Role of Poly-ADP-Ribosylation in Cancer Development

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Abstract

I lucidation of the relationship between poly-ADP-ribosylation and carcinogenesis has
markedly progressed by the recent development of knockout or transgenic mice models
of poly(ADP-ribose) polymerase (Parp)-1, Parp-2, and markedly progressed by the recent development of knockout or transgenic mice models of poly(ADP-ribose) polymerase (Parp)-1, Parp-2, and poly(ADP-ribose) glycohydrolase (Parg). Parp-1 is involved in base excision repair (BER), single- and double-strand break repair, and chromosomal stability. These multiple functions explain why *Parp-1* deficiency enhances carcinogenesis induced by alkylating agents and that in aged animals. Parp-1 is also involved in transcriptional regulation through protein-protein interaction as a coactivator and/or poly-ADP-ribosylation reaction and is possibly involved in epigenetic alteration during carcinogenesis and modulation of tumor phenotypes. Parp-1-dependent cell-death accompanying NAD depletion may be another important issue in carcinogenesis because this process could lead to the selection of *Parp-1* deficient cells due to their survival advantage during cancer growth. The relationship of Parp-2, Parp-3, tankyrase and Parg with carcinogenesis is also discussed.

Introduction

Carcinogenesis is a multistage process that involves multiple pathways and each cancer arises though different combinations of a variety of genetic and epigenetic changes.^{1,2} Compared to the pathogenesis process of other diseases, carcinogenesis involves a wider range of aberrations of biological processes, including genomic stability, induction of cell death, differentiation, control of cell cycle and proliferation. The poly-ADP-ribosylation reaction and the Parp-1 molecule are involved in each of the above processes and thus should be related to carcinogenesis.³ In this chapter, we give an overview of the impact of dysfunction of the poly-ADP-ribosylation reaction on carcinogenesis in various experimental models, and discuss their mechanistic bases in relation to human cancer.

Mouse Models of Carcinogenesis

Three types of Parp-1 knockout mice established by disruption of either exon 1^4 , 2^5 , or $4⁶$ were examined for their susceptibility to carcinogenesis. As shown in Table 1, an increased frequency of the development of hepatocellular carcinomas (HCC) in *Parp-1 -/-* mice, harboring exon 2 disruption of the *Parp-1* gene was observed in aged mice as reported by Tong et al.⁷ In developed HCC, frequent occurrence of genomic instability, loss of expression of E-cadherin and accumulation of β -catenin were observed. In our experiments, although spontaneous tumor development was not observed at 7 and 9 months of age, 8.9 the

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 $*(\rightarrow)$ no change, (1) elevated, (\downarrow) reduced incidence, compared to wild-type mice, respectively

frequency of HCC development was increased in 21-23-month-old *Parp-1 -/-* mice, whereas no tumors were observed in other tissues (Masutani et al unpublished). Administration of N-nitrosobis(2-hydroxypropyl)amine (BHP) resulted in the development of liver hemangioma and hemangiosarcoma at significantly higher frequencies in *Parp-1 -/- than* in *Parp-1 ÷/+* mice. 8 Another alkylating agent, azoxymethane also enhanced the frequency of tumor development both in the colon and liver in *Parp-1^{-/-}* compared with that in *Parp-1*^{+/+} mice.⁹ In addition to the differences in tumor incidence, the size of tumors, mainly adenocarcinoma, was larger in *Parp-1⁻¹* than in *Parp-1*^{+/+} mice in the colon, suggesting that loss of Parp-1 affects tumor growth. In sharp contrast, the frequency of hepato- and pulmonary carcinogenesis was not different among *Parp-1⁻¹*, *Parp-1^{+/-}* and *Parp-1^{+/+} mice administered IQ* (2-amino-3-methylimidazo[4,5-fquinoline), a cooked food-borne heterocyclic amine that produces bulky adducts on DNA (Ogawa et al unpublished). 4-Nitrosoquinoline 1-oxide (4NQO) mimics ultraviolet (UV)-induced damage and generates a DNA adduct, which is removed mainly by nucleotide excision repair involving XPA (xeroderma pigmentosum group A). It was reported that development of oral tumors in mice given 4NQO was markedly higher in XPA^{-/-} than in wild-type mice.¹⁰ In contrast, there was no difference in tumor incidence between *Parp-1 -/-* and *Parp-1 ÷/÷* mice after 4NQO administration in drinking water (Gunji et al unpublished). These experiments strongly suggest that susceptibility to carcinogenesis under *Parp-1* deficiency depends substantially on the type of DNA damage and implies the significant contribution of Parp-1 in BER and/or DNA strand break repair pathways to prevent carcinogenesis.

