**INK4a-ARF alterations in liver cell adenoma**

A Tannapfel, C Busse, F Geißler, H Witzigmann, J Hauss, C Wittekind

*Gut* 2002;51:253–258

**LIVER DISEASE**

**INK4a-ARF alterations in liver cell adenoma**

**Background:** The INK4a-ARF (CDKN2A) locus on chromosome 9p21 encodes two tumour suppressor proteins, p16^INK4a^ and p14^ARF^, whose functions are inactivated in many human cancers.

**Aims:** To evaluate p14^ARF^ and p16^INK4a^ alterations in liver cell adenoma.

**Methods:** After microdissection, DNA from 25 liver cell adenomas and corresponding normal liver tissue were analysed for INK4A-ARF inactivation by DNA sequence analysis, methylation specific polymerase chain reaction, restriction enzyme related-polymerase chain reaction (RE-PCR), mRNA expression, microsatellite analysis, and immunohistochemistry. In addition, microdeletion of p14^ARF^ and p16^INK4a^ were assessed by differential PCR.

**Results:** Methylation of p14^ARF^ was found in 3/25 cases (12%) and alterations in p16^INK4a^ occurred in 6/25 liver cell adenomas (24%) which correlated with loss of mRNA transcription. We failed to detect microdeletions or specific mutations of both exons. p16^INK4a^ methylation appeared in the context of unmethylated p14^ARF^ promoter in six cases. In normal liver tissue, p14^ARF^ or p16^INK4a^ alterations were not observed.

**Conclusions:** Our data suggest that p14^ARF^ methylation occurs independently of p16^INK4a^ alterations in liver cell adenomas. Furthermore, methylation of p14^ARF^ and p16^INK4a^ may be a result of cell cycle deregulation and does not seem to be a prerequisite of malignancy.

**MATERIALS AND METHODS**

**Patients and tissue samples**

Twenty-five patients with LCA undergoing partial hepatectomy (segmental or lobar resection) between 1990 and 1999 were included in this retrospective study.

Each tumour was re-evaluated with regard to typing (WHO 2000). In all cases, slides prepared from four different paraffin blocks of tissue, sampled from different tumour areas, were examined.

**DNA samples**

For each LCA sample, the histopathological lesions of interest were first identified on routinely stained slides. Parallel sections were cut with the microtome set at 6 μm, and the slides dried overnight at 37°C. Corresponding areas of interest were delineated and microdissected after rapid staining with haematoxylin and eosin. Thereafter the tissue was scraped off the slide sections were covered by 25 μl of Tris buffer 0.05 mol with the tip of a sealed glass pipette and then sucked into a microcapillary tube. Tissue samples were placed in Eppendorf tubes and incubated with proteinase K at 37°C overnight. Proteinase K activity was inactivated by heating to

**Abbreviations:** LCA, liver cell adenoma; MSP, methylation specific polymerase chain reaction; RE-PCR, restriction enzyme-related polymerase chain reaction; RT-PCR, reverse transcription-polymerase chain reaction; SSCP, single strand conformational polymorphism.

See end of article for authors’ affiliations

Correspondence to:
Dr A Tannapfel, Institute of Pathology, University of Leipzig, Liebigstraße 26, 04103 Leipzig, Germany; tann@medizin.uni-leipzig.de

Accepted for publication 4 December 2001
95°C for 10 minutes. For DNA extraction, standard methods were used: after incubation with proteinase K at 37°C overnight, the tissue was extracted twice in phenol and twice in chloroform, followed by ethanol precipitation.

