

Consanguinity, Genomic

- Balazs, I., Baird, M., Clyne, M. and Meade, E. (1989). Human population genetic studies of five hypervariable DNA loci. *American Journal of Human Genetics* **44**: 182-190.
- Beier, D. R. (1993). Single-strand conformation polymorphism (SSCP) analysis as a tool for genetic mapping. *Mammalian Genome* **4**: 627-631.
- Bellamy, R. J., Inglehearn, C. F., Jalili, I. K., Jefferys, A. J. and Bhattacharya, S. S. (1991). Increased band sharing in DNA fingerprints of an inbred human population. *Human Genetics* **87**: 341-347.
- Ben Hamida, C., Doerflinger, N., Belal, S., Linder, C., Reutenauer, L., Dib, C., Gyapay, G., Vignal, A., *et al.* (1993). Localization of Friedreich ataxia phenotype with selective vitamin E deficiency to chromosome 8q by homozygosity mapping. *Nature Genetics* **5**: 195-200.
- Bowcock, A. M., Ruiz-Linares, A., Tomfohrde, J., Minch, E., Kidd, J. R. and Cavalli-Sforza, L. L. (1994). High resolution of human evolutionary trees with polymorphic micro-satellites. *Nature* **368**: 455-457.
- Broman, K. W. and Weber, J. L. (1999). Long homozygous chromosomal segments in reference families from the Centre d'Étude du Polymorphisme Humain. *American Journal of Human Genetics* **65**: 1493-1500.
- Chakraborty, R. and Daiger, S. P. (1991). Polymorphisms at VNTR loci suggest homogeneity of the white population of Utah. *Human Biology* **63**: 571-587.
- Chakraborty, R. and Jin, L. (1993). Determination of relatedness between individuals using DNA fingerprinting. *Human Biology* **65**: 875-895.
- Chakraborty, R., Smouse, P. E. and Neel, J. V. (1988). Population amalgamation and genetic variation: Observations on artificially agglomerated tribal populations of Central and South America. *American Journal of Human Genetics* **43**: 709-725.
- Chakraborty, R. and Zhong, Y. (1994). Statistical power of an exact test of Hardy-Wemberg proportions of genotype data at a multiallelic locus. *Human Heredity* **44**: 1-9.
- Chapman, N. H. and Wijsman, E. M. (1998). Genome screens using linkage disequilibrium tests: optimal marker characteristics and feasibility. *American Journal of Human Genetics* **63**: 1872-1885.
- Charlesworth, D. and Wright, S. I. (2001). Breeding systems and genome evolution. *Current Opinion in Genetics and Development*. **11**: 685-690.
- Deka, R., Chakraborty, R. and Ferrell, R. E. (1991). A population genetic study of six VNTR loci in three ethnically defined populations. *Genomics* **11**: 83-92.

- Deng, H., Chen, W. and Recker, R. R. (2000). QTL fine mapping by measuring and testing for Hardy-Weinberg and linkage disequilibrium at a series of linked marker loci in extreme samples of populations. *American Journal of Human Genetics* **66**: 1027-1045.
- Durham, L. K. and Feingold, E. (1997). Genome scanning for segments shared identical by descent among distant relatives in isolated populations. *American Journal of Human Genetics* **61**: 830-842.
- Eaves, I. A., Merriman, T. R., Barber, R. A., Nutland, S., Tuomilehto-Wolf, E., Tuomilehto, J., Cucca, F. and Todd, J. A. (2000). The genetically isolated populations of Finland and Sardinia may not be a panacea for linkage disequilibrium mapping of common disease genes. *Nature Genetics* **25**: 320-323.
- Edwards, A., Civitello, A., Hammond, H. A. and Caskey, C. T. (1991). DNA typing and genetic mapping with trimetric and tetrameric tandem repeats. *American Journal of Human Genetics* **49**: 746-756.
- Edwards, A., Hammond, H. A., Jin, L., Caskey, C. T. and Chakraborty, R. (1992). Genetic variation at five trimetric and tetrameric tandem repeat loci in four human population groups. *Genetics* **12**: 241-253.
- Edwards, J. H. (1988). Evidence of incest based on homozygosity. The use of multiple hypervariable probes for the probable detection or exclusion of incest. *Annals of Human Genetics* **52**: 351-353.
- Farrall, M. (1994). Homozygosity mapping: familiarity breeds debility. *Nature Genetics* **5**: 107-108.
- Génin, E. and Clerget-Darpoux, F. (1996). Association studies in consanguineous populations. *American Journal of Human Genetics* **91**: 861-866.
- Génin, E. and Clerget-Darpoux, F. (1996). Consanguinity and sib-pair method: an approach using identity by descent between and within individuals. *Annals of Human Genetics* **59**: 1149-1162.
- Guo, S. W. (1997). Computation of multilocus prior probability of autozygosity for complex inbred pedigrees. *Genetic Epidemiology* **14**: 1-15.
- Houwen, R. H. J. (1994). Genome screening by searching for shared fragments: mapping a gene for benign recurrent intrahepatic cholestasis. *Nature Genetics* **8**: 380-386.
- Katshya, T., Higaki, J., Miki, T., Nakera, J., Ikegami, H. and Morishita, R. (1991). Substrain comparison of genetically hypersensitive rats using DNA fingerprinting, and genetic analysis of blood pressure in the inbred rats. *Tohoku Journal of Experimental Medicine* **165**: 253-260.
- Kong, A. (1991). Effective methods for computing linkage likelihoods of recessive diseases in inbred pedigrees. *Genetic Epidemiology* **8**: 81-104.