The impact of the combination of deficiency of *Parp-1 and DNA-PKorp53* was also studied in mice. SCID mice harbor a mutation in the gene encoding a catalytic subunit of the DNA-PK complex and show immunodeficiency due to the lack of V[D]J recombination to produce mature T and B cells. In *Parp-1⁻¹SCID* mice, a marked increase of the frequency of T-cell lymphoma was observed from an early age compared to SCID mice, although the frequency of B-cell lymphoma was not increased.¹¹

P53 is a major genome guardian and is involved in the regulation of both proper cell cycle and apoptosis after DNA damage. Mice lacking $p53$ ($p53^{-/-}$) show a high incidence of spontaneous tumors as well as an increase in various types of genomic instabilities after DNA damage.¹² Tong et al reported that the deficiency of $p53$ in *Parp-1⁻¹* mice, harboring exon 2 disruption of *Parp-1,* significandy promotes the development of thymic lymphoma, colon and breast carcinomas. 13 A transgenic mouse, which overexpresses the DNA binding domain of Parp-1, as a dominant negative mutant (PARP-DBD), also showed increased incidence of T-cell lymphomagenesis in $p53^{-/2}$ mice with a significantly shorter tumor latency period.¹⁴ It is possible that the suppressive effect of PARP-DBD on DNA repair promotes the accumulation of genomic instability and contributes to lymphomagenesis.

Another intriguing finding is the spontaneous development of medulloblastoma in the cerebellum of 8-week-old *p53-/-Parp-1 -/-* mice and that nearly half of these mice harbor medulloblastoma by 6 months of age.¹⁵ Lee et al reported the spontaneous development of medulloblastoma in the knockout mice harboring both *DNA ligase IV and p53* disruption. 16 Since DNA ligase IV is a key enzyme in nonhomologous end joining (NHEJ) repair and accumulating evidence implies that Parp-1 also participates in NHEJ repair, it is possible that the NHEJ-dependent DSB repair is important in prevention of medulloblastoma formation in the cerebellum.

Different consequences of p53 *and Parp-1* deficiencies were reported by Conde et al in *p53-/-Parp-1 -/-* mice, harboring exon 4 disruption in *Parp-1* gene. These mice show a lower frequency of thymic lymphoma compared to $p53^{-/2}$ mice.¹⁷ In relation to this, H-ras-transformed fibroblasts derived from $p53^{-1}$ *Parp-1⁻¹* mice showed reduction of *inducible nitric oxide synthase (iNOS)* expression, nitric oxide release and decreased potential of cell growth and tumorigenesis compared to those derived from $p53^{-/-}$ mice.¹⁷ The diminished cell growth is likely to be related to the decreased level of nitric oxide, since the stimulatory role of nitric oxide in proliferation and its inhibitory role in apoptosis have been reported.¹⁸ We suggest that the role of Parp-1 in cell proliferation significantly affects tumorigenesis under certain conditions. Notably, B-cell lymphoma development was not increased either in SCIDParp-1⁻¹ ⁻¹¹ or in $p53^{-1}$ *Parp-1*^{-/-} mice¹³ whereas T-cell lymphoma development was augmented in these cases. Since impairment of S-phase entry of the B-cell population in splenocytes was also observed in *Parp-1⁻¹* mice, ¹⁹ the evidence indicates the possibility that Parp-1 is required for B-cell lymphoma development by supporting its cell proliferation potential. The genetic background of mice may also affect the extent of contribution of Parp-1 in cell proliferation, since we observed that *Parp-1⁻¹⁻* mice of the C57BL/6 congenic strain show partial lethality during late embryogenesis¹⁹ and reduced body-weight gain (Ogawa et al unpublished), whereas those of ICR/129Sv mixed genetic background do not show such phenotypes.

