 (n = 635)	0.17
Female	481	70.5 (n = 147)	67.8 (n = 334)	0.026
Male	488	66.2 (n = 187)	66.1 (n = 301)	0.92
MSS CRC*				
Female	417	70.8 (n = 123)	67.31 (n = 294)	0.007
Male	432	66.7 (n = 171)	66.4 (n = 216)	0.81
SCCHN	157	60.2 (n = 57)	61.2 (n = 99)	0.62

MSS, microsatellite stable.

Early onset uterine leiomyosarcomas

All 68 leiomyosarcoma samples were successfully analysed. The frequencies of the genotypes were similar to the healthy controls (31% wild type (n = 21), 53% heterozygotes (n = 36), and 16% homozygotes (n = 11)). The median age of disease onset was somewhat higher in individuals with wild type (40.9 years, n = 21) than in heterozygous or homozygous SNP309 carriers (39.3 years, n = 47), but this difference did not reach statistical significance (p = 0.24). The possible impact of SNP309 to disease onset was further analysed by comparing the genotype distribution in two subgroups: patients <41 years (n = 33) and in patients \geq 41 years (n = 35) at diagnosis; however, no differences were observed (p = 0.44). There was also no difference observed when the genotype distribution was analysed between local and diffuse tumours (p = 0.21). Finally, the SNP status was analysed according to family history of cancer, but no significant associations were detected between patients with no family history (n = 21) and patients with at least one first degree relative with cancer (n = 36; p = 0.47) (tables 1, 2).

CRC

Of the 1042 CRC samples, 969 were successfully analysed for SNP309. The frequencies of the genotypes were similar in CRC patients (34% wild type (n = 334), 48% heterozygotes (n = 465), 18% homozygotes (n = 170)) and in healthy controls (p = 0.44). The median age of the CRC patients at diagnosis was 67.8 years in wild type individuals, and 66.8 and 67.5 years in SNP309 heterozygotes and homozygotes, respectively. SNP309 was more frequent in women than in men (p = 0.024). In women, SNP309 was associated with a slightly earlier disease onset (2.7 years, p = 0.026), and patients with microsatellite stable CRC were more frequently homozygous for SNP309 than patients with microsatellite unstable CRC (p = 0.036). Analysis of genotype distribution according to a history of a second cancer at any site (n = 130, including 20 patients with a second CRC) showed a trend towards a slightly higher frequency of homozygous mutations in patients with multiple cancer (24% v 16.5% in patients with a single CRC), although this difference did not reach statistical significance (p = 0.096). The frequencies of the genotypes were also analysed according to tumour grade (p = 0.395), Duke's stage (p = 0.235), and family history (no familial cancer v one or more cancer in a first degree relative; p = 0.703), but no significant correlations were observed (table 1–2).

HNSCC

In total, 157 HNSCC samples were successfully analysed for SNP309. In this cohort, 37% (n = 58) of the patients were wild type, 48% (n = 75) heterozygous, and 15% (n = 24) homozygous for SNP309, thus the genotypic distribution was similar to the healthy controls (p = 0.47). The median age of the HNSCC patients at diagnosis was 60.2 years in the group

of individuals with wild type alleles, and 60.4 and 63.8 years in heterozygotes and homozygotes, respectively. The genotypes were further analysed between patients \leq 61 years (n = 84) and >61 years (n = 73) at disease diagnosis, but no significant differences in the genotype distribution were observed (p = 0.45). The frequency of SNP309 was also analysed according to tumour size (T1 v T \geq 2 tumours, p = 0.60), disease progression (p = 0.88), and nodal stage (N0 v N+, p = 0.14) but no evidence to support the involvement of SNP309 in any of these variables was obtained (tables 1, 2).

DISCUSSION

Alterations in *p53* are among the most common genetic changes observed in human malignancies; for instance, in more than 50% of colon adenocarcinomas, *p53* is mutated.² In microsatellite unstable CRCs, *p53* mutations occur less frequently, but approximately 50% of these tumours display frameshift mutations in the *BAX* gene, which is involved in the *p53* regulated pathway for induction of apoptosis.¹¹ Alterations in *p53* are also commonly detected in HNSCC; mutations in *p53* have been reported in 40–80% of HNSCCs and inactivation of *p53* through interaction with high risk human papillomavirus in 14–60% of cases.^{12–15} The presence of *p53* mutations seems to correlate with worse response to radiotherapy and 5-fluorouracil-cisplatin based chemotherapy in HNSCC, but in both HNSCC and CRC, the prognostic value of *p53* remains controversial.^{2 16–19 21 20} Adenoviral *p53* gene transfer therapy developed for HNSCC has shown some degrees of success, rendering *p53* a gene of potential clinical relevance in this tumour type.²² Abnormalities in both *p53* and *MDM2* genes have been reported also in human sarcomas. The *MDM2* gene appears to be amplified in about a third of soft tissue sarcomas, and alterations in *p53* have been detected in 17–62% of leiomyosarcomas.^{5 23–27} Sample sizes in these studies have been relatively small, and thus no firm conclusion can be drawn.

