

Instituto Juan March
de Estudios e Investigaciones

62

CENTRO DE REUNIONES
INTERNACIONALES SOBRE BIOLOGÍA

1996
Annual Report

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Instituto Juan March
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Depósito legal: M. 127/1997

Impresión: Ediciones Peninsular. Tomelloso, 27. 28026 Madrid.



Headquarters of the Fundación Juan March
(Home of the Centre for International Meetings on Biology)

Instituto Juan March (Madrid)

Small, focused meetings of this kind allow the progress in a limited area of science to be critically evaluated. In the transcription field this is particularly valuable because the multiplicity of related proteins, the many target genes, and the complex regulation of activity can only be unraveled by integrating the efforts of many laboratories. Other fields would benefit from such focused meetings from which reports such as this can convey progress to the rest of the community.

**Baeuerle, P.A. and Baltimore, D. (1996).
NF- κ B: Ten Years After. (Meeting Review).
Cell 87, 13-20.**

INSTITUTO JUAN MARCH DE ESTUDIOS E INVESTIGACIONES
CENTRE FOR INTERNATIONAL MEETINGS ON BIOLOGY

1996 ANNUAL REPORT

CONTENTS

	<u>PAGE</u>
Foreword	9
The Centre for International Meetings on Biology	11
1996 Meetings Schedule	13
Transcriptional Regulation at a Distance	17
From Transcript to Protein: mRNA Processing, Transport and Translation	29
Mechanisms of Expression and Function of MHC Class II Molecules	39
Enzymology of DNA-Strand Transfer Mechanisms	49
Vascular Endothelium and Regulation of Leukocyte Traffic	59
Cytokines in Infectious Diseases	69
Molecular Biology of Skin and Skin Diseases	79
Programmed Cell Death in the Developing Nervous System	89
NF- κ B/I κ B Proteins. Their Role in Cell Growth, Differentiation and Development	99

	<u>PAGE</u>
Chromosome Behaviour: the Structure and Function of Telomeres and Centromeres	109
RNA Viral Quasispecies	121
Absciscic Acid Signal Transduction in Plants	131
Oxygen Regulation of Ion Channels and Gene Expression	141
XV Juan March Lectures	151
Sessions Open to the Public	155
Reviews in Scientific Journals	159
1997 Meetings Schedule	163
Scientific Council	167
Index of Personal Names	171

FOREWORD

This publication covers the activities of the Centre for International Meetings on Biology during the year 1996. All of them were announced in brochures, posters, advertisements in scientific journals and articles in other periodicals.

The core of the Centre's work during 1996 was the organization of 13 workshops on different biological topics. An introduction to each of these meetings is presented here, followed by a list of invited speakers and participants selected from among the applications received. In total, 248 speakers were invited to these workshops, and 380 participants were chosen from among the 537 applications received.

A booklet was published on each of these meetings, which included the abstracts of the contributions presented by the participating scientists. About 400 copies of each booklet were distributed to research groups and laboratories working on problems relating to the subject of each meeting.

A new series of the Juan March Lectures on Biology, a tradition in the Centre since 1982, was organized in 1996. Information on these lectures is also included in the following pages. Another two sessions open to the general public were held to coincide with meetings mentioned above.

A short report is given of the reviews published during 1996 in scientific journals, regarding workshops organized by the Centre.

The schedule of meetings to take place in 1997 is also offered in this book.

Instituto Juan March de Estudios e Investigaciones

THE CENTRE FOR INTERNATIONAL MEETINGS ON BIOLOGY

The Centre for International Meetings on Biology endeavours actively and systematically to promote close cooperation and interaction among Spanish and foreign scientists working in the field of Biology. This scientific field is understood in the widest sense, and emphasis is given to advanced lines of research.

The Centre's activities stem from the Plan for International Meetings on Biology, initiated by the **Fundación Juan March** in January 1989 and ending in December 1991. A wide range of meetings and scientific activities were organized under this Plan. The Fundación Juan March, in addition to its well-known support of the fine arts and culture in general, has devoted particular attention to the biological sciences since its creation in 1955 by the Spanish financier Juan March Ordinas.

The Centre for International Meetings on Biology was established on January 1992 within the **Instituto Juan March de Estudios e Investigaciones**, a private foundation created in October 1986 and recognized by the Spanish Ministry of Education and Culture. This foundation complements the work of the Fundación Juan March, as an entity specializing in scientific activities. The Board of Trustees of the Instituto comprises: Juan March (Chairman), Carlos March (Deputy Chairman), Leonor March, Alfredo Lafita, Antonio Rodríguez Robles, Pablo Vallbona, Enrique Piñel and Jaime Prohens (Secretary). José Luis Yuste is the Managing Director of the Institute.

The Centre for International Meetings on Biology is located at Calle Castelló 77, Madrid. The Director of the Centre is Andrés González.

1996 Meetings Schedule

INSTITUTO JUAN MARCH

CENTRE FOR INTERNATIONAL MEETINGS ON BIOLOGY

1996 MEETINGS SCHEDULE

Date	Meeting Subject	Organizers
15-17 January	Transcriptional Regulation at Distance	W. Schaffner. Universität Zürich. V. de Lorenzo. Centro de Investigaciones Biológicas. Madrid. J. Pérez-Martin. Centro de Investigaciones Biológicas. Madrid.
11-13 March	From Transcript to Protein: mRNA Processing, Transport and Translation	I. Mattaj. European Molecular Biology Laboratory. Heidelberg. J. Ortin. Centro Nacional de Biotecnología. Madrid. J. Valcárcel. University of Massachusetts Medical Center. Worcester.
25-27 March	Mechanisms of Expression and Function of MHC Class II Molecules	B. Mach. University of Geneva. A. Celada. Facultad de Biología. Universidad de Barcelona.
15-17 April	Enzymology of DNA-Strand Transfer Mechanisms	E. Lanka. Max-Planck-Institut für Molekulare Genetik. Berlin. F. de la Cruz. Universidad de Cantabria. Santander.
20-22 May	Vascular Endothelium and Regulation of Leukocyte Traffic	T. Springer. Center for Blood Research. Boston. M. O. de Landázuri. Hospital de la Princesa. Madrid.
3-5 June	Cytokines in Infectious Diseases	A. Sher. National Institute of Health. Bethesda. M. Fresno. Centro de Biología Molecular «Severo Ochoa». Madrid. L. Rivas. Centro de Investigaciones Biológicas. Madrid.
17-19 June	Molecular Biology of Skin and Skin Diseases	D. R. Roop. Baylor College of Medicine. Houston. J. L. Jorcano. CIEMAT. Madrid.
1-3 July	Programmed Cell Death in the Developing Nervous System	R. W. Oppenheim. The Bowman Gray School of Medicine. Winston-Salem. E. M. Johnson. Washington University. St. Louis. J. X. Comella. Facultad de Medicina. Lérida.
8-10 July	NF κ B/I κ B Proteins. Their Role in Cell Growth, Differentiation and Development	R. Bravo. Bristol-Myers Squibb Pharmaceutical Research Institute. Princeton. P. S. Lazo. Facultad de Medicina. Oviedo.
23-25 September	Chromosome Behaviour: the Structure and Function of Telomeres and Centromeres	B. Trask. University of Washington. Ch. Tyler-Smith. University of Oxford. F. Azorin. Centro de Investigación y Desarrollo. Barcelona. A. Villasante. Centro de Biología Molecular «Severo Ochoa». Madrid.
7-9 October	RNA Viral Quasispecies	S. Wain-Hobson. Institut Pasteur. Paris. E. Domingo. Centro de Biología Molecular «Severo Ochoa». Madrid. C. López Galíndez. Centro Nacional de Biología Celular y Retrovirus. Madrid.
28-30 October	Absciscic Acid Signal Transduction in Plants	R. Quatrano. University of North Carolina. Chapel Hill. M. Pagès. Centro de Investigación y Desarrollo. Barcelona.
25-27 November	Oxygen Regulation of Ion Channels and Gene Expression	E. Kenneth Weir. University of Minnesota. J. López-Barneo. Facultad de Medicina. Sevilla.

All meetings will take place on the premises of the Instituto Juan March:

Castelló, 77
Telephone: 34-1-435-4240
Fax: 34-1-576-3420
28006 Madrid (Spain)

Individual advertisements for every meeting, with more detailed information, are published with sufficient anticipation.

Transcriptional Regulation At a Distance

Organized by

W. Schaffner, V. de Lorenzo and J. Pérez-Martín

15th-17th January, 1996

The discovery of enhancer elements about one dozen years ago has been one of the major landmarks in modern Molecular Biology. The notion that discrete DNA sequences and cognate DNA-binding proteins can control the activity of promoters located at considerable distances has provided the key to understand the molecular basis of major biological phenomena such as tissue-related gene expression as well as the organization of complex regulatory cascades in developmental systems. The last few years have witnessed an amazing progress in the analysis of the various components which account for activation at a distance, in particular the nature of the regulatory proteins and auxiliary factors involved.

From the information available at the moment, we know that *cis*-acting regulatory elements of eukaryotic genes include promoter sequences located around the transcription initiation site and enhancer sequences located farther away. A promoter often consists of an initiator sequence, a TATA box and one or more upstream sequences where regulatory proteins can bind. Transcription initiation by RNA polymerase II involves the assembly of a multifactor complex at the TATA box and initiation site. While the promoter is the assembly site of the preinitiation complex, enhancers confer additional regulatory information (i.e. cell-type specificity) to the promoter. Eukaryotic transcription factors are divided, in one hand, into the *general transcription factors*, which bind to common motifs (TATA box, initiator motif) and constitute the preinitiation complex, and the *sequence-specific transcription factors* which bind to upstream promoter or enhancer elements. On the other hand, sequence-specific transcription factors are thought to influence the rate of transcription initiation by interacting with the general transcription factors, RNA polymerase II and chromatin components. The main features of a sequence-specific transcription factor include the DNA-binding domain, the nuclear localization signal and the transactivation domain. A common (and somewhat naive) view of the process assumes that once the initiation complex is assembled, the collection of transcription factors create a constellation of protein-protein interactions that, through a largely undisclosed mechanism, enables the polymerase to initiate transcription. On top of this, the pivotal role of chromatin and chromatin-associated proteins in transcriptional control is becoming an emerging (and expanding) issue in nearly every system where its role has been examined.

Needless to say that these views are under permanent challenge, since new factors and mechanisms are coming into play, mostly from research on transcriptional regulation in yeasts and *Drosophila*. These two experimental systems are the best beneficiaries at the power of the genetics that can be applied to solve otherwise intractable questions. Complex issues on the mechanism of transcription initiation by RNA polymerase II (for example, recruitment of the holoenzyme to the promoter mediated by transcriptional factors) are amenable to experimental scrutiny, to this day, almost exclusively through genetic means. In addition to the reverse genetics with mammalian cell cultures and the increasing availability of transgenic animals, yeast genetics has become the major driving force to raise a wealth of opportunities for fundamental explorations into the mechanisms of transcription in

eukaryotes. One example is the control of the mating types of *S. cerevisiae*, one of the most complex -and most fascinating- paradigms of regulation of gene expression in the biological world. Similarly, the study of novel elements such as the chromatin insulators of *Drosophila* that inhibit the function of enhancers, is greatly facilitated in systems with a good repertoire of tools for genetic analysis.

What was believed to be distinct of eukaryotic promoters happens to occur also in prokaryotic systems. A number of observations made in the mid-80s in the Laboratory of B. Magasanik on regulation of nitrogen-starvation systems of *Escherichia coli*, notably the *glnAp2* promoter and its cognate regulator, the protein NRI (widely known by its alternative name, NtrC), indicated that remote transcriptional control was not a privilege of higher cells. *glnAp2* turned out to be the prototype of a novel class of promoters depending on the alternative σ^{54} factor. These are unique in that they are activated at a distance by specific regulators bound to upstream, enhancer-like sequences (UAS). These unusual properties are to be explained by the eukaryotic-like structure of the σ^{54} factor itself and that of the cognate regulatory proteins. In a subset of σ^{54} -dependent promoters, a binding site for the histone-like protein IHF site is found between the binding sites of the RNAP- σ^{54} holoenzyme and the UAS. The major (but perhaps not the sole) role of IHF as co-activator in the σ^{54} -promoters is believed to assist formation of a DNA loop or even a nucleoprotein complex to stabilize contacts between the RNAP and the activator protein bound to the UAS. There is also an increasing evidence that other prokaryotic histone-like proteins (such as HU) play a role in the assembly of the transcription initiation complex.