The elucidation of the relationship of other Parp family members to carcinogenesis awaits the results of further experiments including those using the transgenic animal models. Recent studies reported the involvement of Parp-2 in BER processes,²⁰ of Parp-3 in centrosome regulation²¹ and of tankyrase in telomere length regulation.²² Hence, dysfunction of these molecules may cause genomic instability and is expected to have certain impacts on carcinogenesis.

Compared to the poly-ADP-ribosylation reaction, the involvement of poly(ADP-ribose) degradation by Parg on carcinogenesis has not been elucidated yet. *Parg-deficient* embryonic stem (ES) cells²³ and *Drosophila*²⁴ have become available recently. Since *Parg*-deficient ES cells show increased sensitivity to alkylating agents and γ -irradiation and undergo early apoptosis (Fujihhara et al unpublished), dysfunction of the *Panggene* may also be involved in carcinogenesis possibly through regulation of recovery from DNA damage.

Effect of PARP Inhlbitors on Carcinogenesis

Several carcinogenesis experiments have been carried out using Parp inhibitors or modulating NAD level, summarized in Table 2. Parp inhibitors including 3-aminobenzamide and 3-methoxybenzamide augment²⁵⁻²⁹ or decrease³⁰⁻³² the incidence of tumors depending on the treatment protocol of inhibitors, carcinogens, tissue, or animals used in the studies.³³ The exact explanation for this phenomenon is still not available. Since Parp inhibitors also block activity of Parp family members other than Parp-1, the inhibition of various Parp family proteins should have a substantial influence on the susceptibility to carcinogens. The experimental model of Boyonoski et al manipulated NAD levels in vivo and showed that NAD deficiency increases the incidence of tumors and leukemia, 34 whereas supplementation with the NAD precursor niacin delayed the onset of HCC.³⁵ These results suggest that maintenance of cellular NAD levels prevents or delays carcinogenesis.

In vitro transformation systems using cultured cells in combination with various types of carcinogens have been also described. The effects of Parp inhibitors exhibit a wide spectrum as depicted in Table 3. Parp inhibitors suppressed transformation induced by various type of carcinogens,³⁶ not only methylating agents but also one inducing bulky adducts, benzo[a]pyrene,³⁶ as well as ionizing irradiation $\left(\text{IR}\right)^{37,38,42}$ and UV.^{37,39} In contrast, against ethylating agents, such as ethylnitrosourea and ethylmethanesulfonate,⁴⁰⁻⁴² Parp inhibitors enhanced such transformation. The enhancement of in vitro transformation was observed in a time-specific manner. Simultaneous treatment with carcinogen and Parp-inhibitor was effective whereas Parp inhibitor treatment 24 hr after carcinogen exposure was not.⁴¹ These in vitro transformation systems use immortalized cells and the cell proliferation potential may be the major factor that influences the overall frequency of transformation. It is thus conceivable that Parp inhibitors may reduce the proliferation capacity of cells, leading to a low transformation frequency. However, no plausible explanation is currendy available as to why Parp inhibitors exert the opposite effects on transformation induced by methylating and ethylating agents. Parp inhibitors also increase the transformation of NIH3T3 cells by transfection of SV40 DNA and this was further proven to be due to the increase in integration frequency of SV40 DNA into the genome.⁴³

