



BANBURY CENTER HIGHLIGHTS

THE ARABIDOPSIS GENOME

March 20-23, 1994

Organized by:

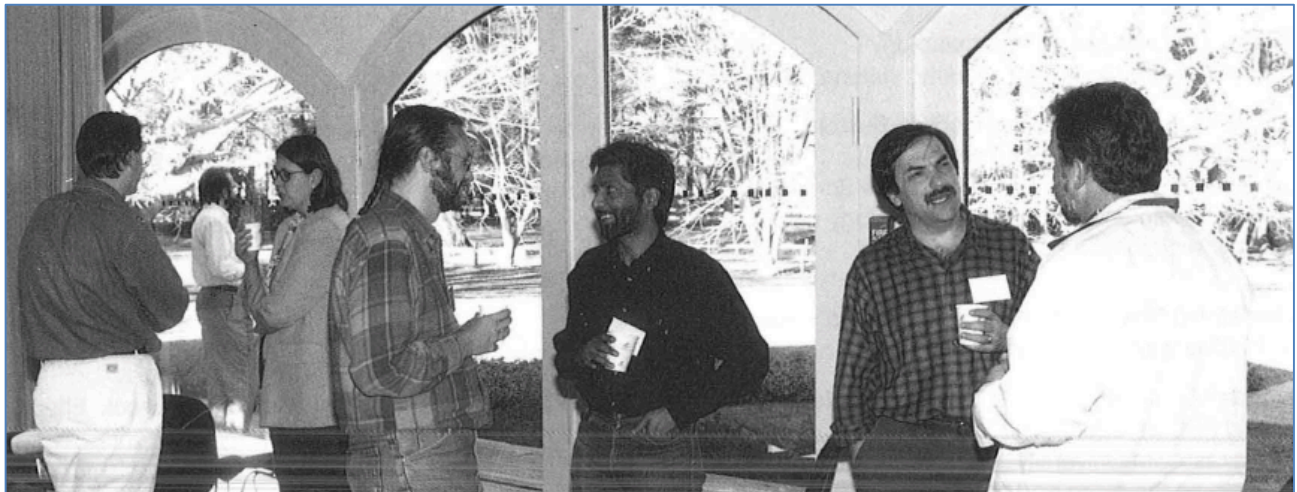
Michael Bevan, John Innes Center, Norwich, United Kingdom
Joseph R. Ecker, University of Pennsylvania, Philadelphia, Pennsylvania
Robert Martienssen, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York

The Banbury Center has established a tradition for meetings dealing with both scientific and policy aspects of genome projects. In this case, a group of scientists working on the Arabidopsis genome came to Banbury to review the scientific progress being made and to make plans for future efforts. The cross-disciplinary nature of genomic research was evident in the first session that included contributions from scientists working on yeast, nematode, fruit fly, and mouse genomes. Following this workshop, the National Science Foundation convened meetings in order to allocate resources (1995) and to coordinate international efforts (1996).

In 1994 there had been great progress in cloning, sequencing, and analyzing the genomes of a variety of organisms. Those efforts were beginning to yield new knowledge of genome evolution and organization, and to provide the basic data for understanding the genetic basis of the ways in which organisms function.

The Arabidopsis Genome meeting was convened at the Banbury Center to review the current status of the multinational *Arabidopsis* genome project; to make a realistic evaluation of what is required for complete sequencing of the 100 Mb *Arabidopsis* genome; and to examine what could be done to further develop and promote a national initiative towards achieving this goal. Participants in the meeting included scientists working on the genome for *Arabidopsis* and other organisms, and representatives from the relevant federal agencies.

This meeting is referenced in: Theologis, A. *Goodbye to 'one by one' genetics*. *Genome Biology* 2:2004.1-2004.9, 2001



E. Richards, R. Schmidt, U. Grossniklaus, V. Sundaresan, P. Scolnik, K. Feldmann



THE ARABIDOPSIS GENOME: Program

Session 1: Large-scale Genome Projects

Chair: Jan A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory, New York

Joseph R. Ecker, University of Pennsylvania, Philadelphia, Pennsylvania
Introductory remarks.

