- 14) White, R. and Lalouel, J.M. 1988. Ann. Rev. Genet. 22: 259-279.
- 15) Gusella, J.F. 1986. Ann. Rev. Biochem. 55: 831-854.
- 16) Melki, J. et al. 1990. Nature 344: 767-768.
- 17) Melki, J. et al. 1990. Lancet (in press).
- 18) Brzustowicz, L.M. et al. 1990. Nature 344: 540-541.
- 19) Gilliam, T.C. et al. 1990. Nature 345: 823-825.
- 20) Kaplan, J. et al. 1990. Hum. Genet. 85 (in press).
- Frézal, J. and Klinger, H.P., eds. 1987. Ninth International Workshop on Human Gene Mapping. Cytogenet. Cell Genet. 46: 1-762.
- 22) Frézal, J. et al. 1989. Genatlas. INSERM/John Libbey, eds. London/Paris.
- 23) Kidd, K.K. et al. 1989. Tenth International Workshop on Human Gene Mapping. Cytogenet. Cell Genet. 51: 1-1147.
- 24) Dean et al. 1990. Nucleic Acids Res. 18: 345-350.
- 25) Carroll, M.C. et al. 1987. Proc. Natl. Acad. Sci. USA 84: 8535-8539.
- 26) Dunham, I. et al. 1987. Proc. Natl. Acad. Sci. USA 84: 7237-7241.
- 27) Carroll, M.C. et al. 1988. J. Exp. Med. 167: 1271-1280.
- 28) Jones, M.E. 1980. Ann. Rev. Biochem. 49: 253-279.
- 29) Enver, T. et al. 1990. Nature 344: 309-313.
- 30) Korenberg, J.R. and Rykowski, M.C. 1988. Cell 53: 391-400.
- 31) Bernardi, G. 1989. Ann. Rev. Genet. 23: 637-661.
- 32) Bird, A.D. 1986. Nature 321: 209-213.
- 33) Weber, J.L. and May, P.E. 1989. Am. J. Hum. Genet. 44: 388-396.
- 34) Antonarakis, S.E. 1988. Adv. Hum. Genet. 17: 27-59.
- 35) Abadie, V. et al. 1989. Genomics 5: 936-939.
- 36) John, S.W.M. et al. 1990. Am. J. Hum. Genet. 46: 970-974.
- 37) Caillaud, C. 1990. MD Thesis, Paris.
- 38) Kerem, B.S. et al. 1989. Science 245: 1073-1080.
- 39) Efstratiadis, A. et al. 1980. Cell 21: 653-668.
- 40) Yen, P.H. et al. 1990. Cell 61: 603-610.

PL-II. THE HUMAN GENOME PROJECT IN JAPAN: CURRENT STATUS AND PROSPECTS

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The human genome consists of 3 billion basepairs (bp) of DNA which are distributed on 24 different chromosomes. Mapping of the estimated 50,000–100,000 genes and sequencing of the entire human genome has become a major interest in medical genetics and human molecular biology. To achieve this goal, a complete understanding of the genetic blue print of human beings, human genome projects have been established in several different countries and the international cooperation is under way. At this congress, I have presented a brief history of the development of the human genome program in Japan and a summary of the current status of the organization and administration of the Monbusho (the Ministry of Education, Science and Culture: MESC) component of the genome program. The MESC's current human genome program consists of five selected topics: 1. human genome mapping, 2. human genome function, 3. DNA technology, 4. bioinformatics, and 5. nonhuman genomes. I have commented on the relationship of this pro-

gram to other governmental genome programs such as Riken project, Yoken project, Genosphere project, and the Human Frontier Science Program. I also discussed some prospects for the future directions of these programs and the applications of genome information.

As a human genome project in my laboratory at Keio University, I have presented the Keio strategy for the physical mapping and fine structure analysis of the smallest human chromosomes, 21 and 22, which contain DNA of approx. 50 Mbp. Although our work is only at the beginning stage, the Keio strategy has proven to be feasible. I have presented a number of new techniques and clone libraries which will be used for isolation of disease-related genes.

Related publications

- Sakai, K., Hirai, M., Minoshima, S., Kudoh, J., Fukuyama, R. and Shimizu, N. 1989. Isolation of cDNAs encoding a substrate for protein kinase C: Nucleotide sequence and chromosomal mapping of the gene for a human 80K protein. *Genomics* 5: 309–315.
- Minoshima, S., Kawasaki, K., Fukuyama, R., Maekawa, M., Kudoh, J. and Shimizu, N. 1990. Isolation of giant DNA fragments from flow-sorted human chromosomes. Cytometry 11: 539-546.
- Shimizu, N. and Minoshima, S. Gene mapping and fine structure analysis of the human genome using flow-sorted chromosomes. *In* Advanced Techniques in Chromosome Research, Adolph, K.W. (ed.), Mercel Dekker Inc., in press.
- Shimizu, N., Minoshima, S., Kudoh, J., Kawasaki, K. and Fukuyama, R. Variation in the organization of the rRNA gene clusters among flow-sorted human acrocentric chromosomes, Cold Spring Harbor Conference of Genome Mapping and Sequencing, New York, Abst. p. 2 (May 1990).
- Shimizu, N., Minoshima, S., Kudoh, J., Fukuyama, R., Sakai, K. and Kawasaki, K. Molecular strategies for physical mapping and fine structure analysis of flow-sorted human chromosome 21, Proceedings of the First International Conference on Electrophoresis, Supercomputing and the Human Genome. Cantor, C. and Lim, H. (eds.), World Scientific, in press.
- Shimizu, N. The human genome project in Japan: Current status and future direction, Proceedings of CIOMS Conference, in press.
- Minoshima, S. and Shimizu, N. Flow-sorting of human chromosome 22 derivatives for physical mapping and fine structure analysis, Proceedings of the Intl. Symp. on Flow Cytometry and Image Analysis for Clinical Applications, Elsevier Science Publ., in press.