Tumorigenesis and Differentiation

Functional loss of Parp modulates tumorigenesis and differentiation of malignant cells as summarized in Table 4. Early studies showed that Parp inhibitors induced differentiation of various types of tumor cell lines. $44-47$ In the case of H_L-60 cells 48 and H-ras transformed NIH3T3 cells, 47 loss of amplified oncogenes, *c-myc* and H-ras genes, was induced after treatment with Parp inhibitors and these changes could reduce the proliferation potential of tumor cells. Teratocarcinoma EC-AI cells also showed differentiation to endodermal cells during tumorigenesis in nude mice.⁴⁴ During cell differentiation, an increase in poly-ADP-ribosylation activity generally occurs at the commitment stage, which is followed by decrease in its activity. Reversion of the tumorigenic phenotype was also observed in vivo with a different type of Parp inhibitor, 5-iodo-6-amino-1, 2-benzopyrone, which is thought to interfere with zinc-finger function of Parp-1.⁴⁹

When $Parp-1$ ^{-/-} mouse ES cells were subcutaneously injected into nude mice, the recipient mice developed teratocarcinoma-like tumors, similar to the case with *Parp-1^{+/+}* ES cells.³⁰ In *Parp-1^{-/-}* tumors, the trophoblast lineage cells, including trophoblast giant cells and spongiotrophoblasts, are preferentially induced and large blood lacuna structures were secondarily induced, probably by the action of trophoblasts. *Parp-1⁻¹* ES cells in culture showed elevated expression levels of trophoblast marker genes, 51 suggesting that loss of Parp-1 promotes commitment to a trophoblast lineage. Trophoblast giant cells emerged after a repeated endoreduplication process and showed up to 1,000N ploidy. Loss of Parp-1 function may, therefore, also enhance endoreduplication. Overexpression of PARP-DBD in HeLa cells also interfered with tumorigenesis in nude mice, accompanied by an increased frequency of apoptosis.⁵² These examples indicate that Parp dysfunction can markedly influence tumor phenotype.

Table 2. Effect of PARP inhibitors on carcinogenesis

Table 3. Effect of PARP inhibitors on in vitro transformation

Parg^{-/-} ES cells produced tumors as in the case of wild-type ES cells (Fujihara et al unpublished). The differentiation potential of ES cells was not different among *Parg* genotypes. Induction of trophoblast lineage was not observed in *Parg*^{-/-} tumors, suggesting that *Parg* deficiency and the resulting impairment of poly(ADP-ribose) degradation is not related to trophoblast induction.

DNA Repair and Genomic Instability

As mentioned above, the spectrum of susceptibility of $Parp-1$ ^{-/-} mice to carcinogens implied a significant contribution of Parp-1 in BER and DNA strand break repair. In BER, after removal of damaged bases, such as 8-hydroxy-dG, or alkylated bases by glycosidases, single

^{*} Differentiation is inhibited depending on the concentration of the inhibitor.

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strand scission is introduced by AP-endonuclease. The recruitment of a molecular scaffold XRCC-1 (X-ray repair cross-complementing factor-I) to the repair site is a critical step in BER because XRCC1 further recruits DNA ligase III α , DNA polymerase β , and polynucleotide kinase. 53 Association of certain polymorphisms in *XRCC1* gene with lung and other cancers was reported by Divine et al.⁵⁴ It was demonstrated that Parp-1 is necessary for the assembly or stability of XRCC-1 nuclear foci at the site of DNA damage. 55 Dantzer et al showed that Parp-1 acts in the strand displacement step of the DNA fill-in reaction by DNA polymerase β and FEN-1 (flap endonuclease-1) and that long-patch BER is substantially delayed, whereas short-patch repair is only slightly affected in extracts from *Parp-1⁻¹* MEF.⁵⁶ Recently, defective poly-ADP-ribosylation in cells from Werner syndrome (WS) was reported following DNA damages introduced by an oxidative or an alkylating agent.⁵⁷ WS protein (WRN) interacts with proteins acting in BER, including polymerase δ , PCNA, FEN-1, replication factor A as well as Parp-1.⁵⁸ WRN may facilitate Parp-1 activation in the BER process. WS is characterized by the early onset of cancer, which may be pardy explained by the defective poly-ADP-ribosylation activity in the BER process. Malanga et al also reported the repair of stalled DNA topoisomerase I (topoI)-DNA covalent complex through reactivation of topoi by Parp-1. 59 In addition, Parp-2 was also shown to be involved in BER by Schreiber et al.²⁰