Steven G. Oliver, UMIST, Manchester, United Kingdom
Yeast as a subject and a tool for genome analysis.

Richard Wilson, Washington University School of Medicine, St. Louis, Missouri
*Sequencing *C. elegans*.*

Michael Palazzolo, Human Genome Center, Berkeley, California
Drosophila human genome project.

William Dietrich, Whitehead Institute Genome Center, Cambridge, Massachusetts
Construction of a dense genetic linkage map of the mouse.

Lee Rowen, University of Washington, Seattle, Washington
Redundancy is our friend: Large scale sequencing of the human and mouse T cell receptor beta loci.

Session II: Physical Mapping and Markers

Chair: Michael Bevan, John Innes Center, Norwich, United Kingdom

Elliot Meyerowitz, California Institute of technology, Pasadena, California
The Arabidopsis genome (structure, size, contents).

Eric Richards, Washington, University, St. Louis, Missouri
Molecular chromosome some in Arabidopsis

Pablo A. Scolnik, E. du Pont de Nemours & Co., Wilmington, Delaware
Mapping and sequencing the Arabidopsis genome: New high throughput markers for genome and mutation analysis.

Marc Zabeau, Keygene n.v., Wageningen, The Netherlands
Progress in physical mapping of the Arabidopsis genome using AFLP markers.

Frederick M. Ausubel, Massachusetts General Hospital, Boston, Massachusetts
Use of RFLP/genomic subtraction to identify large numbers of CAPS (cleaved amplified polymorphic sequences), co-dominant ecotype specific PCR-based markers, for Arabidopsis.

Joseph R. Ecker, University of Pennsylvania, Philadelphia, Pennsylvania
Progress toward a complete map of the Arabidopsis genome.

Renate Schmidt, John Innes Centre, Norwich, United Kingdom
Strategies for completion of the physical maps for chromosomes 4 and 5.

Howard M. Goodman, Massachusetts General Hospital, Boston, Massachusetts
Progress on the physical map and sequence of chromosome II.

Session III: Gene Identification

Chair: Robert Martienssen, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York

Chris R. Somerville, Carnegie Institution of Washington, Stanford, California
MSU Arabidopsis EST project.



Michael Caboche, INRA Versailles, CEDEX, France
Present and future of Arabidopsis genome projects in France.

Claude Gigot, IBMP-CNRS, Strasbourg Cedex, France
Expressed sequence tags obtained by partial sequencing of cDNAs from A. thaliana.

Ronald W. Davis, Stanford University School of Medicine, Stanford, California
A simple genetic map and a proposal of complete cDNA sequencing for the total genome for Arabidopsis thaliana.

John Ryals, Ciba Biotechnology, Research Triangle Park, North Carolina
Acquired resistance in Arabidopsis - A genetic approach - the limitations.

Kenneth A. Feldmann, University of Arizona, Tucson, Arizona
Utility of T-DNA generated populations of Arabidopsis for gene cloning and reverse genetics.

Venkatesan Sundaresan, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York
Exon trapping with transposons.

Session IV: Sequencing and Informatics

Chair: Howard M. Goodman, Massachusetts General Hospital, Boston, Massachusetts

Michael Bevan, John Innes Centre, Norwich, United Kingdom
Arabidopsis genome sequencing the ESSA project.

W. Richard McCombie, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York
Strategies for automated sequence analysis of the genomes of model organisms.

David Searls, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania
Computational gene prediction - Comparative studies in vertebrates, invertebrates, and plants.

Chris Fields, The Institute for Genome Research, Gaithersburg, Maryland
Managing and integrating information from high throughput genome projects.

Thomas G. Marr, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York
The Arabidopsis database

Session V: Policy

Chair: Joseph R. Ecker, University of Pennsylvania, Philadelphia

Remarks by: Joseph R. Ecker, University of Pennsylvania, Philadelphia, Pennsylvania
R. James Cook, USDA-RNI-CGP, Washington, D.C.
Machi W. Dilworth, National Science Foundation, Arlington, Virginia



THE ARABIDOPSIS GENOME: Participants

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