Although σ^{54} -dependent promoters are the most extensively studied case of activation at a distance in prokaryotes, other systems are subjected also to transcriptional control by regulatory devices placed at distant sites. A notable case is that of the T4 enhancer, in which tracking (and not looping) of the replication protein accounts for the effect of distant sites in transcription initiation. Repression at a distance is also a well known phenomenon in prokaryotic systems: early observations can be traced back to the late 70s in the work by Bob Schleif on the arabinose (*ara*) operon of *E. coli*. In spite of having been studied for over two decades, the *ara* system seems to be a permanent source of surprises to this day -and surely the best documented case of remote negative control in bacteria.

What lessons can the prokaryotic systems learn from the more complex eukaryotic promoters and *vice versa*? Perhaps activation at a distance is a general evolutionary strategy to integrate multiple signals for the control of a single promoter. The architecture of some bacterial promoters subjected to distant control may therefore be better understood in light of its evolutionary history and not on the basis of a strict necessity for such a complex setup. An interesting lesson that comes from the prokaryotic side is that DNA structures play an active role in such *signal integration*, instead of being just docking sites for transcription

factors. It seems to be true also for some prokaryotic systems (those dependent of σ^{54}) that the assembly of an upstream nucleoprotein complex gives rise to an enzymatic activity that is not present in the non-assembled components of the complex, an issue rarely examined in eukaryotic promoters.

In summary, it appears that, in spite of the intrinsic differences in the mechanism of activation of prokaryotic and eukaryotic systems subjected to remote control, various common themes will help to gain a better insight in the general biological problem of transcriptional control.

Walter Schaffner
José Pérez-Martín
Víctor de Lorenzo

LIST OF INVITED SPEAKERS

Víctor G. Corces

Department of Biology, The Johns Hopkins University, 144
Mudd Hall/3400 N. Charles St. Baltimore, MD. 21218 (USA).

Michel Débarbouillé

Institut Pasteur, URA 1300 CNRS, Departement des
Biotechnologies,
25 rue du Docteur Roux, 75724 Paris (France).

Ray Dixon

Nitrogen Fixation Laboratory, John Innes Centre,
Colney Lane, Norwich NR4 7UH (U.K.).

E. Peter Geiduschek

Department of Biology, University of California at San
Diego, 9500 Gilman Drive, La Jolla, CA. 92093-0634 (USA).

Jay D. Gralla

Department of Chemistry and Biochemistry and the Molecular
Biology Institute, University of California, 405 Hilgard
Avenue, Los Angeles, CA. 90095 (USA).

Wolfram Hörz

Institut für Physiologische Chemie, Universität München,
Schillerstr. 44, 80336 München (Germany).

Sydney Kustu

Departments of Plant and Molecular and Cell Biology,
University of California, 111 Koshland Hall, Berkeley, CA.
94720 (USA).

Víctor de Lorenzo

Centro Nacional de Biotecnología, UAM, Campus de
Cantoblanco, 28049 Madrid (Spain).

Boris Magasanik

Massachusetts Institute of Technology, 31 Ames Street,
Cambridge, MA. 02139 (USA).

Miguel Angel Peñalva

Centro de Investigaciones Biológicas, CSIC, c/Velázquez 144,
28006 Madrid (Spain).

José Pérez-Martín

Department of Microbiology and Immunology, University of California, San Francisco, 513 Parnassus Ave, Building S-410, Box 0414, San Francisco, CA. 94143-0414 (USA).

Vincenzo Pirrotta

Department of Zoology, University of Geneva, 30 quai E. Ansermet, CH1211 Geneva (Switzerland).

Rudi J. Planta

Department of Biochemistry & Molecular Biology, IMBW, BioCentrum Amsterdam, Vrije Universiteit, 1081 HV Amsterdam (The Netherlands).

Mark Ptashne

Department of Molecular and Cellular Biology, Harvard University, 7 Divinity Avenue, Cambridge, MA. 02138 (USA).

Jasper D. Rine

Division of Genetics, Department of Molecular and Cellular Biology, 401 Barker Hall, University of California, Berkeley, CA. 94720 (USA).

Margarita Salas

Centro de Biología Molecular "Severo Ochoa", CSIC, Universidad Autónoma, 28049 Madrid (Spain).

Paolo Sassone-Corsi

IGBMC, BP 163, 67404 Illkirch, CU de Strasbourg (France).

Walter Schaffner

Institute of Molecular Biology (II), University of Zürich Winterthurer Str. 190, CH-8057 Zürich (Switzerland).

Robert Schleif

Biology Department, The Johns Hopkins University, 3400 N. Charles St., Baltimore, MD. 21218 (USA).

Bernt Eric Uhlin

Department of Microbiology, Umeå University, S-901 87 Umeå (Sweden).

LIST OF PARTICIPANTS

Daniel Aberdam

IMSERM U 35, "Biologie et Physiopathologie de la Peau",
Université de Nice-Sophia Antipolis, Avenue de Valombrose,
06034 Nice (France).

Paola Ballario

Centro di Studio per gli Acidi Nucleici CNR) Dept. of
Genetics and Molecular Biology, University of Rome "La
Sapienza", P.zale A. Moro 7, 00185 Roma (Italy).

Giovanni Bertoni

Centro de Investigaciones Biológicas, CSIC,
c/ Velázquez 144, 28006 Madrid (Spain).

August Böck

Institute of Genetics and Microbiology, University of
Munich, Maria-Ward-Strasse 1a, 80638 München (Germany).

Manuel Carmona

Department of Biology, Massachusetts Institute of
Technology, Room 68-258D, 77 Massachusetts Ave, Cambridge,
MA. 02139 (USA).

Ildefonso Cases

Centro de Investigaciones Biológicas, CSIC, Velázquez 144,
28006 Madrid (Spain).

Irwin Davidson

IGBMC, CNRS/INSERM, Université Louis Pasteur, Parc
d'Innovation, 1 rue Laurent Fries, B.P. 163, 67404
Illkirch, C.U. Strasbourg (France).

M^a Trinidad Gallegos

CSIC, Department of Biochemistry and Molecular and
Cellular Biology of Plants, DOT Group, Box 419,
18008 Granada (Spain).

Rozenn Gardan

Département des Biotechnologies, Unité de Biochimie
Microbienne, Institut Pasteur, 25 rue du Dr. Roux,
75724 Paris Cedex 15 (France).

Jin-Soo Kim

Howard Hughes Medical Institute and Department of Biology,
Massachusetts Institute of Technology, 77 Massachusetts
Ave, Cambridge, MA. 02139 (USA).

Mónica Lamas

IGBMC, CNRS - INSERM, Université Louis Pasteur, Parc
d'Innovation, 1 rue Laurent Fries, Illkirch - C.U. de
Strasbourg (France)

Qiao Li

Department of Cell and Molecular Biology, Medical Nobel
Institute, Karolinska Institutet, S-171 77 Stockholm
(Sweden).

Silvia Marqués

CSIC, Department of Biochemistry and Molecular and
Cellular Biology of Plants, DOT Group, Box 419,
18008 Granada (Spain)

Bidyut K. Mohanty

Department of Microbiology, Duke University Medical
Center, Box 3020, Durham, NC. 27710 (USA)

María Monsalve

Centro de Biología Molecular "Severo Ochoa", (CSIC-UAM),
Cantoblanco, 28049 Madrid (Spain).

B. Tracy Nixon

Department of Biochemistry & Molecular Biology, The
Pennsylvania State University, 327 South Frear Lab.
University Park, PA. 16802 (USA).

José Antonio Oguiza

Área de Microbiología, Facultad de Biología, Universidad
de León, 24071 León (Spain).

Amos B. Oppenheim

Department of Molecular Genetics, Hebrew University-
Hadassah Medical School, P.O. Box 12272,
Jerusalem 91120 (Israel).

Ariella Oppenheim

The Hebrew University-Hadassah Medical School,
Jerusalem 91120 (Israel).

Jacqueline Plumbridge

Institut de Biologie Physico-chimique, 13 rue P. et M.
Curie, 75005 Paris (France).

Juan Luis Ramos

CSIC, Department of Biochemistry, 18008 Granada (Spain).

Javier Rey Campos

Centro de Investigaciones Biológicas, CSIC,
c/ Velázquez 144, 28006 Madrid (Spain).

Fernando Rojo

Centro Nacional de Biotecnología, CSIC, Campus de la
Universidad Autónoma de Madrid, Cantoblanco,
28049 Madrid (Spain).

Gloria Rudenko

The Netherlands Cancer Institute, Plesmanlaan 121,
1066 CX Amsterdam (The Netherlands).

Tomás Ruiz-Argüeso

Laboratorio de Microbiología, Departamento de
Biotecnología, ETS Ingenieros Agrónomos, Universidad
Politécnica de Madrid, 28040 Madrid (Spain).

Eduardo Santero

Departamento de Genética, Facultad de Biología,
Universidad de Sevilla, Ap.1095, 41080 Sevilla (Spain).

Verena Weiss

Department of Biology, University of Konstanz, D-78434
Konstanz (Germany).

**From Transcript to Protein: mRNA Processing,
Transport and Translation**

Organized by
I. Mattaj, J. Ortín and J. Valcárcel
11th-13th March, 1996

Biological research very frequently involves reductionist experimental approaches on very specialized aspects of the cell structure, regulation or fate. However, it is becoming more evident every day that biological phenomena are profoundly and extensively interrelated and interdependent. For a virologist like me, an outsider in the Cell Biology field, it was quite a surprise when work of our group, as well as others, showed that the influenza virus NS1 protein, a small non-structural protein, was able to alter several aspects of the gene expression program of the cell, including pre-mRNA splicing, nucleocytoplasmic transport and mRNA translation. Therefore, it was not a fully altruistic idea to propose to the Centre of International Meetings on Biology ("Instituto Juan March de Estudios e Investigaciones") a Workshop to integrate discussions on the post-transcriptional steps involved in gene expression. Looking at the state of the field, I felt that it was particularly appropriate to look at the recent advances with an integrative perspective and that the Spanish scientists, myself included, could learn very much from it.

The organization of such a meeting would have been impossible without the active role of relevant researchers in the field. I was very lucky to have Iain Mattaj and Juan Valcárcel as co-organizers, who helped very much in the difficult task of selecting, among the many excellent scientists covering these topics, those that would make an appropriate blend for a successful meeting.

It was the purpose of the meeting to find interconnections between the several steps that take place from the point a primary transcript is synthesized up to the moment its corresponding mRNA is actively translated and, eventually, degraded. After three days of intensive exchange of ideas, the outcome of the workshop exceeded our expectations. Indeed, both the oral and poster presentations, as well as the very active discussions, supported previously suspected connections and opened our minds to unexpected new ones. Thus, the mechanisms of nucleo-cytoplasmic trafficking can no longer be separated into nuclear import and export, since evidence is accumulating that suggest that both processes might be tightly connected and might share common factors.

In the same line, some of the newly discovered signals that stimulate the export from the nucleus (NESSs) appear to overlap with nuclear import signals (NLSs). Furthermore, in addition to the long studied dependence of mRNA stability on its capacity to be translated, it appears now that a safe ward might exist to avoid the normal splicing of pre-mRNAs in which premature termination codons would impair the biological activity of the potential translation product. These observations, together with the known relationship between polyadenylation and mRNA translatability, indicate that profound feed-back information loops should exist between distant (both temporally and physically) post-transcriptional events in the gene expression process.