Parp-1 is also activated by double-strand break (DSB) and participates in NHEJ catalyzed by DNA-PK complex. Parp-1 activates auto-phosphorylation activity of DNA-PK and Ku70/ 80 complex, ⁶⁰ whereas Parp-1 activity is suppressed by DNA-PK.⁶¹ In *SCIDParp-1⁻¹* T-lymphocytes, $V[D]$ J recombination, which is carried out by NHEJ, is partially restored.¹¹

Furthermore, in a recombination-inducible SCID cell line, poly(ADP-ribose) formation was shown to occur during the resolution stage of V[D]J recombination where nascent opened coding ends are generated. Poly(ADP-ribose) formation colocalized with foci positive for the recombination protein Mrel I and facilitated coding-end resolution. In contrast, this response was not observed in wild-type cells possessing a functional catalytic subunit of DNA-dependent protein kinase.⁶² WRN protein physically interacts also with Parp-1,⁶³ and Ku70/80-induced stimulation ofWRN exonucleolytic activity was interfered with poly-ADP-ribosylation of Ku70/ 80 by Parp-1. 64 Parp-1 may thus regulate the exonudeolytic activity of WRN and prevent accidental recombination reaction during NHEJ.

Treatment of *Parp-1⁻¹* mice with BHP, an alkylating agent, did not enhance the frequency of point mutation, but rather increased the deletion frequency compared with *Parp-1 +'+* mice (Shibata et al unpublished). This finding supports the current evidence that Parp-1 is involved in the NHEJ process. Lack of elevation in point mutation under *Parp-1* deficiency also suggests that Parp-1 is probably not required in BER, at least until the removal of the damaged base, but may function after DNA strand break introduction by preventing further conversion of single strand breaks into DSBs, which will be predominantly repaired by NHEJ. Thus, Parp-1 is possibly involved in the repair of DSBs that occur during the process of the BER reaction.

Chromosome Instability and Cell-Cycle Checkpoints Controls

Hallmarks of chromosome instability in cancer cells include aneuploidy, hyperploidy, gene amplification, loss of heterozygosity (LOH) and gene rearrangement. Tong et al⁷ reported that $Ku80$ haploinsufficiency in *Parp-1⁻¹*- mice increased the incidence of HCC and the presence of chromosome instability in those tumors, such as chromatid/chromosome breaks, end-to-end fusions and recurrent nonreciprocal translocations. Hyperploidy was observed in spontaneously immortalized *Parp-1⁻¹* MEFs.⁶⁵⁻⁶⁷ Comparative genomic hybridization analysis revealed that chromosome gain and loss were enhanced in *Parp-1^{-/-}* compared with *Parp-1^{+/+}* MEFs.⁶⁵ Parp-1^{-/-} cells showed increased sister-chromatid exchange frequencies (SCEs) and micronuclei formation.^{6,68}

One of the possible mechanisms for these gross chromosome instabilities is deregulation of cell-cycle checkpoints. Parp-1 directly interacts with p53⁶⁹ and was shown to be involved in p53-mediated G1 arrest after DNA damage.⁷⁰⁻⁷² Parp-1 was further found to complex with PCNA and p21 after DNA damage introduced by *N-methyl-N'nitro-N-nitrosoguanidine* (MNNG) treatment. 73 Moreover, Kanai et al demonstrated that Parp-1 is located in the centrosome and interacts with p53 to regulate centrosome replication and function.⁷⁴ Halappanavar et al showed a defective mitotic checkpoint arrest accompanying down-regulation of cyclinB1/cdk-1 kinase activity in *Parp-1⁻¹* MEFs.⁷⁵ They also found that *Parp-1⁻¹* MEFs with higher ploidy were resistant to apoptosis in the G1 phase compared to wild-type cells, indicating defective post-mitotic checkpoints under *Parp-1* deficiency. Despite the accumulated evidence, it remains to be clarified whether *Parp-1⁺* tumors show higher chromosome instability and a more malignant phenotype compared to *Parp-1 +/÷* tumors. Another important issue is to understand whether Parp-1 or poly-ADP-ribosylation is involved in the formation of LOH during tumorigenesis.