Single nucleotide polymorphisms in the *p53* pathway might explain some of the phenotypic variation in cancer susceptibility. The recent identification of SNP309 in the *MDM2* promoter, resulting in attenuation of the *p53* pathway, provides evidence to support this hypothesis.⁸ In relatively small sets of hereditary and sporadic soft tissue sarcomas, the frequency of SNP309 was similar to population controls, but it was shown to be associated with earlier tumour formation.⁸

We have examined the role of the *MDM2* promoter SNP309 in three different tumour types; uterine leiomyosarcomas, CRC, and HNSCC, known to be associated with the *p53*/*MDM2* pathway. Overall, the frequency of SNP309 was slightly higher in the Finnish population than that reported previously.⁸ We found similar frequencies of SNP309 in all four groups tested: in 68 early onset leiomyosarcomas, 969 CRC samples, 157 HNSCCs, and 185 healthy blood donors.

Analysis of SNP309 genotype distribution according to patients' age at disease onset failed to show a significant

association in the leiomyosarcoma and the HNSCC materials (table 2). Because of limited statistical power, however, subtle changes may have been missed. Bond *et al* reported tumour formation in soft tissue sarcoma occurring 12 years earlier in patients with homozygous SNP309 compared with those without SNP309. Such an association could not be confirmed in our uterine leiomyosarcoma material, although a trend towards a slightly younger age at disease diagnosis was observed in SNP309 carriers. Further studies are needed to confirm the role of SNP309 in other types of sporadic soft tissue sarcomas. Bond *et al* also reported an association of SNP309 with the occurrence of multiple primary tumours in a lifetime in patients with Li-Fraumeni syndrome. None of the leiomyosarcoma patients and only a few HNSCC (n = 3) patients had a second tumour, and thus a similar association could not be tested in our materials.

In the population based CRC material, SNP309 was not significantly associated with patient age at diagnosis (p = 0.17). Interestingly however, SNP309 was detected in higher frequencies in women than in men (p = 0.01, odds ratio 1.4, 95% confidence interval 1.1 to 1.8), and SNP309 in female carriers was linked with an age at diagnosis approximately 2.7 years younger (p = 0.026). In addition, a trend towards a higher incidence of homozygous SNP309 in patients with microsatellite stable CRC was observed, which is of some interest, as microsatellite stable and unstable CRCs are different in view of p53 involvement, with microsatellite stable tumours harbouring more p53 mutations.¹¹ Furthermore, women with microsatellite stable CRC were diagnosed on average 3.5 years earlier (p = 0.007) if they carried SNP309 (tables 1, 2). Because of multiple testing, Bonferroni adjustment was applied and p < 0.005 was considered significant. Thus, no statistically significant association between SNP309 and any clinicopathological parameters remained in the CRC material. Interestingly, germline p53 mutations have been connected with higher cancer risk in female than in male carriers, a difference that cannot be explained by a distortion of sex specific cancer.²⁸⁻²⁹ It is therefore tempting to speculate whether a correlation could also exist between germline MDM2 polymorphisms and sex differences in cancer risk. Subsequent studies are needed to show whether the trends observed in this study hold in other materials.

In conclusion, little evidence was obtained to support the role of SNP309 in cancer predisposition.

ACKNOWLEDGEMENTS

This study was supported by grants from the Academy of Finland (grant 44870, Finnish Center of Excellence Program 2000–2005), the Finnish Cancer Society, the Sigrid Juselius Foundation, the European Commission (QLG2-CT-2001-01861), Finnish Medical Society, and the Foundation of the Finnish Cancer Institute.

Authors' affiliations

P Alhopuro, S K Ylisaukko-oja, P Vahteristo, L A Aaltonen, Department of Medical Genetics, University of Helsinki, Helsinki, Finland
W J Koskinen, L-M Aaltonen, Department of Virology, Haartman Institute, University of Helsinki and HUCH Laboratory Diagnostics, Helsinki, Finland
W J Koskinen, T Atula, R Kontio, A A Mäkitie, S Suominen, L-M Aaltonen, Department of Otorhinolaryngology – Head and Neck Surgery, Helsinki University Central Hospital, Helsinki, Finland
P Bono, Department of Oncology, Helsinki University Central Hospital, Helsinki, Finland
J Arola, I Leivo, Department of Pathology, University of Helsinki and HUCH Laboratory Diagnostics, Helsinki, Finland
H J Järvinen, The Second Department of Surgery, Helsinki University Hospital, Helsinki, Finland
J-P Mecklin, Department of Surgery, Jyväskylä Central Hospital, Jyväskylä, Finland

S Suominen, Department of Plastic Surgery, University Hospital, Helsinki, Finland

Competing interests: none declared

The first three authors contributed equally to the paper.