**Methylation status of the INK4a-ARF locus**

The CpG WIZ p16 methylation assay kit was used (OncoRInc, Gaithersburg, Maryland, USA) according to the manufacturer’s instructions. After an initial bisulphite reaction to modify the DNA, polymerase chain reaction (PCR) amplification with specific primers was performed to distinguish methylated from unmethylated DNA. Primers specific for unmethylated p16 (5′-TTATAGAGGGTTGGGGATG-3′, 5′-CAACCCCCCAACCA CAACCTATAA-3′) or methylated p16 (5′-TTATAGAGGGTTGGGCGGAGATG-3′, 5′-GACCCCGAAGCGCGACCGA TA-3′) were used. DNA (7 µg/100 µl) was denatured by 0.2 M NaOH for 10 minutes at room temperature. DNA Modification Reagent I was added, incubated for 24 hours at 50°C, and subsequently purified by DNA Modification Reagents II and III in 0.3 M NaOH treatment for five minutes followed by ethanol precipitation. For hot start PCR, the PCR mixture contained Universal PCR Buffers (1×, 4 dNTPs (1.25 mM)), and U or M primers (300 ng each per reaction). Annealing temperature was 65°C for 30 cycles. The PCR product was directly electrophoresed on a 3% agarose gel, stained with ethidium bromide, and visualised under UV illumination. The PCR products were amplified for 35 cycles (95°C for 45 seconds, 57°C for 45 seconds, and 72°C for 60 seconds). The RT reaction product (1 µl) was then amplified by PCR using the forward primers of exons 1α and 1β and the reverse primer for exon 2 of the p16β-α exon 1β gene. The primers were as follows: forward exon 1α (sense): 5′-GCTGGCGCGCCGCGACCGA TA-3′; exon 1β (sense): 5′-GCGTGGCTGCTGACGTA A-3′; and reverse primer (antisense) 5′-ACCACCACCGGCTGCAAA-3′. Hot start PCR was performed for 35 cycles (95°C for 45 seconds, 57°C for 45 seconds, and 72°C for 60 seconds). The sizes of the products were 179 bp for p16α and 200 bp for p14α, respectively. PCR products were electrophoresed on a 2% agarose gel and stained. β-actin amplification was performed to show RNA quality.

**Allelic dosage analysis of loss of heterozygosity and homozygous deletion, and DNA sequencing for the INK4a-ARF (CDKN2A) locus**

Allelic dosage analysis of the p14α and p16β genes was performed using differential PCR. PCR fragments were amplified in exon 1β of p14α, exon 3 of p16β, and exon 2 using the following primers: p14α exon 1β: ARF2F 5′-CTGGTGTGATGTAGTCTAGG-3′ and ARF2R 5′-AAGTCTGT TGAAACCCAAGATG-3′; p16 exon 3: p16ex3F: 5′-CGAGATTG GAAGCCAGAGAG-3′ and p16ex3R 5′-ATGACATTACGG TATGGG-3′; and reverse primer (antisense) 5′-ACCACCACCGGCTGCAGAAA-3′. As a negative control, a glioblastoma cell line (LN2343) with a known deletion of the INK4a-ARF locus was used. For positive controls, the hepatocellular carcinoma cell line HepG2 with an intact INK4a-ARF locus was analysed. The ratio of DNA fragment intensities in HepG2 between exon 1β or exon 3 and the internal control interferon γ was used to normalise the ratio. Hemizygous deletion was diagnosed if the ratio of the tumour sample was 50% of the one found in HepG2. If the ratio was less than 40%, the tumour sample was considered to harbour a homozygous deletion (fig 2). To control the data for gene dosage analysis, microsatellite analysis using nine microsatellites of chromosome 9p21 was performed, as described previously. The markers used were D9S161, D9S126, D9S171, D9S172, D9S1748, D9S1747, D9S1749, D9S1751, and IFNA, and were obtained from Research Genetics (Huntsville Alabama, USA) (fig 3).