Epigenetic Instability and Control of Gene Expression

Epigenetic changes in the gene are defined as nongenetic changes inheritable to daughter cells during cell growth. It has been demonstrated that epigenetic alteration of gene expression by hypo- or hyper-methylation substantially contributes to carcinogenesis.⁷⁶ Previous studies reported global hypomethylation in cancer cells and that genome hypomethylation induced by DNA methyltransferase mutation increases tumor incidence in mice.⁷⁷ In contrast, local hypermethylation of CpG islands in promoter regions in various tumor suppressor genes, including $p16^{NKA}$, was observed frequently in cancer cells.⁷⁶ Using the PARP inhibitor

3-aminobenzamide, Zardo et al⁷⁸ reported the presence of a genome-wide negative correlation between DNA methylation and poly-ADP-ribosylation. The promoter region of the $Ht\mathcal{D}$ gene also displayed this negative correlation.⁷⁹ Further studies are needed to investigate whether Parp-1 dysfunction leads to hypermethylation of cancer-related genes, and whether it promotes carcinogenesis.

On the other hand, poly-ADP-ribosylation can be involved in the control of gene expression independent ofDNA methylation. In *Drosophila,* engineered Parp-deficient flies displayed attenuation of the expression of genes located in puff loci, accompanied by the lack of puff formation as well as marked decrease of the induction of immune related genes such as *Diptericine. 8°* Gene expression was also reported to be altered under *Parp-1* deficiency,81 including those of iNOS, ⁸² and histone acetyltransferase. ⁸³ A function of Parp-1 as a coactivator could be involved in these phenomena. These possible functions of Parp-1 in the regulation of gene expression may lead to the alteration of differentiation potential and may ultimately affect tumor phenotypes.

Cancer Cell Selection through Cell Death

During cancer development, cancer cells may encounter various forms of cell-death pressure, depending on the site of their growth and surrounding microenvironment. During rapid proliferation of cancer cells in limited tissue space, hypoxic/anoxic conditions may prevail, which in turn enhance p53-dependent apoptosis. Such conditions may preferentially select *p53-deficient* cancer cells and cells overexpressing bcl-2, an apoptosis inhibitory protein, as described by Graeber et al.⁸⁴ In this regard, $p53$ gene alteration is detected in more than one-half of human tumors and *bcl-2* overexpression is also frequently observed in B-cell lymphoma, prostate cancer and colorectal cancer in humans.

On the other hand, oxidative cell death may be also induced in inflammatory conditions during carcinogenesis. Reactive oxygen species and reactive nitrogen species, including nitric oxide, produced by macrophages, induce rapid activation of Parp-1, leading to NAD depletion and apoptosis-inducing factor (AIF)-dependent cell death. Yu et al demonstrated that Parp-1 is necessary for this process. 85 It may thus be speculated that *Parp-l-deficient* cells may be selected out under such oxidative stress conditions (Fig. 1). Previous studies showed that neuronal cell death⁸⁶ and streptozotocin-induced pancreatic β -cell death were inhibited by either the Parp inhibitor, 3-aminobenzamide, or *Parp-I* deficiency.^{4,87,88} The experiments by Yamagami et al, in which the development of insulinoma in rats treated with streptozotocin was markedly enhanced by treatment with the Parp inhibitor 3-aminobenzamide,²⁵ adds further support for this scenario.