Ethics approval: patient information and samples were obtained with full informed consent. The study was approved by the appropriate ethics review committees (Helsinki University Central Hospital Ethics Committee E8 and Ethics Committee no 9 for Neurosurgery, Ophthalmology and Otorhinolaryngology).

REFERENCES

- Moll UM, Petrenko O. The MDM2-p53 interaction. *Mol Cancer Res* 2003;1:1001–8.
- Grady WM, Markowitz SD. Genetic and epigenetic alterations in colon cancer. *Annu Rev Genomics Hum Genet* 2002;3:101–28.
- Freedman DA, Wu L, Levine AJ. Functions of the MDM2 oncoprotein. *Cell Mol Life Sci* 1999;55:96–107.
- Ries S, Biederer C, Woods D, Shifman O, Shirasawa S, Sasazuki T, McMahon M, Oren M, McCormick F. Opposing effects of Ras on p53: transcriptional activation of mdm2 and induction of p19ARF. *Cell* 2000;103:321–30.
- Oliner JD, Kinzler KW, Meltzer PS, George DL, Vogelstein B. Amplification of a gene encoding a p53-associated protein in human sarcomas. *Nature* 1992;358:80–3.
- Onel K, Cordon-Cardo C. MDM2 and prognosis. *Mol Cancer Res* 2004;2:1–8.
- Tachibana M, Kawamata H, Fujimori T, Omotehara F, Horiuchi H, Ohkura Y, Igarashi S, Kotake K, Kubota K. Dysfunction of p53 pathway in human colorectal cancer: analysis of p53 gene mutation and the expression of the p53-associated factors p14ARF, p33ING1, p21WAF1 and MDM2. *Int J Oncol* 2004;25:913–20.
- Bond GL, Hu W, Bond EE, Robins H, Lutzker SG, Arva NC, Bargonetti J, Bartel F, Taubert H, Wuerl P, Onel K, Yip L, Hwang SJ, Strong LC, Lozano G, Levine AJ. A single nucleotide polymorphism in the MDM2 promoter attenuates the p53 tumor suppressor pathway and accelerates tumor formation in humans. *Cell* 2004;119:591–602.
- Aaltonen LA, Salovaara R, Kristo P, Canzian F, Hemminki A, Peltomäki P, Chadwick RB, Kaariainen H, Eskelinen M, Jarvinen H, Mecklin JP, de la Chapelle A. Incidence of hereditary nonpolyposis colorectal cancer and the feasibility of molecular screening for the disease. *N Engl J Med* 1998;338:1481–7.
- Salovaara R, Loukola A, Kristo P, Kaariainen H, Ahtola H, Eskelinen M, Harkonen N, Julkunen R, Kangas E, Ojala S, Tulikoura J, Valkamo E, Jarvinen H, Mecklin JP, Aaltonen LA, de la Chapelle A. Population-based molecular detection of hereditary nonpolyposis colorectal cancer. *J Clin Oncol* 2000;18:2193–200.
- Rampino N, Yamamoto H, Ionov Y, Li Y, Sawai H, Reed JC, Perucho M. Somatic frameshift mutations in the BAX gene in colon cancers of the microsatellite mutator phenotype. *Science* 1997;275:967–9.
- Balz V, Scheckenbach K, Gotte K, Bockmuhl U, Petersen I, Bier H. Is the p53 inactivation frequency in squamous cell carcinomas of the head and neck underestimated? Analysis of p53 exons 2–11 and human papillomavirus 16/18 E6 transcripts in 123 unselected tumor specimens. *Cancer Res* 2003;63:1188–91.
- Scholes AG, Liloglou T, Sniijders PJ, Hart CA, Jones AS, Woolgar JA, Vaughan ED, Walboomers JM, Field JK. p53 mutations in relation to human papillomavirus type 16 infection in squamous cell carcinomas of the head and neck. *Int J Cancer* 1997;71:796–9.
- Koskinen WJ, Chen RW, Leivo I, Makitie A, Back L, Kontio R, Suuronen R, Lindqvist C, Auvinen E, Mäkitie A, Quint WG, Vaheri A, Aaltonen LM. Prevalence and physical status of human papillomavirus in squamous cell carcinomas of the head and neck. *Int J Cancer* 2003;107:401–6.
- Gillison ML, Koch WM, Capone RB, Spafford M, Westra WH, Wu L, Zahurak ML, Daniel RW, Viglione M, Symer DE, Shah KV, Sidransky D. Evidence for a causal association between human papillomavirus and a subset of head and neck cancers. *J Natl Cancer Inst* 2000;92:709–20.
- Cabelguenne A, Blons H, de Waziers I, Carnot F, Houllier AM, Soussi T, Brasnu D, Beaune P, Laccourreye O, Laurent-Puig P. p53 alterations predict tumor response to neoadjuvant chemotherapy in head and neck squamous cell carcinoma: a prospective series. *J Clin Oncol* 2000;18:1465–73.
- Gallo O, Chiarelli I, Boddi V, Boccia C, Bruschini L, Porfiro B. Cumulative prognostic value of p53 mutations and bcl-2 protein expression in head-and-neck cancer treated by radiotherapy. *Int J Cancer* 1999;84:573–9.
- Blons H, Laurent-Puig P. TP53 and head and neck neoplasms. *Hum Mutat* 2003;21:252–7.
- McDermott U, Longley DB, Johnston PG. Molecular and biochemical markers in colorectal cancer. *Ann Oncol* 2002;13(suppl 4):235–45.
- Tortola S, Marcuello E, Gonzalez I, Reyes G, Arribas R, Aiza G, Sancho FJ, Peinado MA, Capella G. p53 and K-ras gene mutations correlate with tumor aggressiveness but are not of routine prognostic value in colorectal cancer. *J Clin Oncol* 1999;17:1375–81.
- Soong R, Powell B, Elsaleh H, Gnanasampanthan G, Smith DR, Goh HS, Joseph D, Iacopetta B. Prognostic significance of TP53 gene mutation in 995 cases of colorectal carcinoma. Influence of tumour site, stage, adjuvant chemotherapy and type of mutation. *Eur J Cancer* 2000;36:2053–60.