Juan Ortín

LIST OF INVITED SPEAKERS

Montserrat Bach-Elias

Centro de Investigación y Desarrollo, CSIC, Jordi Girona
Salgado 18-26, 08034 Barcelona (Spain).

Joel G. Belasco

Department of Microbiology and Molecular Genetics,
Harvard Medical School, 200 Longwood Avenue,
Boston, MA. 02115 (USA).

Gideon Dreyfuss

Department of Biochemistry and Biophysics, Howard Hughes
Medical Institute, University of Pennsylvania School of
Medicine, 422 Curie Boulevard,
Philadelphia, PA. 19104-6148 (USA).

Matthias W. Hentze

Gene Expression Programme, European Molecular Biology
Laboratory, Meyerhofstrasse 1, D-69117 Heidelberg
(Germany).

Elisa Izaurralde

EMBL, Gene Expression Programme, Meyerhofstrasse 1,
D-69012 Heidelberg (Germany).

Walter Keller

Department of Cell Biology, Biozentrum, University of
Basel, Klingelbergstrasse 70, CH-4056 Basel (Switzerland).

Adrian Krainer

Cold Spring Harbor Laboratory, P.O. Box 100, Cold Spring
Harbor, NY. 11724 (USA).

Angus I. Lamond

Department of Biochemistry, University of Dundee,
Dundee DD1 4HN, Scotland (U.K.)

Pierre Legrain

Laboratoire du Métabolisme des ARN, Department of
Biotechnology, Institut Pasteur, 28 rue du Dr. Roux,
F-75724 Paris (France).

Juan Ortín

Centro Nacional de Biotecnología, CSIC, Universidad
Autónoma, Campus de Cantoblanco, 28049 Madrid (Spain).

Roy Parker

Howard Hughes Medical Institute & Department of Molecular
and Cellular Biology, University of Arizona,
Tucson, AZ. 85721 (USA).

Joel D. Richter

Worcester Foundation for Biomedical Research, 222 Maple
Avenue, Shrewsbury, MA. 01545 (USA).

Michael Rosbash

Brandeis University, Howard Hughes Medical Institute,
Department of Biology, Basine 235,
Waltham, MA. 02254 (USA).

Bertrand Séraphin

EMBL, Gene Expression Programme, Meyerhofstrasse 1,
D-69117 Heidelberg (Germany).

Nahum Sonenberg

Department of Biochemistry, McGill University, 3655
Drummond Street, Montreal, PQ. H3G 1Y6 (Canada)

Joan A. Steitz

Department of Molecular Biophysics and Biochemistry,
Howard Hughes Medical Institute, Yale University
School of Medicine, 295 Congress Avenue,
New Haven, CT. 06536-0182 (USA).

Alan M. Tartakoff

Case Western Reserve University, 2085 Adelbert Road,
Cleveland, OH. 44106 (USA).

Juan Valcárcel

Gene Expression Programme, European Molecular Biology
Laboratory, Meyerhofstrasse 1,
D-69117 Heidelberg (Germany).

LIST OF PARTICIPANTS

M.Mar Albà

Departamento de Genética Molecular, C.I.D./C.S.I.C.,
c/ Jordi Girona 18/26, 08034 Barcelona (Spain).

Said Aoufouchi

MRC, Lab. of Molecular Biology, PNAC Division, Hills Road,
Cambridge CB2 2QH (U.K.).

Graham J. Belsham

Institute for Animal Health, Pirbright Laboratory, Ash
Road, Pirbright, Woking Surrey GU24 0NF (U.K.).

Laura Beretta

INSERM U.153, 17 rue du Fer-à-Moulin,
75005 Paris (France).

Ronald P. Boeck

Department of Molecular & Cellular Biology, 401 Barker
Hall, University of California, Berkeley, CA. 94720 (USA).

Philippe Bouvet

Laboratoire de Biologie Moléculaire Eucaryote,
IB CG du CNRS, 118 route de Narbonne,
31062 Toulouse Cedex (France).

Bryan R. Cullen

Howard Hughes Medical Institute and Department of
Genetics, Duke University Medical Center,
Post Office Box 3025, Durham, NC. 27710 (USA).

Gretchen Edwalds-Gilbert

Department of Molecular Genetics and Biochemistry,
University of Pittsburgh School of Medicine, BST W1207,
Terrace & Lothrop Sts., Pittsburgh, PA. 15261 (USA).

Luis Enjuanes

Centro Nacional de Biotecnología, CSIC, Campus Universidad
Autónoma, Cantoblanco, 28049 Madrid (Spain).

Ruth Espuny Suarez

Centro de Investigación y Desarrollo, CSIC, Jordi Girona
18-26, 08034 Barcelona (Spain).

M^a Angeles Freire-Picos

Departamento de Biología Celular y Molecular, Universidad
de La Coruña, 15009 La Coruña (Spain).

M^a Purificación Fortes
EMBL, Gene Expression Programme, Meyerhofstrasse 1,
69117 Heidelberg (Germany).

Mariano A. García-Blanco
Department of Molecular Cancer Biology, Duke University
Medical Center, Box 3686, Durham, NC. (USA).

Fátima Gebauer
Worcester Foundation for Biomedical Research,
222 Maple Avenue, Shrewsbury, MA. 01545 (USA).

Charles C. Gubser
MRC Laboratory of Molecular Biology, Hills Road,
Cambridge CB2 2QH (U.K.).

César de Haro
Centro de Biología Molecular "Severo Ochoa", CSIC,
Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Fabrizio Loreni
Friedrich Miescher-Institut, P.O. Box 2543,
CH-4002 Basel (Switzerland).

Rosa M^a Marión
Centro Nacional de Biotecnología, CSIC, Universidad
Autónoma, Campus de Cantoblanco, 28049 Madrid (Spain).

Encarnación Martínez-Salas
Centro de Biología Molecular "Severo Ochoa", CSIC,
Universidad Autónoma, de Madrid, Cantoblanco,
28049 Madrid (Spain).

César Milstein
MRC Laboratory of Molecular Biology, Division of Protein
and Nucleic Acid Chemistry, Hills Road, Cambridge CB2 2QH
(U.K.).

Pura Muñoz-Cánoves
Departament de Receptors Cel·lulars, Institut de Recerca
Oncològica, Hospital "Duran i Reynals", Autovía
Castelldefels Km 2.7, 08907 L'Hospitalet de Llobregat,
Barcelona (Spain).

Amelia Nieto
Centro Nacional de Biotecnología, CSIC, Universidad
Autónoma, Campus de Cantoblanco, 28049 Madrid (Spain).

Steffen Nock

Universität Bayreuth, Lehrstuhl für Biochemie,
Universitätsstr. 30, D-95440 Bayreuth (Germany).

Marcel·lí del Olmo

Departament de Bioquímica i Biologia Molecular, Facultat de Ciències, Universitat de València,
c/ Dr. Moliner 50, E-46100 Burjassot, (Spain).

Josefa Salgado

EMBL, Gene Expression Programme, Meyerhofstrasse 1,
D-69117 Heidelberg (Germany).

Helen Salz

Department of Genetics, Case Western Reserve University,
School of Medicine, Cleveland, Ohio 44106-4955 (USA).

Vivian Siegel

CELL, Editorial Offices, 1050 Massachusetts Avenue,
Cambridge, MA. 02138 (USA).

Annie Sittler

CNRS/INSERM, Université Louis Pasteur, Parc d'Innovation,
1 rue Laurent Fries, Illkirch-C.U. de Strasbourg (France).

Christoph Springer

Institute of Microbiology, Biochemistry and Genetics,
Friedrich-Alexander-University, Staudt-Strasse 5, D-91058
Erlangen (Germany).

Eric J. Steinmetz

Department of Biomolecular Chemistry, University of
Wisconsin, 1300 University Avenue,
Madison, WI. 53706-1532 (USA).

Li Su

Department of Biology, Room 68-223, Massachusetts
Institute of Technology, Cambridge, MA. 02139 (USA).

Albert Tauler

Universitat de Barcelona, Facultat de Farmàcia, Dept. de Ciències Fisiològiques Humanes i de la Nutrició,
Av. Diagonal 643, 08028 Barcelona (Spain).

Mechanisms of Expression and Function of MHC Class II Molecules

Organized by
B. Mach and A. Celada
25th-27th March, 1996

The idea of organizing the Workshop on "Mechanisms of expression and function of MHC class II molecules" in Madrid was to cover two objectives: first, to make the point of the recent discoveries in the field of MHC class II molecules. The second objective was to meet other Spanish colleagues working in this field. The major credit for the organization of this meeting is to the co-organizer, Bernard Mach, who helped me in contacting a selected list of brilliant and active investigators in the field of class II molecules. With his prestige, Bernard supported this meeting which, due to the small size and the good facilities of the Juan March Foundation, made for an easy interaction between participants. Without the effort of Bernard this meeting would not have been possible. Finally, I should thank all the participants who spent some of their busy schedules coming to Madrid and making the success of the meeting possible.

I would like to mention that Spanish research in the last 20 years has made a dramatic improvement. This is due, certainly, to the political and economical changes that have occurred with the return of democracy to Spain. The increase in the budgets for research programmes resulted in a large number of publications appearing in scientific journals, produced by groups working in Spain. Another important aspect to science is communication, and we are very glad that some private foundations such as Juan March decided to support with enthusiasm and organize these biology meetings that help the interactions between Spain and the rest of the scientific community. One of the results of this effort is that many of the invited scientists to the workshop made their first visit to Spain, where they could learn through the presentations carried out during the meeting that, although Spanish science still needs to develop, putting our emphasis on the quality of the research, we are traveling in the good direction.

The small number of participants allowed a good interaction during the presentations, the coffee breaks and lunches. Many cooperative projects will start from this meeting, helping all of us to do in a better way one of the things that we enjoy: research. Also, for young participants, it was a unique opportunity to meet one of the best groups of scientists working in the field of class II molecules. I am quite sure that soon some of these participants will apply for training as post-docs in some of the labs that made the presentations.

The immune system has two functions: one is to recognize what comes from outside and what comes from inside, and the other is to induce a reaction that eliminates what is foreign. MHC class II molecules play a key role in the immune system. These molecules are necessary to present to T lymphocytes the peptides that come from the processed antigens. It is very important to define the mechanisms that regulate the expression of MHC class II molecules. Once these molecules have been produced, it is also necessary to know the different steps from the endoplasmic reticulum until the molecules of class II are loaded with peptides and expressed at the cell surface. Therefore, the understanding of the regulation of the expression and functional activity of these molecules is one of the major steps to understand correctly the immune system.

The expression of class II genes is tissue specific and inducible in some cells by cytokines such as interferon gamma (IFN γ). For instance, in B lymphocytes the expression is constitutive, in macrophages it is inducible by IFN γ and in some other cells it is not expressed. This represents a good opportunity to study tissue specific and inducible transcription factors as a way to better understand the regulation of gene expression.

In the study of molecules such as IFN γ that induce the expression of class II molecules, the next step is to define the interaction with the cells at their surface. IFN γ -receptors are proteins in which, after the interaction with the ligands, two tyrosin-kinases, JAK1 and JAK2 become activated.

As a result of the ligand-receptor interaction, a cascade of second signals is produced inside the cell. Some of these signals induce in minutes the expression of some genes (early genes), such as Stat 1, that are required for the subsequent transcription of other genes directly related with the expression of class II molecules.

Upstream of all MHC class II genes there exist three relatively conserved sequences that play an essential role in the transcription regulation of these genes. Some binding proteins are defective in patients with combined immunodeficiency, a disease in which there is no MHC class II expression.

MHC class II molecules assemble with the Invariant chain in the endoplasmatic reticulum and are then moved to endosomal/lysosomal compartments. There, Ii is proteolytically digested but fragments of Ii, designed CLIP, remain in the groove of class II molecules and are removed by HLA-DM, a non-classical MHC class II molecule, so that peptide loading with antigenic peptides can proceed.

