Structure of the c-Ki-ras Gene in a Rat Fibrosarcoma Induced by 1,8-Dinitropyrene

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Restriction enzyme maps were made of the region around exons 1 and 2 of activated c-Ki-ras of a fibrosarcoma (1,8-DNP2) induced in a rat by 1,8-dinitropyrene. Nucleotide sequence analysis revealed that activated c-Ki-ras shows a $G \rightarrow T$ transversion in codon 12 and consequently encodes cysteine instead of glycine in normal rat c-Ki-ras.

1,8-Dinitropyrene, a potent environmental mutagen present in diesel exhaust and polluted air, induced fibrosarcomas when injected subcutaneously into Fischer 344 rats (8). Of seven sarcomas examined, one tumor, 1,8-DNP2, contained an activated c-Ki-*ras* oncogene detected by an NIH 3T3 cell transfection assay (7). Studies of transforming c-Ki-*ras* genes in a wide variety of human and rodent tumors revealed that a single point mutation in codon 12 or 61 of the predicted p21 protein was responsible for the activation of the protooncogene (4, 6, 10, 12). However, the structure of rat c-Ki-*ras* has not yet been reported. Here we report the structure of a portion of c-Ki-*ras* of the rat fibrosarcoma 1,8-DNP2.

An NIH 3T3 primary transformant (1,8-DNP2-2) contain-

that did not. The latter fragment may not be related but may be ligated to c-Ki-*ras* during cloning. The other clone, λ DNP2-2, had a 10.5-kb *Bam*HI insert. The 8.3- and 10.5-kb *Bam*HI fragments from λ DNP2-1 and λ DNP2-2, respectively, were recloned into plasmid pSP64, yielding pDNP2-1 and pDNP2-2, respectively.

The restriction enzyme maps of pDNP2-1 and pDNP2-2 are shown in Fig. 1. The hatched boxes indicate the regions with homology to HiHi380 which covers exons 1 and 2 and a 5' portion of exon 3 of human c-Ki-ras (5). A 0.1-kb SstII-HinfI fragment of HiHi380 (2) was used to detect exon 1 of c-Ki-ras. Exon 3 was distinguished from the others by use of a 0.2-kb XbaI-EcoRI fragment of HiHi3 (2). A 0.5-kb EcoRI-HindIII fragment of pDNP2-1 contained exon 1, an



FIG. 1. Restriction maps of pDNP2-1 and pDNP2-2. Hatched boxes indicate the regions that hybridized with HiHi380. Solid boxes indicate the exons that were examined by nucleotide sequencing. Exon 3 has not yet been analyzed. Restriction endonuclease sites were as follows: B, BamHI; E, EcoRI; H, HindIII; K, KpnI; P, PstI; Pv, PvuII; S, SacI; and Ha, HaeIII. HaeIII sites are mapped only in the EcoRI-EcoRI fragment containing exon 2. EcoRI sites and HaeIII sites in the right half of pDNP2-2 were determined by partial digestion of the end-labeled 5-kb HindIII-BamHI fragment.

ing an activated c-Ki-*ras* gene was obtained by transfection of DNA of the rat fibrosarcoma 1,8-DNP2 (7). Complete digestion of the 1,8-DNP2-2 DNA with *Bam*HI yielded two rat-derived fragments of about 9 and 11 kilobases (kb) that hybridized with HiHi380 (2). These two fragments were ligated to the *Bam*HI site of EMBL3A (3). Three clones that gave a positive signal with the HiHi380 probe were obtained. Clone λ DNP2-1 contained two *Bam*HI inserts: an 8.3-kb fragment that hybridized to the probe and a 7.5-kb fragment 0.8-kb *Eco*RI-*Bam*HI fragment of pDNP2-2 contained exon 3, and the remaining 1.7-kb *Eco*RI fragment contained exon 2. pDNP2-2 was digested with *Hae*III, and the resulting 0.5-kb fragment was found to carry exon 2, which hybridized with the HiHi380 probe but not with the *XbaI-Eco*RI fragment of HiHi3 (Fig. 1).

