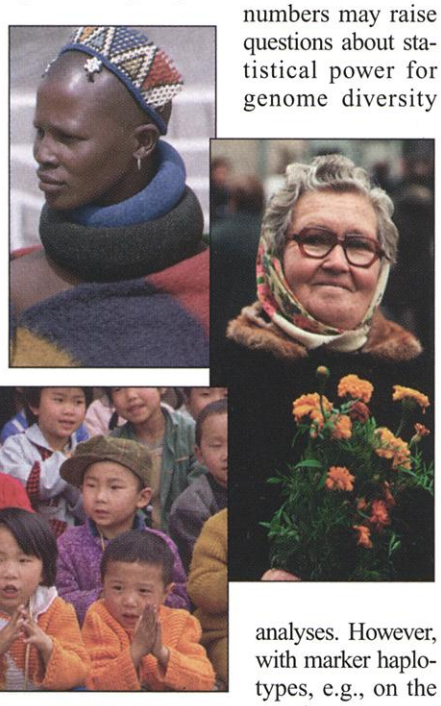
A Human Genome Diversity Cell Line Panel

A RESOURCE OF 1064 CULTURED lymphoblastoid cell lines (LCLs) (*1*) from individuals in different world populations and corresponding milligram quantities of DNA is deposited at the Foundation Jean Dausset (CEPH) (*2*) in Paris. LCLs were collected from various laboratories by the Human Genome Diversity Project (HGDP) (*3*) and CEPH to provide unlimited supplies of DNA for studies of sequence diversity and history of modern human populations. Information for each LCL is limited to sex, population, and geographic origin of the individual. Each LCL is registered in a project-specific database and provided with a CEPH-generated, numeric identifier that labels the LCL, its corresponding DNA, and subject information. Every product derived from an LCL is labeled with a unique alphanumeric bar-code. LCLs were tested for *mycoplasma* infestation by a polymerase chain reaction–based test (*4*). All lines showing infestation were discarded. LCLs were expanded for storage at −196°C and for production of milligram quantities of DNA.

The panel contains LCLs from populations living on all continents. Details of the LCL collections in the resource and a world map showing the 60 positions of the 51 different population samples that contributed blood specimens for production of the cell lines are given in the supplementary material (*5*). The LCLs from each of 47 population samples represent unrelated individuals. In each of four other groups, several relative pairs were sampled, permitting direct inference of their haplotypes (*5*). Notably absent are LCLs from India, rich in genetic diversity (*6*), and Australia, whose founders arrived quite early in the peopling of the world (*7*). There is much to learn from India and Australia, and every effort should be made for exchange and cooperation in genome diversity studies. Most samples intentionally contain an excess of males (*5*). Males are haploid for the X and Y chromosomes, and both males and females can be considered as haploid for mitochondria. Marker types for these genomes are equivalent to genotypes. LCLs from population samples enriched for males enhance the collection of hundreds of Y-linked single nucleotide polymorphisms (SNPs) (*8*). Nonrecombinant Y-linked polymorphisms track male population history; mitochondrial markers (transmitted only by mothers to offspring of both sexes) track female population history. The maximum number of LCLs from a population sample is 51. Twenty-five to 49 LCLs are available from each of 21 population samples. Fourteen Chinese minority groups are represented by only 9 to 10 LCLs each. These numbers may raise questions about statistical power for genome diversity analyses. However, with marker haplotypes, e.g., on the Y chromosome, specific lineages may be differentiated and their origins compared among samples of the resource (*9*). Furthermore, confidence in statistics based on microsatellite loci can be acceptable if sufficiently large numbers of loci are analyzed (*10*).



LCLs will help researchers to study sequence diversity and the history of modern human populations.

One of us (H.T.G.) confirmed that the blood specimens that served as sources of the LCLs were freely donated under conditions of informed consent and confidentiality by reviewing consent forms, institutional review board approvals, or detailed reports from those who organized collections. Only LCLs produced from samples for which he found sufficient evidence of informed consent are included in the resource.

DNA from the LCLs will be distributed to investigators who agree to type all the DNAs with their genetic markers and contribute the results to a central database. LCLs will not be distributed. The DNAs have already been typed with 404 microsatellite markers, mapped throughout the nuclear genome (*11*), including 20 from the X chromosome and seven from the Y. Sixteen LCLs differ for gender indicated on records and that determined by molecular typing (*5*). It is likely that the latter is more reliable. The resource should be useful for SNP discovery, for analyzing SNP and haplotype variability and structure, and for determining global sequence variation at various loci. DNA types at the same loci will accumulate on individuals from each of the populations, essential in light of the extensive genome diversity within populations that accounts for some 85% of the genetic variation around the world (*12*). Finally, cooperative research will be facilitated among researchers who have hitherto been forced into a competitive mode of interaction.