At the end of the meeting, I asked myself if we have answers to all the questions that this exciting workshop provoked. Obviously that is not the case, and not only that, but I think that we have more questions that remain open to new ideas, experiments, etc. This suggests to me that this interesting topic is alive and we will need the help of many scientist to answer all the questions.

Antonio Celada

LIST OF INVITED SPEAKERS

Luciano Adorini

Roche Milano Ricerche, Via Olgettina 58, I-20131 Milano (Italy).

Jeremy M. Boss

Department of Microbiology and Immunology, Emory University School of Medicine, 3001 Rollins Research Center, Atlanta, GA. 30322 (USA).

Antonio Celada

Departament de Fisiologia (Immunologia), Facultat de Biologia, Universitat de Barcelona, Diagonal 645, 08071 Barcelona (Spain).

Peter Cresswell

Howard Hughes Medical Institute, Yale University School of Medicine, 310 Cedar Street, New Haven, CT. 06510 (USA).

Richard A. Flavell

Section of Immunology, Yale University School of Medicine, Howard Hughes Medical Institute, 310 Cedar St., New Haven, CT. 06510 (USA).

Ronald N. Germain

Lymphocyte Biology Section, Laboratory of Immunology, NIAID, National Institutes of Health, Bldg. 10, Rm. 11N311, 10 Center Drive MSC-1892, 20892-1892 Bethesda, MD. (USA)

Laurie H. Glimcher

Harvard School of Public Health, Department of Cancer Biology, 665 Huntington Av. Boston, MA. 02115 (USA).

Günter J. Hämmerling

Division of Molecular Immunology, Tumor Immunology Program, German Cancer Research Center, Im Neuenheimer Feld 280, 69120 Heidelberg (Germany).

Lars Karlsson

The R.W. Johnson Pharmaceutical Research Institute at The Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, CA. 92037 (USA).

Ian M. Kerr

Imperial Cancer Research Fund, 44 Lincoln's Inn Fields,
London WC2A 3PX (U.K.).

H.R. MacDonald

Ludwig Institute for Cancer Research, Chemin des
Boveresses 155, 1066 Epalinges (Switzerland).

Bernard Mach

Jeantet Laboratory of Molecular Genetics, Department of
Genetics and Microbiology, University of Geneva Medical
School, CH-1211 Genève 4 (Switzerland).

Walter Reith

Jeantet Laboratory of Molecular Genetics, Department of
Genetics and Microbiology, University of Geneva Medical
School, CH-1211 Genève 4, (Switzerland).

Andrea J. Sant

University of Chicago, Department of Pathology and
Committee on Immunology, 5841 S. Maryland Ave,
MC1089, Chicago, IL. 60637 (USA).

Robert D. Schreiber

Washington University School of Medicine, 660 South Euclid
Avenue, St. Louis. MO. 63110 (USA).

Viktor Steimle

Jeantet Laboratory of Molecular Genetics, Department of
Genetics and Microbiology, University of Geneva Medical
School, CH-1211 Genève 4, (Switzerland).

Jenny P.-Y. Ting

Lineberger Comprehensive Cancer Center, Department of
Microbiology-Immunology, University of North Carolina,
Chapel Hill, NC. 27599 (USA).

John Trowsdale

Human Immunogenetics Laboratory, Imperial Cancer Research
Fund, Lincoln's Inn Fields, Holborn,
London WC2A 3PX (U.K.).

LIST OF PARTICIPANTS

José Alcamí

Servicio de Microbiología, Centro de Investigación,
Hospital 12 de Octubre, Ctra. de Andalucía s/nº,
28041 Madrid (Spain).

Javier Arroyo

Departamento de Microbiología II, Facultad de Farmacia,
Universidad Complutense, 28040 Madrid (Spain).

Amy Axelrod

Cell Editorial Offices, 1050 Massachusetts Ave,
Cambridge, MA. 02138 (USA).

Youngmee Bae

Department of Biochemistry, University of Oxford,
South Park Road, Oxford OX1 3QU (U.K.).

Cheong-Hee Chang

Section of Immunobiology, Yale School of Medicine,
310 Cedar Street, New Haven, CT. 06510 (USA).

Peter J. van den Elsen

Department of Immunohaematology & Blood Bank, University
Hospital, P.O. Box 9600, 2300 RC Leiden (The Netherlands).

Enric Espel

Departament de Fisiologia (Immunologia), Facultat de
Biologia, Universitat de Barcelona, Av. Diagonal 645,
08028 Barcelona (Spain).

Partho Ghosh

Structural Biology, Department of Molecular and Cellular
Biology, Harvard University, 7 Divinity Avenue,
Cambridge, MA. 02138 (USA).

Eduard Góñalons

Department of Fisiology (Immunology), Faculty of Biology,
University of Barcelona, Diagonal, 645,
08028 Barcelona (Spain).

Dolores Jaraquemada

Immunology Unit, Universitat Autònoma de Barcelona, Ctra.
del Canyet s/nº, 08916 Badalona (Spain).

Harald Kropshofer

German Cancer Research Center, Department of Molecular
Immunology, Im Neuenheimer Feld 280, D-69120 Heidelberg
(Germany).

Janet S. Lee
Memorial Sloan-Kettering Cancer Center, Immunology
Program, 1275 York Avenue, New York, NY. 10021 (USA).

Monika Liljedahl
The R.W. Johnson Pharmaceutical Research Institute at The
Scripps Research Institute, 10666 North Torrey Pines Road,
La Jolla, CA. 92037 (USA).

Jorge Lloberas
Departament de Fisiologia, Facultat de Biologia,
Universitat de Barcelona, Diagonal 645,
08071 Barcelona (Spain).

Hong-Tao Lu
Department of Neurosciences, Research Institute, Cleveland
Clinic Foundation, 9500 Euclid Avenue,
Cleveland, OH. 44195 (USA).

Roberto Mantovani
Dipartimento di Genetica e Biologia dei Microrganismi,
Università degli Studi di Milano, Via Celoria 26,
20133 Milano (Italy).

Mercè Martí
Hospital Universitari "Germans Trias i Pujol" (Unitat
d'Immunologia), Facultat de Medicina, Universitat Autònoma
de Barcelona, Ctra. Canyet s/nº, 08916 Badalona (Spain).

Jorge Martínez Laso
Inmunología, Hospital 12 de Octubre,
Ctra. Andalucía Km 5.4, 28041 Madrid (Spain).

Eduardo Martínez Naves
Inmunología, Facultad de Medicina, Universidad
Complutense, 28040 Madrid (Spain).

Corinne Moulon
Max-Planck-Institut für Immunbiologie, Stübeweg 51,
D-79108 Freiburg (Germany).

Luc Otten
Department of Genetics and Microbiology, University of
Geneva, Medical School, CH-1221 Genève 4 (Switzerland).

Eduardo Pareja
Sección de Biología Teórica, Hospital Virgen de las
Nieves, Dr. Azpitarte, 4 - 4ª planta, Granada (Spain).

José Peña

Servicio de Inmunología, Hospital Universitario "Reina Sofía", Avda. Menéndez Pidal s/nº, 14004 Córdoba (Spain).

José R. Regueiro

Inmunología, Facultad de Medicina, Universidad Complutense, 28040 Madrid (Spain).

Miguel Sánchez-Pérez

Departamento de Microbiología II, Facultad de Farmacia, Universidad Complutense, Plaza Ramón y Cajal s/nº, 28040 Madrid (Spain).

Idit Shachar

Section of Immunology, HHMI, Yale University School of Medicine, 310 Cedar Street, New Haven, CT. 06510 (USA).

Concepció Soler

Departament de Fisiologia (Immunologia), Facultat de Biologia, Fundació Pi i Sunyer, Campus Bellvitge, Universitat de Barcelona, 08071 Barcelona (Spain).

José A. Villadangos

Center for Cancer Research, Massachusetts Institute of Technology, 40 Ames Street, Cambridge, MA. 02139 (USA).

Anne B. Vogt

German Cancer Research Center, Department of Molecular Immunology, Im Neuenheimer Feld 280, D-69120 Heidelberg (Germany)

René de Waal Malefyt

Human Immunology Department, DNAX Research Institute for Cellular and Molecular Biology, Palo Alto, CA. 94304-1104 (USA).

Sabine Zachgo

Max-Planck-Institut, Carl-von-Linne Weg 10, D-50929 Cologne (Germany).

Enzymology of DNA-Strand Transfer Mechanisms

Organized by
E. Lanka and F. de la Cruz
15th-17th April, 1996

This year we celebrate the 50th anniversary of the discovery of bacterial conjugation by Lederberg and Tatum. Since then, conjugation has been a hot matter of active research at various levels: basic advance of knowledge, as a technological tool, by its implication in bacterial ecology (including medically important issues) and evolution, etc.

From a general point of view, we now know it involves the assembly and operation of a complicated structure that can be compared with the small ribosomal subunit, at least in the number of components. Conjugation allows the passage of a single-stranded DNA (that can be as large as the entire bacterial chromosome - a string of 5 million nucleotides) across four bacterial membranes. Amazingly, the process can be of very broad host range, with several known examples of trans-kingdom conjugation. By far the most conspicuous is T-DNA transfer from *Agrobacterium tumefaciens* to plant cells, a process considered to be a specialized form of bacterial conjugation.

Plasmid conjugation is of actuality also because of the use of exogenous DNA in release experiments, an ecological issue that was discussed at a related workshop in this Institute (Thomas et al., 1994).

The molecular complexity of bacterial conjugation allocates it to the intersection of apparently unrelated research topics, from rolling-circle replication and DNA-strand transfer mechanisms to macromolecular transport through biological membranes. We reasoned that first front research in bacterial conjugation should not limit itself to the knowledge produced by inbreeding. We considered it will most profit from the input of leading experts in the above mentioned flanking areas, by adopting an interdisciplinary approach. Thus, we organized the workshop with strong emphasis in the awareness that the contribution of the flanking areas can trigger in our field. As a nice by-product, the achievements of bacterial conjugation research will be better appreciated by a broader audience.

Hopefully, all participants will benefit from provoking questions and ideas launched across the different fields. With this idea in mind, the keynote lecture was chosen to alert the audience on the crucial importance of the knowledge of the 3D structures of proteins to investigate biochemical processes using topoisomerases as a model system.

The first section of the meeting focused on rolling-circle replication systems, which resemble the DNA processing reactions during conjugation. These were compared at a later section to other DNA-strand transferases, such as transposases and resolvases. The core sections included the topics of conjugation and T-DNA transfer. The utilization by bacterial conjugation of a complex DNA transport machinery bears analogies with other processes of macromolecular transport through membranes, which constituted another section of the workshop.

In our opinion, the meeting succeeded in presenting the facts of conjugation in a way that could be discussed as pertaining to the selected fields. Perhaps one of the most difficult

things was to find a suitable and inclusive title for our enterprise. Our initial idea ("Sources of inspiration for bacterial conjugation") found its way as the headline for the final Round Table discussion which involved many of the participants in a lively and "inspiring" discussion. Although gene transmission by bacterial conjugation is being studied now for 50 years, it is only since very recently that questions dealing with the mechanistic principle were asked and could be answered at the molecular level of enzymes. Consequently, "Enzymology of DNA-strand transfer mechanisms" was chosen as the most appropriate title to describe the aims of the workshop.

Fernando de la Cruz and Erich Lanka

LIST OF INVITED SPEAKERS

Juan C. Alonso

Centro Nacional de Biotecnología, CSIC, Campus Universidad
Autónoma de Madrid, Cantoblanco, E-28049 Madrid (Spain).

Tania A. Baker

Department of Biology and Howard Hughes Medical Institute,
Massachusetts Institute of Technology, 68-523,
77 Massachusetts Avenue, Cambridge, MA. 02139 USA)

Silvia Bolland

Laboratory of Biochemical Genetics, box 86,
The Sloan-Kettering Institute, 1275 York Avenue,
New York, NY. 10021 (USA).

Drusilla L. Burns

Center for Biologics Evaluation and Research, FDA,
8800 Rockville Pike, Bethesda, MD. 20892 (USA).