For examination of the genetic alterations of exons 1 and 2, we determined their nucleotide sequences. A 0.5-kb *EcoRI-HindIII* fragment of pDNP2-1 was subcloned into M13mp18 or M13mp19, and a 0.5-kb *HaeIII* fragment of pDNP2-2 carrying exon 2 was subcloned into the phospha-

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a)					1			_	_	_					11	_					_		_	_	21					
1,8-DNP2-2 Ki- <u>ras</u>	GC	CTG	CTG	ала	Met ATG	Thr ACT	Glu GAG	Tyr Tat	Lys AAA	Leu CTT	GTG	GTA	GTT	GIY GGA	GCT GCT	Cys TGT	GGC	GTA	GGC	Lys AAG	Ser AGT	GCC	Leu TTG	Thr ACG	ATA	GIN CAG	CTA	ATT	GIn C A G	ASN AAT
Human c-Ki- <u>ras</u> 2							A									G														
v-Ki- <u>ras</u>			A		 31											λ														
1,8-DNP2-2 Ki- <u>ras</u>	His CAC	Phe TTT	Val GTG	Asp GAT	Glu GAA	Tyr TAT	Asp GAT	Pro CCT	Thr ACG	Ile ATA	Glu G A G																			
Human c-Ki- <u>ras</u> 2	T			c				A	A		 Gln																			
v-Ki- <u>ras</u>											C																			
ь)				41										51										61						
b) 1,8-DNP2-2 Ki- <u>ras</u>	Asp GAC	Ser TCC	Tyr TAC	41 Arg AGG	Lys Aaa	Gln C AA	Val GT A	Val GTA	Ile ATT	Asp Gat	Gly GGA	Glu G AA	Thr ACC	51 Cys TGT	Leu CTC	Leu TTG	Asp GAT	Ile ATT	Leu CTC	Asp GAC	Thr ACA	Ala GCA	Gly GGT	61 Gln C AA	Glu GAG	Glu G A G	Tyr TAC	Ser AGT	Ala GCA	Met ATG
b) 1,8-DNP2-2 Ki- <u>ras</u> Human c-Ki- <u>ras</u> 2	Asp GAC T	Ser TCC	Tyr TAC	41 Arg AGG 	Lys AAA G	Gln CAA	Val GTA	Val GTA	Ile ATT	Asp Gat	Gly GGA	Glu G AA	Thr ACC	51 Cys TGT	Leu CTC	Leu TTG	Asp GAT	Ile ATT	Leu CTC	Asp GAC	Thr ACA	Ala GCA	Gly GGT 	61 Gln C AA	Glu GAG	Glu GAG	Tyr TAC	Ser AGT	Ala GCA	Met ATG
b) 1,8-DNP2-2 Ki- <u>ras</u> Human c-Ki- <u>ras</u> 2 v-Ki- <u>ras</u>	Asp GAC T	Ser TCC	Туг ТаС 	41 Arg AGG 71	Lys AAA G	Gln CAA 	Val GTA 	Val GTA 	Ile ATT 	А з р GAT 	Gly GGA	Glu G AA 	Thr ACC 	51 Cys TGT 81	Leu CTC	Leu TTG	Asp GAT 	Ile ATT	Leu CTC	Asp GAC 	Thr ACA	Ala GCA Thr A	Gly GGT 	61 Gln CAA 91	Glu GAG	Glu GAG 	Tyr TAC 	Ser AGT	Ala GCA	Met ATG
b) 1,8-DNP2-2 Ki- <u>ras</u> Human c-Ki- <u>ras</u> 2 v-Ki- <u>ras</u> 1,8-DNP2-2 Ki- <u>ras</u>	Asp GAC T Arg AGG	Ser TCC Asp GAC	Tyr TAC Gln CAG	41 Arg AGG 71 Tyr TAC	Lys AAA G Met ATG	Gln CAA Arg ÀGA	Val GTA Thr ACT	Val GTA Gly GGG	Ile ATT Glu GAG	Asp GAT Gly GGC	Gly GGA Phe TTT	Glu GAA Leu CTT	Thr ACC Cys TGT	51 Cys TGT 81 Val GTA	Leu CTC Phe TTT	Leu TTG Ala GCC	Asp GAT Ile ATA	Ile ATT Asn AAT	Leu CTC Asn AAT	Asp GAC Thr ACT	Thr ACA Lys AAA	Ala GCA Thr A Ser TCA	Gly GGT Phe TTT	61 Gln CAA 91 Glu GAA	Glu GAG Asp GAT	Glu GAG Ile ATT	Tyr TAC His CAC	Ser AGT His CAT	Ala GCA Tyr TAT	Met ATG Arg AG
b) 1,8-DNP2-2 Ki- <u>ras</u> Human c-Ki- <u>ras</u> 2 v-Ki- <u>ras</u> 1,8-DNP2-2 Ki- <u>ras</u> Human c-Ki- <u>ras</u> 2	Asp GAC T Arg AGG 	Ser TCC Asp GAC 	Tyr TAC Gln CAG 	41 Arg AGG 71 Tyr TAC 	Lys AAA G Met ATG 	Gln CAA Arg ÀGA G	Val GTA Thr ACT	Val GTA Gly GGG 	Ile ATT Glu GAG 	Asp GAT Gly GGC 	Gly GGA Phe TTT	Glu GAA Leu CTT	Thr ACC Cys TGT 	51 Cys TGT 81 Val GTA	Leu CTC Phe TTT	Leu TTG Ala GCC 	Asp GAT Ile ATA 	Ile ATT Asn AAT	Leu CTC Asn AAT 	Asp GAC Thr ACT	Thr ACA Lys AAA	Ala GCA Thr A Ser TCA	Gly GGT Phe TTT	61 Gln CAA 91 Glu GAA	Glu GAG Asp GAT 	Glu GAG Ile ATT	Tyr TAC His CAC	Ser AGT His CAT	Ala GCA Tyr TAT	Met ATG Arg AG