Single strand conformational polymorphism (SSCP) analysis is a technique for the detection of mutations based on the three dimensional conformation taken by a single strand of DNA in a non-denaturing environment. Sequencing gels and flanking intronic sequences of exons 1α, 1β, and 2 of the INK4a-ARF gene were analysed by PCR-SSCP Primer sequences for exons 1α, 1β,
Figure 1  Analysis of p14<sup>ARF</sup> and p16<sup>INK4a</sup> in three liver cell adenomas (case Nos 1, 10, and 11; same patients as in table 1). (A) p14<sup>ARF</sup> analysis with restriction enzyme related-polymerase chain reaction (RE-PCR). The methyl sensitive restriction enzymes used for RE-PCR are indicated (HpaII, KspI); digestion with the non-methyl sensitive enzyme MspI serves as a negative control and undigested DNA (control) serves as a positive control. The p14<sup>ARF</sup> gene is methylated in case No 11 and unmethylated in case Nos 1 and 10. (B) p16<sup>INK4a</sup> analysis with RE-PCR. Similar to (A), the methyl sensitive restriction enzymes used for RE-PCR are indicated (HpaII, KspI); digestion with the non-methyl sensitive enzyme MspI serves as a negative control and undigested DNA (control) serves as a positive control. Methylation of p16<sup>INK4a</sup> is detected in case No 1, but not in case Nos 10 and 11. (C) p16<sup>INK4a</sup> analysis using methylation specific polymerase chain reaction (MSP). Bisulphite treated DNA (which changes the unmethylated but not the methylated cytosines into uracil) is subjected to PCR amplification using primers designed to anneal specifically to the methylated bisulphite modified DNA. MSP results are expressed as unmethylated p16 specific bands (U) or methylated p16 specific bands (M). Bisulphite converted DNA from normal corresponding liver tissue (N) served as a negative control, as indicated by the presence of the U but not the M band. Similar to (B), methylation of p16<sup>INK4a</sup> was detected in case No 1 but not in case Nos 10 and 11. (D) Results of multiplex reverse transcription-PCR (RT-PCR) of p14 mRNA (upper line corresponding to 200 bp) and p16 mRNA (lower line corresponding to 179 bp) for case Nos 1, 10, and 11. (E) Immunostaining of p16<sup>INK4a</sup> protein in liver cell adenoma (LCA). Case No 1 shows methylated p16<sup>INK4a</sup> and complete loss of p16<sup>INK4a</sup> (LCA cells negative for p16 protein) (original magnification ×10). p16<sup>INK4a</sup> is detectable in case Nos 10 and case 11 (dark reaction product within the cell nuclei) (original magnification ×20 and ×40). (F) Immunostaining of p14<sup>ARF</sup> protein in LCA. Case No 1 shows unmethylated p14<sup>ARF</sup> and strong immunoreactivity of the tumour cells for p14 protein (dark reaction product within the tumour cell nuclei). The tumour surrounding fibrous capsule (arrows) is negative (original magnification ×5). Case No 11 shows a methylated p14<sup>ARF</sup> and complete protein loss within the tumour tissue (original magnification ×20).
and 2 have been described previously.\textsuperscript{16} Exon 1\(\beta\) was analysed through two overlapping PCR products generated with the primer pairs P14F1 (5′ TCAGGGAAGGGCCTGC 3′) and P14R1 (5′ GCCCAGGTAGTGAAACCA 3′), which generated a 245 bp product, and the primer pair P14F2 (5′ GCCGGGAGTAGGTTT 3′) and P14R2 (5′ CACCCAGTTACTCTCCTC 3′), which generated a 257 bp product. The primers were labelled with \(^{32}\)P-ATP and each sample was subjected to PCR analysis (denaturing for 30 seconds, annealing for 45 seconds, extension for 30 seconds at 94°C, 55–60°C, and 72°C, respectively). The PCR products were electrophoresed, and the gels dried and autoradiographed. Variant SSCP bands were cut out from the gel and the DNA eluted. Variant bands and 3\(\mu\)l of the eluted DNA were used as templates for unlabelled PCR. After purification of the PCR products, sequencing analysis was performed using the DNA Sequenase Kit (Amersham, Germany) and an automatic sequencing analyser (ABI 373; Applied Biosystems-Perkin-Elmer, Germany). All mutations found were confirmed by direct sequencing of the amplified tumour and corresponding non-tumorous DNA to identify germline mutations and polymorphisms.

**Immunohistochemical analysis and assessment**

Immunohistochemical analysis was performed as described previously.\textsuperscript{16} All cases tumour and non-neoplastic liver tissue was examined.

