52) Genetic analysis of the spontaneously hypertensive rat (SHR) , Wistar-Kyoto rat (WKY) & their F₂ generation using DNA fingerprints T. Nabika, Y. Nara*, K. Ikeda*, M. Sawamura, J. Endo, and Y. Yamori* Dept. of Lab. Med., Dept. of Pathology*, Shimane Med. Univ., Izumo, 693, Japan

Recent genetic studies revealed that WKY showed genetic variance between different sources. In this study, we examined the DNA fingerprints of substrains of SHR to see whether they also show genetic variance. In addition, Fingerprints of F₂ rats between WKY and SHRSP were analyzed to see whether we could detect fingerprinting bands which show linkage with hypertension loci.

Eleven human VNTR and two minisatellite probes ('myo' and 'ins') are generously provided by Dr. Y. Nakamura and Dr. R. Kominami, respectively. Genomic DNA from the livers of the rats were digested with Hae III, Hin fI or Rsa I. Employed strains were 3 stroke-prone SHR (SHRSP) substrains, 4 stroke-resistant SHR (SHRSR) substrains and WKY from Izumo colony and SHRSP, SHRSR and WKY from NIH colony. The digested DNA were analyzed by Southern hybridization using ³²P-labeled probes. Prehybridization and hybridization were performed at 60°C in 6x SSC/0.5% SDS. The prehybridization buffer included 5x Denhardt solution. Hybridized membranes were then washed twice in 1x SSC/0.1% SDS at room temperature for 30-60 min and were autoradiographed for 10 to 72 hrs.

DNA fingerprints of SHRSR using 'myo' showed substantial genetic difference between the rats from NIH colony and from Izumo colony. By contrast, 4 SHRSR substrains of Izumo colony had a similar DNA fingerprinting pattern, indicating that they have a close genetic background. These results implied that the genetic difference of SHRSR from different sources causes biochemical and/or physiological differences, and that one has to be careful to use SHR and WKY of different sources in comparison studies. On the contrary, SHRSP from Izumo and NIH colonies shared similar fingerprint pattern.

DNA fingerprinting patterns between WKY and SHRSP were obtained with 10 of the 11 human VNTR probes. Among these fingerprinting bands, 52 polymorphic bands were observed in Hae III-digested panels. Hin fI- & Rsa I-digested panels were less polymorphic. To examine whether these polymorphic bands can be applied to segregation study of hypertension in F₂ generation, we studied the DNA fingerprints of two groups of F₂ rats which had either highest (HB) or lowest blood pressures (LB). The results suggested that some polymorphic bands distinguished by VNTR probes showed distorted distribution between the HB and the LB groups although they were not statistically significant. This observation imply that this strategy is useful to examine multiple loci for the segregation with hypertension quickly.