FIG. 2. Nucleotide sequences and predicted amino acid sequences of exons 1 (a) and 2 (b) of c-Ki-*ras* derived from 1,8-DNP2. Corresponding regions of v-Ki-*ras* and normal human c-Ki-*ras*2 determined by others (5, 11) are also shown. Dashes indicate nucleotides that are identical to those in c-Ki-*ras* derived from 1,8-DNP2.

tase-treated *SmaI* site of M13mp10. The nucleotide sequences were determined by the dideoxy method of Sanger et al. (9). Coding regions were assigned by comparison of the DNA sequences with those of the v-Ki-*ras* (11) and human c-Ki-*ras*2 (5) genes. Consensus splicing sequences that were identical to those of human genes were found at intron-exon boundaries (data not shown).

The nucleotide sequences of exons 1 and 2 cloned from 1,8-DNP2-2, encoding a sequence of 97 amino acids at the N terminus, were compared with the corresponding sequences of human c-Ki-ras and v-Ki-ras (Fig. 2). The nucleotide sequence was more homologous with that of v-Ki-ras than with that of human c-Ki-ras. In fact, 1,8-DNP2-2 Ki-ras and v-Ki-ras differed in only three nucleotides in the coding regions, the first letters of codons 12, 37, and 59, although these all resulted in differences in the predicted amino acid sequence. The amino acid sequence encoded by 1,8-DNP2-2 Ki-ras than to that encoded by v-Ki-ras; the only difference was that at codon 12. Rat c-Ki-ras of the primary transformant 1,8-DNP2-2 encoded cysteine, whereas normal human c-Ki-ras?

Codon 12 of the genomes from normal rats and the original tumors were analyzed further by oligodeoxynucleotide hybridization. Two synthetic 19-mers spanning the region from nucleotide 25 in codon 9 to nucleotide 43 in codon 15 of the human c-Ki-ras gene (Pharmacia P-L Biochemicals), one containing GGT (glycine) and the other containing TGT (cysteine) at codon 12, were used as probes after being labeled with ³²P in a polynucleotide kinase reaction. Consistent with the restriction map shown in Fig. 1, in double digests with SacI and EcoRI of DNAs of normal rat kidney, sarcoma 1,8-DNP2, and the primary transformant 1,8-DNP2-2, exon 1 of rat c-Ki-ras was found in a 1.5-kb fragment. The 1.5-kb EcoRI-SacI fragments of normal rat kidney and of 1,8-DNP2 but not of 1,8-DNP2-2 hybridized with the probe of 19-mer containing GGT (glycine) at codon 12 by direct gel hybridization (1). The 19-mer containing TGT (cysteine) at codon 12 hybridized with the DNAs of 1,8-DNP2 and of 1,8-DNP2-2 but not of normal rat kidney (data not shown).

From the results on nucleotide sequencing and oligo-

deoxynucleotide hybridization, we conclude that glycine is encoded at codon 12 of normal rat c-Ki-*ras*, that a G \rightarrow T transversion has occurred at the first letter of codon 12 in 1,8-DNP2 c-Ki-*ras*, and that 1,8-DNP2 is a heterozygote of normal and activated c-Ki-*ras*. The same mutation has been observed in activated c-Ki-*ras* of human tumors (6, 12), and the transforming activity of c-Ki-*ras* encoding cysteine as amino acid 12 was first determined by using chimeric genes (10). From these results, it is conceivable that the somatic mutation (G \rightarrow T) in 1,8-DNP2 is responsible for the activation of c-Ki-*ras*.

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