The following antibodies were used: p16 (polyclonal; rabbit, dilution 1:500; Pharmingen, San Diego, California, USA), and p14 (polyclonal; rabbit, dilution 1:100; Zymed Laboratories, South San Francisco, California, USA).

Sections known to stain positively were included in each batch and negative controls were also performed by replacing the primary antibody with mouse or goat ascsites fluid (Sigma-Aldrich Biochemicals, St Louis, Missouri, USA).

**RESULTS**

**Analysis of INK4a-ARF deletions and mutations**

Twenty five normal/tumour pairs were interpreted for allelic dosage analysis (table 1, fig 2). The allelic balance of the two genes was determined using the interferon \(\gamma\) gene as an internal control (fig 2). The two genes, p14\textsuperscript{ARF} and p16\textsuperscript{INK4a}, were expressed in all cases examined; deletions were not observed. No exclusive loss of either p16\textsuperscript{INK4a} or p14\textsuperscript{ARF} was found in our tumours. Loss of heterozygosity analysis revealed an identical status of the microsatellite markers used in paired samples of LCA and corresponding liver (fig 3).

Mutations of exons 1 and 2 were analysed by SSCP-PCR followed by direct sequencing of the cases with anomalous migrating bands. In nine cases, abnormal bands were visible. However, we failed to detect specific mutations within both exons. In one case, a polymorphism was identified in normal liver but not within LCA tissue (c442G >A; A148T).

**Methylation status of the p14\textsuperscript{ARF} and p16\textsuperscript{INK4a} genes**

Promoter methylation of p14\textsuperscript{ARF} was present in 3/25 cases (12%). In all patients, corresponding non-neoplastic liver tissue was also analysed; no p14\textsuperscript{ARF} promoter methylation was observed in any case. Analysis of the methylation status of the adjacent p16\textsuperscript{INK4a} gene revealed that 6/25 LCA (24%) examined showed aberrant methylation at the 5′CpG island. Despite microdissection, amplification of unmethylated templates was also detected to some degree, probably because of contaminated normal intratumorous tissue (fibroblasts, endothelial cells, inflammatory cells). In normal LCA surrounding liver tissue, methylation of p16\textsuperscript{INK4a} or p16\textsuperscript{INK4a} was not observed.

All six LCA with methylated p16\textsuperscript{INK4a} exhibited an unmethylated p14\textsuperscript{ARF} promoter. A coincidence of both p14\textsuperscript{ARF} and p16\textsuperscript{INK4a} methylation was not found. Thus the methylation status of p14\textsuperscript{ARF} and p16\textsuperscript{INK4a} promoters does not seem to be directly related.

Real time PCR of those samples with a methylated p16\textsuperscript{INK4a} gene showed a level of methylation of approximately 75%.

All six cases with aberrant methylation of the p16\textsuperscript{INK4a} or p14\textsuperscript{ARF} gene showed complete loss of immunoreactivity (fig 1E, F) within the tumour tissue. In the 19 cases shown to lack p16\textsuperscript{INK4a} promoter methylation, nuclear staining of p16\textsuperscript{INK4a} protein was observed in nearly all LCA cells with a moderate to strong intensity of immunoreactivity. In normal liver tissue, p16\textsuperscript{INK4a} protein was detected in all cases (fig 1E, F). Three LCA with a methylated p14\textsuperscript{ARF} promoter lacked specific p14\textsuperscript{ARF} immunostaining (fig 1E, F).
downregulated p16 detected in 22/25 tumours (fig 1D). Among the tumours with p16
the remainder p16
lial tumour of the liver. We examined the status of p14
chromosome 9p21 in LCA, the most important benign epithe-
agus, and pancreas.
been reported not only in various types of carcinomas but also
in early preneoplastic lesions in the lung, stomach, oesoph-
alterations in these genes may function as cooperative or
alternative mechanisms in the pathogenesis of these tumours.