Howard M. Cann,* CEPH; **Claudia de Toma**, CEPH; **Lucien Cazes**, CEPH; **Marie-Fernande Legrand**, CEPH; **Valerie Morel**, CEPH; **Laurence Piouffre**, CEPH; **Julia Bodmer**, Cancer Research UK; **Walter F. Bodmer**, Cancer Research UK; **Batsheva Bonne-Tamir**, Sackler Faculty of Medicine; **Anne Cambon-Thomsen**, Inserm U 558; **Zhu Chen**, Human Genome Center at Shanghai; **Jiayou Chu**, Chinese Academy of Medical Sciences; **Carlo Carcassi**, "R. Binaghi" Hospital; **Licinio Contu**, "R. Binaghi" Hospital; **Ruofu Du**, Chinese Academy of Sciences; **Laurent Excoffier**, University of Geneva; **G. B. Ferrara**, National Cancer Research Institute; **Jonathan S. Friedlaender**, Temple University; **Helena Groot**, Universidad de los Andes; **David Gurwitz**, Sackler Faculty of Medicine; **Trefor Jenkins**, South African Institute of Medical Research; **Rene J. Herrera**, Florida International University; **Xiaoyi Huang**, Harbin Medical University; **Judith Kidd**, Yale University School of Medicine; **Kenneth K. Kidd**, Yale University School of Medicine; **Andre Langaney**, University of Geneva; **Alice A. Lin**, Stanford University School of Medicine; **S. Qasim Mehdi**, Biomedical and Genetic Engineering Laboratories; **Peter Parham**, Stanford University School of Medicine; **Alberto Piazza**, University of Turin; **Maria Pia Pistillo**, National Cancer Research Institute; **Yaping Qian**, Chinese Academy of Medical Sciences; **Qunfang Shu**, Chinese Academy of Sciences; **Jiujin Xu**, Chinese Academy of Sciences; **S.**

Zhu, Chinese Academy of Sciences; **James L. Weber**, Marshfield Medical Research Foundation; **Henry T. Greely**, Stanford University Law School; **Marcus W. Feldman**, Stanford University; **Gilles Thomas**, CEPH; **Jean Dausset**, CEPH; **L. Luca Cavalli-Sforza**, Stanford University School of Medicine.

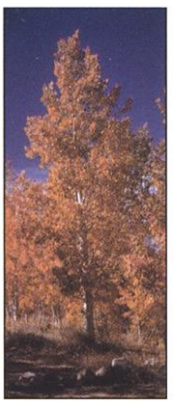
*To whom correspondence should be addressed. Foundation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France. E-mail: howard@cephb.fr

References and Notes

1. B. J. Bolton, N. K. Spurr, in *Culture of Immortalized Cells*, R. J. Freshney, M. G. Freshney, Eds. (Wiley-Liss, New York, 1996), pp. 283–299.
2. J. Dausset *et al.*, *Genomics* **6**, 575 (1990).
3. L. L. Cavalli-Sforza, A. C. Wilson, C. R. Cantor, R. M. Cook-Deegan, M.-C. King, *Genomics* **11**, 490 (1991).
4. G. Rawadi, O. Dussurget, *PCR Methods Applic.* **4**,199 (1995).
5. Supplementary material is available on *Science* Online at www.sciencemag.org/cgi/content/full/296/5566/261/DC1.
6. M. Bamshad *et al.*, *Genome Res.* **6**, 994 (2001).
7. R. M. Jones, in *The Human Revolution: Behavioural and Biological Perspectives on the Origins of Modern Humans*, P. Mellars, C. Stringer, Eds. (Princeton Univ. Press, Princeton, NJ, 1989), pp. 743–782.
8. P. A. Underhill *et al.*, *Nature Genet.* **26**, 358 (2000).
9. O. Semino *et al.*, *Science* **290**, 1155 (2000).
10. D. Goldstein *et al.*, *Mol. Biol. Evol.* **13**, 1213 (1996).
11. K. W. Broman, J. C. Murray, V. C. Sheffield, R. L. White, J. L. Weber, *Am. J. Hum. Genet.* **63**, 861 (1998).
12. G. Barbujani, A. Magagni, E, Minch, L. L. Cavalli-Sforza, *Proc. Natl. Acad. Sci. U.S.A.* **94**, 4516 (1997).
13. We thank the individuals who contributed blood specimens for LCL production; the various researchers, physicians, and anthropologists who participated in specimen collection; and the laboratories that produced and contributed LCLs. Construction of the panel was supported in part by the Ellison Medical Foundation.

Trees, Homologs, and Poisons

I AM QUOTED OUT OF CONTEXT IN THE recent news article on forest biotechnology (News Focus, 1 Mar., p. 1627) by Charles Mann and Mark Plummer. I indicated that "a tree is essentially a mountain of poisons" to give some context to considerations of the possible ecological effects of new, taxon-specific transgenes that increase pest resistance—not to indicate that dicotyledonous trees such as poplars (genus Populus) are not extensively genomically homologous to well-studied annual dicot plants like *Arabidopsis*. In fact, I recently submitted a proposal for which a primary goal is a detailed comparative genomic analysis of the full *Arabidopsis* and the soon-to-be-determined poplar genome sequences. Woody species such as poplar will certainly have embellished and at least somewhat distinctive genomic content compared with *Arabidopsis* as a result of their different adaptive and phyletic histories, but making use of the structural and functional homologies between annual and woody plants—whether for basic tree physiology or biotechnology—can easily keep generations of tree-loving scientists productively occupied.



STEVEN H. STRAUSS

Department of Forest Science, Oregon State University, Corvallis, OR 97331–5752, USA. E-mail: Steve.Strauss@orst.edu

Stocking the Stacks

UNIVERSITY LIBRARIES' BATTLE TO KEEP scientific journals on their shelves despite soaring subscription costs and unfavorable exchange rates is the subject of Dennis Normile's recent article ("Libraries seek ways to keep costs down," News of the Week, 18 Jan., p. 429). This scenario is common in developing countries, where university libraries are not able to maintain

CREDIT: SHERRY BALLARD/CALIFORNIA ACADEMY OF SCIENCES