Role of PARP in Human Carcinogenesis

Molecular and biochemical studies as well as animal model studies suggest that PARP is involved in carcinogenesis, although the relation of the functional loss of PARP to human carcinogenesis is largely undetermined yet. Several pioneering studies investigated the changes in *PARP-1* gene expression and gene structure in human cancers. In a series of studies, Bhatia et al89-91 demonstrated that a *PARP-1* pseudogene on chromosome 13q33-qter presents a two allele (A/B) polymorphism and that the frequency of the B allele is higher in African Americans and is associated with endemic Burkitt lymphomas (1.7-fold), multiple myeloma and prostate cancers in the African American population. Enhanced activity and expression of *PARP-1* in Ewing's sarcoma cell lines were reported by Prasad et al.⁹² The same group later reported that enhancement of *PARP-1* gene expression is due to activation of transcription factors *ets-1* in Ewing's sarcoma cells. 93 Bieche et a194 showed that weak expression of the *PARP-1* gene is associated with higher genomic instability in breast cancer. They also showed that chromosome lq41-42, where the *PARP-1* gene is located, is frequently amplified in cancers that overexpress *PARP-1.* Other studies reported low formation of poly(ADP-ribose) induced by bleomycin treatment in peripheral lymphocytes from laryngeal cancer patients,⁹⁵ suggesting

Figure 1. A possible model for selection of Parp-l-deficient cells during carcinogenesis. Hypoxic or anoxic conditions often prevail in tumors, which may lead to thepreferential selection *ofp53-deficient* cancer cells and cells overexpressing the anti-apoptotic protein bcl-2.⁸⁴ We speculate that, in contrast, *Parp-1*-deficient cells may be selected under oxidative or nitrosative stress conditions, which also may prevail during cancer formation. For details, see text.

that low PARP activity correlates with a higher risk of laryngeal cancer. We found that the gastric cancer cell line MKN28 harbored a structural alteration in *PARP-1* gene, 96 although it is not known yet whether this affects the function of PARP-1.

Recent biochemical studies suggest that dysfunctions of PARP-2 and PARP-3 are also closely related to carcinogenesis. In this regard, Augustin et al²¹ indicated that the *PARP-3* gene is located at chromosome 3p21.1-3p21.31, where LOH is frequently observed in the early stages of lung cancer. Extensive investigation of genetic alterations of these PARP family genes may facilitate our understanding of the role of PARP in human carcinogenesis.

Concluding Remarks

Carcinogenesis in humans generally increases dramatically with age and it is considered that five or more genetic or epigenetic events may be necessary for development of cancer. 1,2 Each event leads to evolution of a certain tumor cell population from the selective pressure given from the microenvironment. Several lines of evidence obtained from research over the years imply that Parp-1 is involved in epithelial carcinogenesis and lymphomagenesis as a tumor suppressor factor. On the other hand, Parp-1 seems to be required for carcinogenesis and lymphomagenesis through its function in promotion of cell proliferation and inflammatory responses. Moolgavkar and Luebeck proposed that intervention strategies aimed at reducing the rate of clonal expansion of initiated/premalignant cells should be more effective than those designed to decrease the rate of early mutational events in the multistage process of human carcinogenesis. 97 In this context, a better understanding of the roles of poly-ADP-ribosylation

in transcription, cell-cycle-control, cell proliferation and modulation of immune responses is also important, especially for cancer development at an advanced age.

It was reported that haploinsufficiency of caretaker genes, such as histone $H2AX$ ^{98,99} and *NBS*¹⁰⁰ genes significantly enhances the susceptibility to carcinogenesis. Since Parp-1 functions as both a caretaker and gate-keeper of the genome, haploinsufficiency *of Parp-1* may also enhance carcinogenesis. In this context, susceptibility of *Parp-1 +/-* animals should be further investigated over extended time periods after application of various stimuli. The combination of haploinsufficiency in either caretaker genes or gate-keeper genes may further enhance the carcinogenic process during the long lifespan of human beings.

The identification of various Parp family members as well as Parg evoked intriguing questions on their functions, including whether these proteins are related to carcinogenesis, and further studies using animal models should clarify the impact of their deficiency on susceptibility to carcinogenesis.

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