DISCUSSION
Recently, aberrant methylation of the p16
promoter has been reported not only in various types of carcinomas but also
in early preneoplastic lesions in the lung, stomach, oesoph-
agous, and pancrea.17–21 Ours is the first study to examine alterations in the INK4a-ARF (also termed CDKN2A) locus on chromosome 9p21 in LCA, the most important benign epithelial tumour of the liver. We examined the status of p14
and p16
simultaneously to answer the question of whether alterations in these genes may function as cooperative or alternative mechanisms in the pathogenesis of these tumours.

Our study showed that the p14
promoter was inactivated in 12% of cases. In 24% of all LCA examined, promoter methylation of the neighbouring gene p16
was observed. We failed to detect simultaneous methylation of both genes and conclude that p14
methylation is independent of p16
. Thus the p14
promoter demonstrates selective epigenetic silencing independent of that of p16
. The strong correlation between promoter methylation and transcriptional inactivation, as examined by multiplex RT-PCR, indicates that aberrant methylation is a major mechanism of inactivation of the INK4a-ARF locus in LCA.

In concordance with data reported for cell lines, we failed to detect specific mutations of the p14
or p16
gene.18–22 p14
can also be lost by (homozygous) deletion but this loss also targets p16
in the vast majority of cases.19–22 Only a few examples currently exist of specific p14
deletions that spare the remainder p16
coding region: a melanoma cell line and a glioma xenograft.23

In human cells, transcriptional silencing usually involves methylation of CpG rich sequences (CpG islands) in the promoters of affected genes. Such silencing is clonal and thought to be physiologically irreversible in somatic cells. Neoplastic cells often display aberrant methylation of multiple genes, including genes that regulate critical processes such as cell cycle control, DNA repair, and angiogenesis.12–14 The cause(s) of aberrant promoter methylation in neoplastic cells remains to be elucidated. It has been proposed that age related methylation identifies and contributes to an acquired predisposition to neoplasia (for example, colon cancer) because it parallels an age related increased cancer incidence and has the potential to alter the physiology of aging cells and tissues.24–26 This hypothesis predicts that higher levels of age related methylation may be present in conditions of rapid cell turnover that mimic premature aging. In LCA, an increase in cellular proliferation is often histologically. The proliferative activity of the neoplastic hepatocytes is significantly higher than in adenoma surrounding non-neoplastic liver tissue.2,27 Therefore, we hypothesise that methylation and consecutive silencing of the p16
and p14
promoter may cause induction of increased cell turnover via affecting the G1/S phase transition of the cell cycle. In contrast with Rashid et al who found aberrant methylation of p16
in approximately 73% of tubulovillous colon adenoma,28 a clear precancerous lesion, we detected aberrant methylation only in 24% of LCA. Together with the observation that altered methylation is also observed in liver cirrhosis,29 our data favour the hypothesis that methylation is a phenomenon of increased cellular proliferation and immortalisation rather than a conditio-sine-quanon of malignant transformation.

Table 1 Pathohistological data and INK4a-ARF alterations

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Table entries: RE-PCR, restriction enzyme related-polymerase chain reaction; MSP, methylation specific PCR; EXP, gene mRNA expression analysed by reverse transcription PCR; ND, not detected (wild-type, both alleles expressed as defined by multiplex PCR); NI, not informative.

Multiplex RT-PCR for p16
and p14
mRNA
Using specific sense primers for exon 1α and exon 1β, and a common reverse primer for exon 2, both transcripts were simultaneously amplified in a single reaction. p16
mRNA was amplified in 19/25 cases and p14
transcripts were detected in 22/25 tumours (fig 1D). Among the tumours with downregulated p16
or p14
mRNA, methylation of the corresponding promoters was observed in six and three cases, respectively.

Authors’ affiliations
A Tannapfel, C Busse, C Wittekind, Institute of Pathology, University of Leipzig, Liebigstr 26, 04103 Leipzig, Germany
F Geijler, H Witzigmann, J Hauss, Department of Abdominal, Vascular, and Transplantation Surgery II, University of Leipzig, Liebigstr 20a, 04103 Leipzig, Germany

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Gut 2002 51: 253-258
doi: 10.1136/gut.51.2.253

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