- 22 **Nemuncitis J**, Khuri F, Ganly I, Arseneau J, Posner M, Vokes E, Kuhn J, McCarty T, Landers S, Blackburn A, Romel L, Randlev B, Kaye S, Kirn D. Phase II trial of intratumoral administration of ONYX-015, a replication-selective adenovirus, in patients with refractory head and neck cancer. *J Clin Oncol* 2001;**19**:289–98.
- 23 **Seki A**, Kodama J, Miyagi Y, Kamimura S, Yoshinouchi M, Kudo T. Amplification of the *mdm-2* gene and p53 abnormalities in uterine sarcomas. *Int J Cancer* 1997;**73**:33–7.
- 24 **Hall KL**, Teneriello MG, Taylor RR, Lemon S, Ebina M, Linnoila RI, Norris JH, Park RC, Birrer MJ. Analysis of Ki-ras, p53, and MDM2 genes in uterine leiomyomas and leiomyosarcomas. *Gynecol Oncol* 1997;**65**:330–5.
- 25 **Patterson H**, Gill S, Fisher C, Law MG, Jayatilake H, Fletcher CD, Thomas M, Grimer R, Gusterson BA, Cooper CS. Abnormalities of the p53 MDM2 and DCC genes in human leiomyosarcomas. *Br J Cancer* 1994;**69**:1052–8.
- 26 **Jeffers MD**, Farquharson MA, Richmond JA, McNicol AM. p53 immunoreactivity and mutation of the p53 gene in smooth muscle tumours of the uterine corpus. *J Pathol* 1995;**177**:65–70.
- 27 **Miyajima K**, Tamiya S, Oda Y, Adachi T, Konomoto T, Toyoshiba H, Masuda K, Tsuneyoshi M. Relative quantitation of p53 and MDM2 gene expression in leiomyosarcoma; real-time semi-quantitative reverse transcription-polymerase chain reaction. *Cancer Lett* 2001;**164**:177–88.
- 28 Hwang SJ, Lozano G, Amos CI, Strong LC. Germline p53 mutations in a cohort with childhood sarcoma: sex differences in cancer risk. *Am J Hum Genet* 2003;**72**:975–83.
- 29 **Chompret A**, Brugieres L, Ronsin M, Gardes M, Dessarps-Freichay F, Abel A, Hua D, Ligot L, Dondon MG, Bressac-de Paillerets B, Frebourg T, Lemerle J, Bonaiti-Pellie C, Feunteun J. P53 germline mutations in childhood cancers and cancer risk for carrier individuals. *Br J Cancer* 2000;**82**:1932–7.