—Brief data report—

Linkage Mapping of the Rat Poly(ADP-ribose) Glycohydrolase (*Parg*) Gene to Chromosome 16

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Species: Rat (*Rattus norvegicus*)

Locus name: Poly(ADP-ribose) glycohydrolase

Locus symbol: *Parg*

Map position: D16Rat12 - 2.9 cM - *Parg*, D16Mit2 - 4.8 cM - D16Mit5

Method of mapping: Linkage mapping using a (F344 × ACI)_{F1} × ACI (FAA) backcross panel generated with 139 backcross progeny and 155 microsatellite markers by Map Manager QT version 3.0b8 [4].

Database deposit information: Rat *Parg* cDNA (AB019366), an intron sequence of rat *Parg* (AB022043).

Molecular reagents: A primer set used to amplify the rat *Parg* intron (AB022043) was 5'-TATTACCACTTGGATGGATAC-3' and 5'-TCTGCACAGAACTCATCATG-3' (nucleotide position 367 to 387 and 448 to 467 of rat *Parg* cDNA, respectively). Primer sequences designed from the above intron sequence and used for the linkage analysis by PCR were RPG-MIS; 5'-TGTCAGTAGTGGTTATAGAC-3' and RPG-MIA; 5'-TTAAGCTTACCTCTATCTCAG-3' (nucleotide position 218 to 238 and 363 to 383 of AB022043, respectively). All microsatellite markers were purchased from Research Genetics (Huntsville, AL, USA).

Allele detection: Nucleotide changes from F344 to ACI were G to A and C to G at nucleotide positions 270 and 280 of the *Parg* intron (AB022043), respectively. The 166 bp PCR product, which was obtained with a primer set, RPG-MIS and RPG-MIA, and encompassed these two polymorphisms were subjected to single strand conformation polymorphism (SSCP) analysis [6] as shown in Fig. 1.

Previously identified homologues: Human *PARG* gene is mapped to human Chr 10q11.23-21.1 [8] and between *D10S604* and *D10S220* [2].

Discussion: Poly(ADP-ribose) glycohydrolase (*PARG*) degrades poly(ADP-ribose) molecules attached to various nuclear proteins [5] synthesized by poly(ADP-ribose) polymerase (*PARP*) [9]. Since poly(ADP-ribosyl)ation is considered to play a key role in DNA repair [3, 10] and cell-death induction [1], *PARG* could also be involved in the cellular responses against DNA damaging agents, and consequently in carcinogenesis. Therefore, the information of precise chromosomal localization of *Parg* as well as *Parp* will provide us a powerful tool for investigating the roles of *Parg* in carcinogenesis and various other diseases.

Two base-change type polymorphisms between F344

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Fig. 1. PCR-SSCP analysis for genotyping. PCR-SSCP analysis was performed as described [6] with a primer set, RPG-M1S and RPG-M1A. Each backcross rat (lanes 1–10) was genotyped according to the presence of F344 and/or ACI allele. The bands with closed arrow heads are derived from ACI allele, and those with open arrow heads from F344 allele. The rats of lanes 1, 2, 6, 7, 9 were genotyped as homozygous for ACI allele (ACI/ACI) and those of lanes 3, 4, 5, 8, 10 as heterozygous (F344/ACI).

and ACI were identified by PCR-SSCP analysis in a 575 bp intron sequence of the rat *Parg*, which intervenes the rat *Parg* cDNA between nucleotide position 417 and 418 (Fig. 1). A linkage analysis using a panel of 139 FAA backcross rats mapped the *Parg* gene to the distal region of rat Chr 16p at the same position with *D16Mit2*, giving a lod score of 41.8 (Fig. 2). Rat Chr 16 shares homology with human Chr 10q11–23 [7]. Our linkage data showed that rat *Parg* is localized in this syntenic region.

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Fig. 2. Linkage mapping of rat *Parg* to Chr 16. Genetic distances between markers are shown to the left of the genetic map. Haplotype figure from the FAA backcross is shown in the right panel. The open boxes represent the homozygous ACI allele, and the closed boxes the F344/ACI allele. The number of animals with each haplotype is given at the bottom of each column.

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