Fernando de la Cruz

Departamento de Biología Molecular, Universidad de
Cantabria, C. Herrera Oria s/n, 39011 Santander (Spain).

S. Dusko Ehrlich

Génétique Microbienne, Institut National de la Recherche
Agronomique, Domaine de Vilvert, 78352 Jouy en Josas Cedex
(France).

Manuel Espinosa

Centro de Investigaciones Biológicas, CSIC, Velázquez 144,
E-28006 Madrid (Spain).

Stephen K. Farrand

Departments of Crops Sciences and Microbiology, University
of Illinois at Urbana-Champaign, Urbana, IL. 61801 (USA).

Elisabeth Haggård-Ljungquist

Department of Genetics, Stockholm University, Svante
Arrhenius Våg 16, S-106 91 Stockholm (Sweden).

Stephen E. Halford

Department of Biochemistry, Centre for Molecular
Recognition, School of Medical Sciences, University of
Bristol, University Walk, Bristol BS8 1TD (U.K.).

Barbara Hohn

Friedrich Miescher-Institut, P.O. Box 2543,
CH-4002 Basel (Switzerland).

Paul J.J. Hooykaas

Institute of Molecular Plant Sciences, Leiden University,
Clusius Laboratory, Wassenaarseweg 64,
2333 AL Leiden (The Netherlands).

Scott Hultgren

Washington University School of Medicine, Department of
Molecular Microbiology, 660 South Euclid Avenue,
St. Louis, MO. 63110-1093 (USA).

Erich Lanka

Max-Planck-Institut für Molekulare Genetik,
Innestrasse 73, Dahlem, D-14195 Berlin (Germany).

Matxalen Llosa

Departamento de Biología Molecular, Universidad de
Cantabria, C. Herrera Oria s/n, 39011 Santander (Spain).

Steven W. Matson

Department of Biology, University of North Carolina, Coker
Hall, Chapel Hill, NC. 27599 (USA).

Richard P. Novick

Skirball Institute, New York University Medical School,
540 First Avenue, New York, NY. 10016 (USA).

Anthony P. Pugsley

Unité de Génétique Moléculaire, (CNRS URA1149), Institut
Pasteur, 25 rue du Dr. Roux, Paris 75724 Cedex 15
(France).

Marjorie Russel

The Rockefeller University, 1230 York Avenue, New York,
NY. 10021 (USA).

Wolfram Saenger

Institut für Kristallographie, Freie Universität Berlin,
Takustr. 6, D-14195 Berlin (Germany).

Patrick Trieu-Cuot

Laboratoire de Microbiologie, Faculté de Médecine Necker-
Enfants Malades, 75730 Paris Cedex 15 (France).

James C. Wang

Department of Molecular and Cellular Biology, Harvard
University, 7 Divinity Avenue, Cambridge, MA. 02138 (USA).

Patricia Zambryski

Department of Plant Biology, 111 Koshland Hall, University
of California, Berkeley, CA. 94720 (USA).

LIST OF PARTICIPANTS



Itziar Alcorta

Departamento de Bioquímica y Biología Molecular, Facultad de Ciencias, Universidad del País Vasco, Apartado 644, 48080 Bilbao (Spain).

Lars Andrup

Department of Toxicology and Biology, National Institute of Occupational Health, Lersø Parkallé 105, DK-2100 Copenhagen (Denmark).

Pilar Avila

Departamento de Biología Molecular, Universidad de Cantabria, c/Cardenal Herrera Oria s/n, 39011 Santander (Spain).

Irantzu Bernales

Departamento de Biología Molecular, Universidad de Cantabria, c/Cardenal Herrera Oria s/n, 39011 Santander (Spain).

George Bonheyo

University of Illinois at Urbana-Champaign, Department of Microbiology, 131 Burrill Hall, 407 South Goodwin Avenue, Urbana, IL. 61801 (USA)

Elena Cabezón

Departamento de Biología Molecular, Universidad de Cantabria, c/Cardenal Herrera Oria s/n, 39011 Santander (Spain).

Inés Canosa

Centro Nacional de Biotecnología, CSIC, Campus Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Josep Casadesús

Departamento de Genética, Facultad de Biología, Universidad de Sevilla, 41080 Sevilla (Spain).

Michael Chandler

Laboratoire de Microbiologie et de Génétique Moléculaire du CNRS, 118 route de Narbonne, 31062 Toulouse Cedex (France).

Ramón Díaz Orejas

Centro de Investigaciones Biológicas, CSIC, c/Velázquez 144, 28006 Madrid (Spain).

Félix M. Goñi

Departamento de Bioquímica y Biología Molecular, Facultad
de Ciencias, Universidad del País Vasco, Apartado 644,
48080 Bilbao (Spain).

A. Marika Grahm

Department of Biosciences and Institute of Biotechnology,
University of Helsinki, Viikinkaari 5,
FIN-00014 Helsinki (Finland).

Elisabeth Grohmann

Centro de Investigaciones Biológicas, (CSIC),
Velázquez 144, 28006 Madrid (Spain).

Andrea Güttler

National Research Centre for Biotechnology,
Department of Microbiology, Mascheroder Weg 1,
D-38124 Braunschweig (Germany).

Leda Guzmán

Centro de Investigaciones Biológicas, CSIC,
Velázquez 144, E-28006 Madrid (Spain).

Jana Haase

Max-Planck-Institut für Molekulare Genetik, Ihnestraße 73,
D-14195 Berlin (Germany).

Antonio Juárez

Departament de Microbiologia, Facultat de Biologia,
Universitat de Barcelona, Avda. Diagonal 645,
08028 Barcelona (Spain).

Saleem A. Khan

Department of Molecular Genetics and Biochemistry,
University of Pittsburgh School of Medicine,
Pittsburgh, PA. 15261 (USA).

Gabriel Moncalián

Departamento de Biología Molecular de la Universidad de
Cantabria, C/Cardenal Herrera Oria s/n,
39011 Santander (Spain).

Vladimir Pelicic

Unité de Génétique Mycobactérienne, Mycobacterial Genetics
Unit, Institut Pasteur, 25 rue du Dr. Roux,
75724 Paris Cedex 15 (France).

Susana Rivas

Departamento de Bioquímica y Biología Molecular, Facultad
de Ciencias, Universidad del País Vasco, Aptdo. 644,
48080 Bilbao (Spain).

Andrzej Stasiak

Université de Lausanne, Lab. d'Analyse Ultrastructurale,
Bâtiment de Biologie, niveau 1,
CH-1015 Lausanne-Dorigny (Switzerland).

Heimo M. Strohmaier

Institut für Mikrobiologie, Universität Graz,
Universitätsplatz 2, A-8010 Graz (Austria).

José Tormo

Department of Biochemistry, University of Oxford, South
Parks Road, Oxford OX1 3QU (U.K.).

Ellen L. Zechner

Institut für Mikrobiologie, Karl-Franzens-Universität
Graz, A-8010 Graz (Austria).

Vascular Endothelium and Regulation of Leukocyte Traffic

Organized by

T. A. Springer and M. O. de Landázuri

20th-22nd May, 1996

The circulatory and migratory properties of white blood cells have evolved to allow efficient surveillance of tissues for infectious pathogens and rapid accumulation at sites of injury and infection. Lymphocytes continually patrol the body for foreign antigen by recirculating from blood, through tissue, into lymph, and back to blood. Lymphocytes acquire a predilection, based on the environment in which they first encounter foreign antigen, to home to or to recirculate through that same environment.

The first critical step in lymphocyte migration from circulation into tissue is the adhesion of lymphocytes to vascular endothelium. In lymphoid organs, lymphocyte adherence and transendothelial migration occur at specialized postcapillary vascular sites called high endothelial venules (HEVs). Although HEVs are particularly abundant in the T-cell areas surrounding the B-cell follicles, they serve as the sites of entry both for T and B lymphocytes. In humans, HEVs are found in all secondary lymphoid organs (with the exception of spleen, where lymphocyte emigration occurs via the blood sinusoids in the marginal zone), including hundreds of lymph nodes dispersed in the body, tonsils and adenoids in the pharynx, Peyer's patches in the small intestine, appendix, and small aggregates of lymphoid tissue in the stomach and large intestine. Moreover, HEV-like vessels are observed in chronically inflamed nonlymphoid tissues and are believed to support lymphocyte recruitment in these sites. In contrast to the endothelial cells from other vessels, the high endothelial cells of HEVs have a distinctive appearance, express specialized ligands for lymphocytes and are able to support high levels of lymphocyte extravasation.

The different homing and recirculation behaviors of lymphocytes depend on expression of specific adhesion receptors by lymphocytes, endothelial cells, and tissue cells and on interactions with the extracellular matrix. Expression of these receptors is finely regulated according to cell type, functional state, and anatomical localization, and builds up a complex network in interactions that simultaneously involve several of these receptors working as "traffic signals" or "postcodes" for lymphocyte migration and homing. There are five main families of adhesion molecules: immunoglobulin superfamily, integrins, selectins, cadherins, and mucin-like molecules.

Many different adhesion systems are known to be subject to regulation, but the most-studied and best-understood class is the integrin. Integrins are known to be regulated at several levels. Modulation of the affinity of the adhesion receptor for ligand (called affinity modulation) is a well-documented mechanism for the activation of platelet aggregation and is thought to underlie activation of leukocyte adhesion. Adhesive strengthening by the clustering of adhesion receptors or by cytoskeletal-dependent processes such as cell spreading is known to be crucial for strong cell attachment, the control of cell growth and cell motility. These regulatory changes occur either in response

to intracellular event (hence, sometimes called inside-out signalling), as a result of EC ligand binding (often called postreceptor occupancy events), or in many instances from both.

Regulation of integrin-mediated adhesion may involve conversions among several different states. For example, leukocyte exhibit several different adhesive behaviours as they interact with endothelial cells of vessel wall during homing or extravasation at sites of inflammation. In the now classic three-step model, under the high shear forces present in flowing blood, leukocytes first become tethered and then roll along the vessel surface. When a local signal (for example, a cytokine) is released in their vicinity, they arrest, develop firm adhesion, and then migrate across the endothelium. Until recently, it has been thought that the rolling phase was mediated solely by the selectins, a family of carbohydrate-binding adhesion molecules implicated in leukocyte homing. Arrest and tightening of adhesion are known to result from the activation of leukocyte integrins. However, it has been recently shown that a single type of integrin can mediate all adhesive phases, including the initial tethering and rolling. For example, $\alpha 4 \beta 1$ (VLA-4) mediates tethering and rolling on vascular cell adhesion molecule 1 (VCAM-1), an endothelial integrin ligand belonging to the immunoglobulin superfamily. As expected, this integrin can also become activated to bring about arrest and tight adhesion. Thus, prior to activation, the integrin exhibits binding properties that support tethering and rolling.

The HEV endothelium is unique amongst vascular endothelium by virtue of its capacity to recruit large numbers of lymphocytes. In the human body it is estimated that as many as 5×10^6 lymphocytes extravasate from the blood through HEVs every second. The specificity and efficiency of this process is explained by specialized features of the HEV endothelium, such as the expression of mucin-like glycoproteins decorated with HEV-specific oligosaccharide. In the future, it will be important to define precisely the molecular mechanisms involved in the induction and maintenance of the specialized HEV phenotype.

HEV-like vessels induced by chronic inflammation in extra lymphoid sites appear to be phenotypically and functionally similar to HEVs from lymphoid tissues. Thus, a better understanding of the mechanisms controlling development and maintenance of HEVs could provide the basis of a novel therapeutic approaches for the treatment of human chronic inflammatory diseases, including rheumatoid arthritis and inflammatory bowel diseases, in which HEV-like vessels facilitate large-scale influx of lymphocytes, leading to amplification and maintenance of chronic inflammation.

T.A. Springer and M.O. de Landázuri

LIST OF INVITED SPEAKERS

Kari Alitalo

Molecular / Cancer Biology Laboratory, Haartman Institute,
University of Helsinki, POB 21, 00014 Helsinki (Finland).