- Krontiris, T. G. (1995). Minisatellites and human disease. *Science* **269**: 1682-1683.
- Kruglyak, L., Daly, M. J. and Lander, E. S. (1995). Rapid multipoint linkage analysis of recessive traits in nuclear families, including homozygosity mapping. *American Journal of Human Genetics* **56**: 519-527.
- Lander, E. S. and Botstein, D. (1987). Homozygosity mapping: a way to map human recessive traits with the DNA of inbred children. *Science* **236**: 1567-1570.
- Lander, E. S. and Schork, N. J. (1994). Genetic dissection of complex traits. *Science* **265**: 2037-2048.
- Leutenegger, A. L., Prum, B., Genin, E., Verny, C., Lemaître, A., Clerget-Darpoux, F. and Thompson, E. A. (2003). Estimation of the inbreeding coefficient through use of genomic data. *American Journal of Human Genetics* **73**: 516-523.
- Lynch, M. (1990). The similarity index and DNA fingerprinting. *Molecular Biological Evaluation* **7**: 478-484.
- Martin, E. R., Lai, E. H., Gilbert, J. R., Rogala, A. R., Afshari, A. J. and Riley, J. (2000). SNPing away at complex diseases: analysis of single-nucleotide polymorphisms around APOE in Alzheimer disease. *American Journal of Human Genetics* **67**: 383-394.
- Morell, R., Liang, Y., Asher, J. H., Weber, J. L., Hinnant, J. T., Winata, S., Arhya, I. N. and Friedman, T. B. (1995). Analysis of short tandem repeat (STR) allele frequency distributions in a Balinese population. *Human Molecular Genetics* **4**: 85-91.
- Mueller, R. F. and Bishop, D. T. (1993). Autozygosity mapping, complex consanguinity, and autosomal recessive disorders. *Journal of Medical Genetics* **30**: 798-799.
- Najmabadi, H., Neishabury, M., Sahebjam, F., Kahrizi, K., Shafaghati, Y., Nikzat, N., Jalalyand, M., Aminy, F., *et al.* (2003). The Iranian Human Mutation Gene Bank: a data and sample resource for worldwide collaborative genetics research. *Human Mutation* **21**: 146-150.
- Neel, J. V., Satoh, C., Smouse, P., Asakwa, J., Takahashi, N., Goriki, K., Fujita, M., Kageoka, T., *et al.* (1988). Protein variants in Hiroshima and Nagasaki: tales of two cities. *American Journal of Human Genetics* **43**: 870-893.
- Nielsen, D. M., Ehm, M. G. and Wier, B. S. (1999). Detecting marker-disease association by testing for Hardy-Weinberg disequilibrium at a marker locus. *American Journal of Human Genetics* **63**: 1531-1540.
- Overall, A. D., Ahmad, M., Thomas, M. G. and Nichols, R. A. (2003). An analysis of consanguinity and social structure within the UK Asian population using microsatellite data. *Annals of Human Genetics* **67**: 525-537.

- Peters, C., Schneider, V., Epplen, J. T. and Pöche, H. (1991). Individual-specific DNA fingerprinting in man using the Oligonucleotide probe (GTG) 5/ (CAC)5. *European Journal of Clinical Chemistry and Clinical Biochemistry* **29**: 321-325.
- Peterson, A. C. (1995). The distribution of linkage disequilibrium over anonymous genome regions. *Human Molecular Genetics* **4**: 887-894.
- Pöche, H., Petters, C., Wrobel, G., Schneider, V. and Epplen, J. T. (1991). Determining consanguinity by oligonucleotide fingerprinting with (GTG)5/(CAC)5. *Electrophoresis* **12**: 397-402.
- Pollak, M. R., Chou, Y.-H. W., Cerda, J. J., Steinmann, B., La Du, B. N., Seidman, J. G. and Seidman, C. E. (1993). Homozygosity mapping of the gene for alkalptonuria to chromosome 3q2. *Nature Genetics* **5**: 201-204.
- Reiter, R. S., Williams, J. G. K., Feldman, K. A., Rafalski, J. A., Tingey, S. V. and Scolnik, P. A. (1992). Global and local genome mapping in Arabidopsis-Thaliana by using recombinant inbred lines and random amplified polymorphic DNAs. *Proceedings of the National Academic Science (USA)* **89**: 1477-1481.
- Risch, N. and Zhang, H. (1995). Extreme discordant sib pairs for mapping quantitative trait loci in humans. *Science* **268**: 1584-1589.
- Samaha, H., Rahal, E. A., Abou-Jaoude, M., Younes, M., Dacchache, J. and Hakime, N. (2003). HLA class II allele frequencies in the Lebanese population. *Molecular Immunology* **39**: 1079-1081.
- Stewart, C. A., Horton, R., Allcock, R. J., Ashurst, J. L., Atrazhev, A. M., Coggill, P., Dunham, I., Forbes, S., *et al.* (2004). Complete MHC haplotype sequencing for common disease gene mapping. *Genome Research* **14**: 1176-1187.
- Wang, W., Sullivan, S. G., Ahmed, S., Chandler, D., Zhivotovsky, L. A. and Bittles, A. H. (2000). A genome-based study of consanguinity in three co-resident endogamous Pakistan communities. *Annals of Human Genetics* **64**: 41-49.
- Wang, W., Wise, C., Baric, T., Black, M. L. and Bittles, A. H. (2003). The origins and genetic structure of three co-resident Chinese Muslim populations: the Salar, Bo'an and Dongxiang. *Human Genetics* **113**: 244-252.
- Wells, R. A., Wonke, B. and Thein, S. L. (1988). Prediction of consanguinity using human DNA finger prints. *Journal of Medical Genetics* **25**: 660-662.
- Wiehe, T., Mountain, J., Parham, P. and Slatkin, M. (2000). Distinguishing recombination and intragenic gene conversion by linkage disequilibrium patterns. *Genetic Research* **75**: 61-73.