Ulrich H. von Andrian

The Center for Blood Research, Harvard Medical School,
200 Longwood Avenue, Boston, MA. 02115 (USA).

Elisabetta Dejana

Istituto di Ricerche Farmacologiche Mario Negri, Vascular
Biology Laboratory, Via Eritrea 62, 20157 Milano (Italy).

Detlev Drenckhahn

Institute of Anatomy, Ludwig-Maximilians University of
Würzburg, Koellikerstraße 6, D-97070 Würzburg (Germany).

Martha B. Furie

Department of Pathology, School of Medicine, State
University of New York at Stony Brook, Stony Brook,
NY. 11794-8691 (USA).

John M. Harlan

Division of Hematology, University of Washington, RM-10,
Seattle, WA. 98195 (USA).

Thomas B. Issekutz

Departments of Medicine and Immunology, University of
Toronto, 585 University Avenue, Toronto,
ON. M5G 2C4 (Canada).

Mark A. Jutila

Veterinary Molecular Biology, Montana State University,
S 19th and Lincoln, Bozeman, MT. 59717-0360 (USA).

Francis W. Luscinskas

Department of Pathology, Brigham and Women's Hospital,
221 Longwood Avenue, Boston, MA. 02115 (USA).

Charles Mackay

LeukoSite Inc., 215 First Street, Cambridge,
MA. 02142 (USA).

Rodger P. McEver

W.K. Warren Medical Research Institute, University of
Oklahoma, 825 NE 13th Street, Oklahoma City,
OK. 73104 (USA).

Manuel O. de Landázuri

Sección de Inmunología, Hospital de la Princesa,
c/Diego de León 62, 28006 Madrid (Spain).

Francisco Sánchez-Madrid

Sección de Inmunología, Hospital de la Princesa,
c/Diego de León 62, 28006 Madrid (Spain).

C. Wayne Smith

Department of Pediatrics, Baylor College of Medicine,
Clinical Care Center, Suite 1130, Houston,
TX. 77030-2399 (USA).

Timothy A. Springer

Center for Blood Research, Harvard Medical School,
200 Longwood Avenue, Room 251, Boston, MA. 02115 (USA).

Dietmar Vestweber

Institute of Cell Biology, ZMBE, University of Münster,
Mendelstr. 11, D-48149 Münster (Germany).

Irving L. Weissman

Department of Pathology, Stanford University School of
Medicine B257, Stanford, CA. 94305-5428 (USA).

Timothy J. Williams

Division of Applied Pharmacology, Imperial College School
of Medicine at the National Heart & Lung Institute,
Dovehouse Street, London SW3 6LY (U.K.).

LIST OF PARTICIPANTS

Pedro Aparicio

Departamento de Bioquímica B e Inmunología, Facultad de Medicina, Universidad de Murcia, Campus de Espinardo, 30100 Murcia (Spain).

Alicia G. Arroyo

Howard Hughes Medical Institute, Center for Cancer Research and Department of Biology, Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA. 02139 (USA).

Carlos Cabañas

Departamento de Bioquímica, Facultad de Medicina, Universidad Complutense, Ciudad Universitaria, 28040 Madrid (Spain).

José M. Casasnovas

The Center for Blood Research and Harvard Medical School, 200 Longwood Avenue, Boston, MA. 02115 (USA).

Pablo Engel

Fundació Clínic per a la Recerca Biomèdica, Hospital Clínic i Provincial, c/Villarroel 170, 08036 Barcelona (Spain).

Britta Engelhardt

Max-Planck-Institut für Physiologische und Klinische Forschung, W.G. Kerckhoff-Institut, Abt. Molekulare Zellbiologie, 61231 Bad Nauheim (Germany).

Paul S. Frenette

The Center for Blood Research and Department of Pathology, Harvard Medical School, 800 Huntington Avenue, Boston, MA. 02115 (USA).

María García-Barcina

Departamento de Biología Celular y Ciencias Morfológicas, Facultad de Medicina y Odontología, Universidad del País Vasco, 48940 Leioa, Vizcaya (Spain)

Angeles García-Pardo

Centro de Investigaciones Biológicas, CSIC, c/ Velázquez 144, 28006 Madrid (Spain).

José Manuel Gasalla

Servicio Bioquímica Clínica, Hospital Virgen de la Salud,
Avda. Barber 30, 45005 Toledo (Spain).

Jean-Philippe Girard

Laboratoire de Biologie Moléculaire Eucaryote du CNRS
(LBME-CNRS), 118 route de Narbonne,
31062 Toulouse (France).

Guttorm Haraldsen

Institute of Pathology, University of Oslo, The National
Hospital, N-0027 Oslo (Norway).

Manel Juan

Servei Immunologia, Fundació Clínic, Hospital Clínic i
Provincial, c/Villarroya 170, 08036 Barcelona (Spain).

Yvette van Kooyk

Department of Tumor Immunology, University of Nijmegen,
Philips van Leydenlaan 25, 6525 EX Nijmegen
(The Netherlands).

Roy R. Lobb

Biological Research, Biogen Inc., 14 Cambridge Center,
Cambridge, MA.02142 (USA).

Margarita López Trascasa

Unidad de Inmunología, Hospital La Paz, Paseo de la
Castellana 261, 28046 Madrid (Spain).

Alfonso Luque

Departamento de Bioquímica, Facultad de Medicina,
Universidad Complutense, 28040 Madrid (Spain).

Reina E. Mebius

Department of Cell Biology and Immunology, Medical Faculty
Vrije Universiteit, van der Boechorststraat 7,
1081 BT Amsterdam (The Netherlands).

María C. Montoya

Servicio de Inmunología, Hospital Universitario de la
Princesa, UAM, c/ Diego de León 62, 28006 Madrid (Spain).

Pilar Navarro

Istituto di Ricerche Farmacologiche «Mario Negri»,
Via Eritrea 62, 20157 Milano (Italy).

Manuel Patarroyo

Microbiology and Tumor-Biology Center (MTC), Karolinska
Institute, S-171 77 Stockholm (Sweden).

Pilar Pizcueta

Fundació Clínic per a la Recerca Biomèdica, Hospital
Clínic i Provincial, c/ Villarroel 170,
08036 Barcelona (Spain).

Miguel A. del Pozo

Servicio de Inmunología, Hospital de la Princesa,
Universidad Autónoma, c/Diego de León 62,
28006 Madrid (Spain).

Juan Miguel Redondo

Servicio de Inmunología, Hospital de la Princesa,
Universidad Autónoma, c/ Diego de León 62,
28006 Madrid (Spain).

Marei Sammar

German Cancer Research Center, FSP 0710, Im Neunheimer
Feld 280, D-69120 Heidelberg (Germany).

Luis F. Santamaria Babi

Laboratorios Almirall, Centro de Investigación,
c/ Cardener 68-74, 08024 Barcelona (Spain).

María Jesús Sanz

Applied Pharmacology, National Heart & Lung Institute,
Imperial College of Science Technology and Medicine,
Dovehouse Street, London SW3 6LY (U.K.).

Dulce Soler

LeukoSite, Inc., 215 First Street,
Cambridge, Ma. 02142 (USA).

Joaquín Teixidó

Centro de Investigaciones Biológicas, Departamento de
Inmunología, c/ Velázquez 144, 28006 Madrid (Spain)

Jürgen Westermann

Zentrum Anatomie, Medizinische Hochschule Hannover,
Abteilung Funktionelle und Angewandte Anatomie,
D-30623 Hannover (Germany).

Cytokines in Infectious Diseases

Organized by
A. Sher, L. Rivas and M. Fresno
3rd-5th June, 1996

In recent years it has become clear that cytokines play an important role in controlling both the inductive and the effector arm of the immune response. Moreover, the host cytokines response is a key determinant of the outcome of infection-governing both host resistance and immunopathology. For this reason, prophylaxis or treatment with cytokines has emerged as an important strategy for immunologic intervention in many infectious diseases.

In addition, parasite infections provide paradigms for addressing some fundamental questions concerning the innate host response to infection. What parasite molecules stimulate cytokine production? What causes in some cases, the abnormally high cytokine production that lead to severe pathology? Is this genetically regulated? The study of cytokine function in infectious disease has been revolutionized by the advent of engineered mouse strains with genetic disruptions in cytokine and cytokine receptor genes. In addition to identifying cytokine requirements for host resistance and pathology, these animals have provided new insights into redundancies in the cytokine network itself. Such investigations have highlighted the important lessons learned from the infection disease models on the mechanism underlying the selective induction of different immune responses.

There are two main types of helper T (Th) cells according to cytokine secretion. Th1 cells produce IL-2, INF- γ , and TNF but not IL-4. By the contrary, Th2 cells preferentially secrete IL-4, but not no IFN- γ . Their polarized expression in different disease states frequently determines host resistance or susceptibility and it is strongly influenced by events triggered early in infection, involving innate recognition mechanisms. The early induction of IL-12 by APCs, which in turn trigger IFN- γ , is a key determinant of Th1 response induction while the initiation of Th2 responses depends on IL-4. Thus, the balance of IL-12 and IL-4 triggered early after pathogen invasion forms the basis of the subsequent selection of T cell subsets and their protective versus disease promoting influence on infection. In many diseases, such as Leishmaniasis, Toxoplasmosis, Tuberculosis, Th1 responses are protective whereas Th2 are detrimental. Others, as Chagas or Malaria have a more complex pattern.

Th cell polarization is a complicated process controlled by a number of factors including: the nature of the antigen and of the APCs, accessory molecules expressed on APCs that deliver different co-activation signals to T cells, cytokines produced early after exposure to a pathogenic agent or immunization with an antigen, etc. There is now growing evidence that cells other than APC, encountered by pathogens early after host entry, such as

neutrophils and epithelial cells are also capable of producing IL-12. Besides, CD4⁺NK1.1⁺ cells, and in the case of the *Leishmania* model, a subset of CD4⁺ cells with a limited TCR repertoire, have been implicated as sources of the IL-4 in addition to T and mast cells.

In addition to their role in initiating T cell subset differentiation, cytokines are crucial for maintaining and regulating adaptive immune responses. The lymphokines IL-2, IL-4, IFN- γ and the anti-inflammatory cytokines IL-10 and TGF- β are key players at this stage. An important effector mechanism involved in the control of many different infectious agents is the production of nitric oxide (NO). The synthesis of this toxic metabolite is induced by the action of the Th1 cytokines and regulated by both Th2 and anti-inflammatory cytokines.

Pathogens have also evolved complex strategies to ensure survival in an immunologically hostile host environment. Thus, many parasites have coevolved molecules that can alter the production of either immunoregulatory or effector cytokines, important to control the infection, by macrophages.

Although clearly important in both the establishment and maintenance of resistance, the cytokine response to infectious agents can also be host detrimental and has been described as a "double-edged sword". Most of the pro-inflammatory cytokines and lymphokines associated with the Th1 response (e.g. TNF- α , IL-12 and IFN- γ) are toxic when induced in an excessive or uncontrolled manner. Some of this toxicity results from the subsequent production of NO but also from more complex down-stream phenomena. Cytokine biology offers an important approach for understanding the pathogenesis of these disorders. Finally, as should be obvious, the exogenous manipulation of deleterious cytokine responses offers a potentially powerful strategy for preventing or treating infectious disease pathology.

Animal studies on a number of important infectious diseases have provided testable strategies for the use of cytokines in disease treatment as well as prevention. The further elucidation of the function role of cytokine regulation in human infection and the continued introduction into the clinic of novel cytokine based strategies for disease intervention remain important goals for this field. The Juan March Workshop has provided a forum to address some of those questions in detail and to exchange knowledge from different infectious diseases in this dynamic field.

Manuel Fresno, Alan Sher.

LIST OF INVITED SPEAKERS

Mario Clerici

Cattedra di Immunologia, Università degli Studi di Milano,
Facoltà di Medicina e Chirurgia, Istituto di Patologia
Generale, Via Venezian 1, 20133 Milano (Italy).

Mariano Esteban

Centro Nacional de Biotecnología, CSIC, Campus Universidad
Autónoma, Cantoblanco, 28049 Madrid (Spain).

Fred D. Finkelman

Department of Medicine, University of Cincinnati School of
Medicine, P.O. Box 670563,
Cincinnati, OH. 45267-0563 (USA).

Manuel Fresno

Centro de Biología Molecular "Severo Ochoa", CSIC, Campus
Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Manfred Kopf

Basel Institute for Immunology, Grenzacherstrasse 487,
CH-4005 Basel (Switzerland).

Dominic Kwiatkowski

University Department of Paediatrics, Institute of
Molecular Medicine, John Radcliffe Hospital,
Oxford OX3 9DU (U.K.).

Jean Langhorne

Department of Biology, Imperial College of Science,
Technology and Medicine, London SW7 2BB (U.K.).

F.Y. Liew

Department of Immunology, University of Glasgow, Western
Infirmary, Glasgow G11 6NT, Scotland (U.K.).

Richard M. Locksley

Department of Medicine, University of California San
Francisco, 521 Parnassus Ave.,
San Francisco, CA. 94143-0654 (USA).

Jacques A. Louis

WHO Immunology Research and Training Center, Institute of
Biochemistry, University of Lausanne, Chemin des
Boveresses 155, CH-1066 Epalinges-sur-Lausanne
(Switzerland).

Enrico Maggi

Clinical Immunology and Allergology Dept., Istituto di
Medicina Interna e Immunoallergologia, University of
Florence, Viale Morgagni 85, 50134 Firenze (Italy).

Carlos Martínez-A.

Departamento de Inmunología y Oncología, Centro Nacional
de Biotecnología, CSIC, Campus Universidad Autónoma,
Cantoblanco, 28049 Madrid (Spain).

Werner Müller

Institute for Genetics, University of Cologne,
Weyertal 121, D-50931 Köln (Germany).

Anders Örn

MTC, Box 280, Karolinska Institutet, Mikrobiologiskt och
Tumorbologiskt Centrum, S-171 77 Stockholm (Sweden).

Isabelle P. Oswald

Laboratoire associé INRA-ENVT de Physiopathologie et
Toxicologie Expérimentales, 23 chemin des Capelles,
31076 Toulouse, Cedex (France)

Luis Rivas

Centro de Investigaciones Biológicas, CSIC, Velázquez 144,
28006 Madrid (Spain).

Luigina Romani

Microbiology Section, Department Experimental Medicine and
Biochemical Sciences, University of Perugia,
Via del Giochetto, 06122 Perugia (Italy).

Phillip Scott

Department of Pathology, School of Veterinary Medicine,
University of Pennsylvania, 3800 Spruce Street,
Philadelphia, PA. 19104 (USA).

Alan Sher

Immunology Section, Laboratory of Parasitic Diseases,
NIAID, Bldg. 4, Room 126, Bethesda, MD. 20892 (USA).

Giorgio Trinchieri

The Wistar Institute, 3601 Spruce Street,
Philadelphia, PA. 19104 (USA).

LIST OF PARTICIPANTS

Antonio Alcamí

Sir William Dunn School of Pathology, University of
Oxford, South Parks Road, Oxford OX1 3RE (U.K.).

Juan Anguita

Department of International Medicine, Section of
Rheumatology, LCI 610, Yale University, 333 Cedar St.,
New Haven, CT. 06520-8031 (USA).

Amedeo Capetti

Ospedale Luigi Sacco, 1ª Divisione di Malattie Infettive e
Servizio di Allergologia, Via G.B. Grassi 74,
20157 Milano (Italy).

Ricardo Corral

Laboratorio de Virología, Hospital de Niños "Dr. R.
Gutiérrez", Gallo 1330, 1425 Buenos Aires (Argentina).

Juana Luisa de Diego

Centro de Biología Molecular "Severo Ochoa", CSIC,
Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Jacques Dornand

INSERM U-431, Université de Montpellier II, Place E.
Bataillon, Case courrier 100, F-34095 Montpellier,
Cedex 05 (France).

Enric Espel

Departamento de Fisiología, Facultad de Biología,
Universidad de Barcelona, Diagonal 645,
08028 Barcelona (Spain).

Angel Ezquerro

CISA-INIA, 28130 Valdeolmos, Madrid (Spain).

Ramón Gimeno

Departamento de Inmunología, Hospital de la Santa Creu i
Sant Pau, Avda. Pare Claret 167, 08025 Barcelona (Spain).

Manuel Gómez del Moral

CISA - INIA, Departamento de Sanidad Animal, 28130
Valdeolmos, Madrid (Spain).

Rosa María Gonzalo

Centro Nacional de Biotecnología, CSIC, Campus Universidad
Autónoma, Cantoblanco, 28049 Madrid (Spain).

Stephanie James

National Institute of Allergy and Infectious Diseases,
Division of Microbiology and Infectious Diseases, 6003
Executive Blvd. Room 3A-10, Rockville, MD. 20852 (USA).

Peter Kima

Department of Epidemiology and Public Health, Yale
University School of Medicine, 60 College Street,
New Haven, CT. 06520-8034 (USA).

Tominori Kimura

Department of Microbiology, Kansai Medical University,
Moriguchi, Osaka 570 (Japan).

Enrique Lara

Unidad de Biología Molecular, Hospital de la Princesa,
Universidad Autónoma, Diego de León 62,
28006 Madrid (Spain).

Pascal Launois

WHO-IRTC, Institute of Biochemistry, University of
Lausanne, 155 Chemin des Boveresses,
1066 Epalinges (Switzerland).

Franziska Lechner

Institute of Veterinary Virology, University of Bern,
Laenggass-Str. 122, 3012 Bern (Switzerland).

Rudolf Lucas

Laboratory of Immunopathology, Department of
Anaesthesiology, Pharmacology and Surgical Intensive Care,
University of Geneva, 1 rue Michel-Servet,
Ch-1211 Genève 4 (Switzerland).

José A. Melero

Centro Nacional de Biología Celular y Retrovirus,
Instituto de Salud Carlos III, Ctra. de Majadahonda-
Pozuelo Km. 2, 28220 Majadahonda, Madrid (Spain).

Francisco Javier Moreno

Centro Nacional de Microbiología, Instituto de Salud
Carlos III, Servicio de Parasitología,
Ctra. de Majadahonda-Pozuelo Km. 2,
28220 Majadahonda, Madrid (Spain).

M^a Angeles Muñoz-Fernández

Servicio de Inmunología, Hospital General Universitario
"Gregorio Marañón", Doctor Esquerdo 46,
28007 Madrid (Spain).

Shreemanta K. Parida

Institute for Medical Microbiology & Infection Immunology,
Justus-Liebig University, Frankfurterstrasse 107, D-35392
Giessen (Germany).

M. Dora Pascual-Salcedo

Inmunología, Hospital La Paz, Paseo de la Castellana 261,
28046 Madrid (Spain).

Patricia B. Petray

Laboratorio de Virología, Hospital de Niños "Dr. R.
Gutiérrez", Gallo 1330, 1425 Buenos Aires (Argentina).

Marian Rocha

Division of Cellular Immunology, German Cancer Research
Center, Im Neuenheimer Feld 280,
D-69120 Heidelberg (Germany).

Elizabeth A. Sabin

Department of Microbiology and Immunology, Cornell
University, College of Veterinary Medicine,
Ithaca, NY. 14853-6401 (USA).

George Thyphronitis

CIBP-INSERM U167, Institut Pasteur, 1 Rue du Prof.
Calmette, 59019 Lille (France).

Irina Udalova

Department of Paediatrics, IMM, John Radcliffe Hospital,
University of Oxford, Oxford OX3 9DU (U.K.).

Marta Velasco

Instituto de Bioquímica, CSIC, Facultad de Farmacia,
Universidad Complutense, 28040 Madrid (Spain).

Ramón Vilella

Servei d'Immunologia, Hospital Clínic i Provincial,
c/Villarreal 170, 08036 Barcelona (Spain).

Molecular Biology of Skin and Skin Diseases

Organized by
D. R. Roop and J. L. Jorcano
17th-19th June, 1996

The skin is the largest organ of the human body. Its importance is well known as a protective barrier against the aggression of many external agents, physical, chemical and biological (bacteria, fungus, virus, etc.). Nonetheless, attention to and research on this tissue have long been scarce, even though dermatological diseases affect a large number of patients (for instance, psoriasis, chronic ulcers and cutaneous tumors are high-incidence diseases in industrialized countries).

In recent years, this situation has changed. Recognition that the epidermis forms a complex, interesting and highly-ordered system in which the processes of proliferation, differentiation and cell death can be studied has attracted the attention of a growing number of investigators. In a spectacular race against the clock, the molecular basis of several skin diseases has been described and significant progress has been made in understanding the mechanisms controlling proliferation and differentiation in this tissue, as well as in the identification of the factors that intervene in these processes. Due to the barrier function of the skin, special attention should be given to the advances in cytoskeletal organization and its role in the maintenance of epithelial structure and function, and in particular to the keratins and to the molecules and structures of cell adhesion (desmosomes and hemidesmosomes, integrins, cadherins, etc.).

The external corporal localization of the skin and the identification of those sequences that direct gene activity in this tissue have made the use of transgenic animals a flexible and widely-used technique which permits the acquisition of important information *in vivo*. The skin has thus become one of the tissues on which more research is being done and more progress is being made.

From the clinical point of view, three novel characteristics have attracted considerable attention to this tissue:

- 1) The finding that the skin produces interleukins and other cytokines of enormous importance in the infectious and inflammatory processes of this tissue. Given the large area of the skin, it is hypothesized that these epidermal cytokines, after passing to the circulation, may also play a very important systemic role.
- 2) At present, the skin is the organ with the highest incidence of tumors, and this frequency continues to increase. There is evidence that many of these tumors are caused by increased exposure of the skin to ultraviolet radiation, due as much to the deteriorating ozone layer as to reigning esthetic fashions. Skin carcinogenesis is an area in which considerable work is being done.

3) *In vitro* culture and expansion of human keratinocytes are recently-developed methods of great relevance, both in patients with major cutaneous lesions (such as, for example, those with burns covering a large body area, insuperable until this new technique was introduced) and in the treatment of ulcers which do not respond to classical therapies. In addition, however, accumulated experience and the relative ease of *in vitro* culture of epidermal keratinocytes and their subsequent transplant in patients make the epidermis an ideal tissue for the development of gene therapy protocols, for both hereditary and tumoral diseases. Recent advances in the identification and isolation of epidermal stem cells are particularly relevant in this context, as is the development of methods which permit the stable or transitory expression of therapeutic genes in keratinocytes.

These subjects were addressed in depth and actively discussed in the present Workshop.

D.R. Roop and J.L. Jorcano.

LIST OF INVITED SPEAKERS

Rosemary J. Akhurst

Department of Medical Genetics, Glasgow University,
Yorkhill Hospitals, Glasgow G3 8SJ (U.K.).

John C. Ansel

Emory University School of Medicine, Department of
Dermatology, 5311 Woodruff Memorial Bldg.
Atlanta, GA. 30322 (USA).

Yann Barrandon

Department of Biology, Ecole Normale Supérieure,
46 rue d'Ulm, 75230 Paris (France).

Paul Basset

IGBMC, CNRS / INSERM / ULP, B.P. 163,
67404 Illkirch (France).

Robert E. Burgeson

The Department of Dermatology, Harvard Medical School, and
the Cutaneous Biology Research Center, Massachusetts
General Hospital, Boston, MA. (USA).

Andrzej A. Dlugosz

LTVB/NCI/NIH, Bldg. 41/Rm C111,
Bethesda, MD. 20892-5055 (USA).

Mark W.J. Ferguson

School of Biological Sciences, University of Manchester,
3.239 Stopford Building, Oxford Road,
Manchester, M13 9PT. (U.K.).

Wendy L. Havran

Department of Immunology, IMM-8, The Scripps Research
Institute, 10666 North Torrey Pines Road,
La Jolla, CA. 92037 (USA).

D. Hohl

Dermatology, CHUV, Beaumont, CH-1011 Lausanne
(Switzerland).

José Luis Jorcano

CIEMAT, Unidad de Biología Molecular y Celular, IMA,
Avenida Complutense 22, 28040 Madrid (Spain).

Thomas S. Kupper

Harvard Skin Disease Research Center, Brigham and Women's
Hospital, 75 Francis Street, Boston, MA. 02115 (USA).

E. Birgitte Lane

CRC Cell Structure Research Group, Department of Anatomy & Physiology, Medical Sciences Institute, University of Dundee, Dundee DD1 4HN, Scotland (U.K.).

Dennis R. Roop

Baylor College of Medicine, Department of Cell Biology, One Baylor Plaza, Houston, TX. 77030-3498 (USA).

Arnoud Sonnenberg

Division of Cell Biology, The Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam and Department of Dermatology, University Groningen, Groningen (The Netherlands).

Tung-Tien Sun

Ronald Perelman Department of Dermatology and Department of Pharmacology, New York University Medical School, 550 First Avenue, New York, NY. 10016 (USA).

Jouni Uitto

Departments of Dermatology and Cutaneous Biology, and Biochemistry and Molecular Biology, Jefferson Medical College, Philadelphia, PA. 19107-5541 (USA).

Fiona M. Watt

Imperial Cancer Research Fund, 44 Lincoln's Inn Fields, London WC2A 3PX (U.K.)

Sabine Werner

Max-Planck-Institut für Biochemie, Am Klopferspitz 18a, 82152 Martinsried (Germany).

Stuart H. Yuspa

Laboratory of Cellular Carcinogenesis and Tumor Promotion, National Cancer Institute, 37 Convent Drive MSC 4255, Bethesda, MD. 20892-4255 (USA).

LIST OF PARTICIPANTS

Rhoda M. Alani

Harvard Medical School, Department of Pathology,
200 Longwood Avenue, Bldg. B2 - Room 113,
Boston, MA. 02115 (USA)

Pedro Aparicio

Department of Biochemistry and Molecular Biology, School
of Medicine, University of Murcia, 30100 Murcia (Spain).

Claudia Bagutti

Imperial Cancer Research Fund, Room 602, 44 Lincoln's Inn
Fields, London, WC2A 3PX (U.K.).

Miroslav Blumenberg

NYU Medical Center, The Ronald O. Perelman Department of
Dermatology, 550 First Avenue, New York, NY. 10016 (USA).

Dirk Breitkreutz

Division 0240, German Cancer Research Center, (DKFZ),
Heidelberg (Germany).

Joseph M. Carroll

Keratinocyte Laboratory, Imperial Cancer Research Fund, PO
Box 123, 44 Lincoln's Inn Fields, London WC2A 3PX (U.K.).

M^a de los Llanos Casanova

CIEMAT, Departamento de Biología Molecular y Celular,
Edif. 7, Avda. Complutense 22, 28040 Madrid (Spain).

John Compton

Laboratory of Skin Biology Genetic Studies Section, NIAMS,
NIH, Building 6, Room 429, 6 Center Dr. MSC 2757,
Bethesda, MD. 20892- 2757 (USA).

Claudio J. Conti

The University of Texas, M.D. Anderson Cancer Center,
Dept. of Carcinogenesis, Science Park, PO Box 389,
Smithville, TX. 78957 (USA).

Philippe Djian

CEREMOD, CNRS, 9 rue Jules Hetzel, 92190 Meudon-Bellevue
(France).

Pilar Frontelo
Instituto de Investigaciones Biomédicas del CSIC, Arturo
Duperier 4, 28029 Madrid (Spain).

Alberto Gandarillas
Imperial Cancer Research Fund, Keratinocyte Laboratory,
44 Lincoln's Inn Fields, P.O. Box 123,
London WC2A 3PX (U.K.).

Griseldis Hübner
Max Planck-Institut für Biochemie, Am Klopferspitz 18a,
82152 Martinsried (Germany).

Saewha Jeon
Department of Cell Biology, Harvard Medical School,
240 Longwood Ave, Boston, MA. 02115 (USA).

Sibylle Kaiser
Boehringer Ingelheim Research Group, SFB-311, I. Medical
Department, Johannes Gutenberg-University, Obere
Zahlbacher Str. 63, D-55131 Mainz (Germany).

Fernando Larcher
Cell and Molecular Biology Department, IMA, CIEMAT,
22 Complutense Avenue, 28040 Madrid (Spain).

Michele de Luca
IDI, Istituto Dermopatico dell'Immacolata, Via dei
Castelli Romani 83/85, 00040 Pomezia, Roma (Italy).

Guerrino Meneguzzi
INSERM U385, Faculté de Médecine, Ave de Valombrose,
06107 Nice (France).

Rebecca J. Morris
Lankenau Medical Research Center, 100 Lancaster Avenue
West of City Line, Wynnewood, PA. 19096 (USA).

Rodolfo Murillas
Departamento de Biología Molecular y Celular, CIEMAT,
Avda. Complutense 22, 28040 Madrid (Spain).

Jesús M. Paramio
Department of Cell and Molecular Biology, CIEMAT, 22
Complutense Avenue, 28040 Madrid (Spain).

Esther Pascual

Unidad de Farmacocinética Clínica, Hospital del Aire,
Madrid (Spain).

Graziella Pellegrini

IDI, Istituto Dermopatico dell'Immacolata, Via dei
Castelli Romani 83/85, 00040 Pomezia, Roma (Italy).

Susana Puig

Institut de Recerca Oncològica, Hospital Duran i Reynals,
Avia. Castelldefels Km 2.7, 08907 L'Hospitalet de
Llobregat, Barcelona (Spain).

Miguel Quintanilla

Instituto de Investigaciones Biomédicas, CSIC, Arturo
Duperier 4, 28029 Madrid (Spain).

Angel Ramírez

Departamento de Biología Molecular y Celular, CIEMAT,
Avda. Complutense 22, 28040 Madrid (Spain).

Julia Reichelt

Rheinische Friedrich-Wilhelms-Universität, Institut für
Genetik, Abt. Molekulargenetik, D-53117 Bonn (Germany).

Luis Ríos

Servicio de Dermatología, Hospital de la Princesa,
Diego de León 62, 28006 Madrid (Spain).

M. Rosario Romero

Keratinocyte Laboratory, Imperial Cancer Research Fund, PO
Box 123, 44 Lincoln's Inn Fields, London WC2A 3PX (U.K.).

Marcia Simon

University Hospital, Department of Oral Biology and
Pathology, and Department of Dermatology, SUNY,
Stony Brook, NY. 11794-8702 (USA).

Programmed Cell Death in the Developing Nervous System

Organized by

R. W. Oppenheim, E. M. Johnson and J. X. Comella

1st-3rd July, 1996

Although the existence of a large scale loss of cells during development has long been recognized, it is only in the last twenty years that the significance of programmed, naturally occurring cell death has been appreciated. Because, with the possible exception of the immune system, the programmed cell death of developing neurons has been studied longer and more extensively than that of any other cell type, it is perhaps not surprising that knowledge about the normal biology of cell death in the nervous system is also more complete. However, even in the nervous system our understanding of many aspects of cell death is still fragmentary. Although many aspects of cell death in the nervous system (especially molecular pathways) appear to be similar to that of cell death outside of the nervous system, there are also important differences that make neuronal cell death novel and unique. For example, control of cell death of neurons often involves interactions between neurons and interconnecting populations of synaptic targets and afferents that are absent in other cell types undergoing cell death. Another difference is that physiological activity, including synaptic transmission, plays a role in the regulation of cell death in the nervous system, whereas similar signals are probably not involved outside of the nervous system. Collectively, it is these unique and shared properties of cell death in nervous and non-nervous tissue that provided a major rationale for the first workshop on *Programmed Cell Death in the Developing Nervous System* held at the Juan March Foundation in Madrid. Because of similarities between cell death in nervous and other tissues, the information discussed at the meeting will be of interest to a wide spectrum of investigators in the cell death field. By focusing the meeting on the developing nervous system, however, it was assured that the many unique aspects of neuronal and glial cell death were the major topic of discussion.

The participants at the workshop represented an international group of prominent investigators with diverse interests, backgrounds, research strategies, animal models and viewpoints. Because of this diversity it was possible to address virtually all of the important issues in the field. These included the following topics: What is the biological significance of cell death in the nervous system and does this differ for cell types, brain regions and species; What role do targets and afferents play in the regulation of cell death and does this differ between vertebrates and invertebrates; What are the similarities and differences between cell death of neurons and glia; What neurotrophic agents and growth factors (and receptors) regulate survival in the nervous system and how do these act at the biochemical and molecular levels to promote survival; How are other cell-cell signals such as activity and hormones involved in regulating death and survival; What are the biochemical/molecular pathways that result in cellular degeneration and do these differ for different cells, brain regions and species; What genes are involved in mediating death and survival in the nervous system and how are these similar or different across species.

Although consensus was reached on our present understanding of many of these issues, for others there were differences of opinion and a general agreement that more information is needed for a final resolution. Despite the lingering differences of opinion on some key issues, however, all of the participants felt that the meeting was a great success in assessing the present state of knowledge in the field and in identifying the critical important issues that remain for future investigations. The organizers and participants would like to thank Andrés González and the staff of the Juan March Foundation for their hard work, generosity and perception in supporting this timely inaugural meeting on *Programmed Cell Death in the Developing Nervous System*.

R.W. Oppenheim, E.M. Johnson and J.X. Comella

LIST OF INVITED SPEAKERS

Barbara A. Barres

Stanford University School of Medicine, Department of
Neurobiology, Sherman Fairchild Science Building,
Stanford, CA. 94305-5401 (USA).

Dale E. Bredesen

Program on Aging, La Jolla Cancer Research Foundation,
10901 N. Torrey Pines Road, La Jolla, CA. 92037 (USA).

Peter G.H. Clarke

Institute of Anatomy, University of Lausanne,
Rue du Bugnon 9, 1005 Lausanne (Switzerland).

Joan X. Comella

Unit of Molecular Neurobiology, Departament de Ciències
Mèdiques Bàsiques, Universitat de Lleida,
Av. Rovira Roure, 44, E-25198 Lleida (Spain).

Alun M. Davies

Bute Building, University of St. Andrews, St. Andrews,
Fife KY16 9TS, Scotland (U.K.).

Monica Driscoll

Department of Molecular Biology and Biochemistry, Center
for Advanced Biotechnology and Medicine, Rutgers
University, Piscataway, NJ. 08855 (USA).

Lloyd A. Greene

Department of Pathology, Columbia University College of
Physicians and Surgeons, 630 W. 168th Street,
New York, NY. 10032 (USA).

Christopher E. Henderson

INSERM U.382, IBDM, Campus de Luminy - Case 907,
13288 Marseille Cedex 09 (France)

H. Robert Horvitz

Howard Hughes Medical Institute, Department of Biology,
MIT, 77 Massachusetts Avenue, Cambridge, MA. 02139 (USA).

Michael D. Jacobson

MRC Laboratory for Molecular Cell Biology and Department
of Biology, University College London, Gower St.
London WC1E 6BT (U.K.).

Eugene M. Johnson

Departments of Neurology and Molecular Biology and
Pharmacology, Washington University Medical School,
St. Louis, MO. 63110 (USA).

José R. Naranjo

Cajal Institute, C.S.I.C., Av. Dr. Arce 37,
28002 Madrid (Spain).

Ernie J. Nordeen

Department of Brain and Cognitive Sciences, University of
Rochester, Meliora Hall, Rochester, NY. 14627 (USA).

Ronald W. Oppenheim

Department of Neurobiology and Anatomy and the
Neurosciences Program, Bowman Gray School of Medicine of
Wake Forest University, Winston-Salem, NC. 27157 (USA).

Edwin W. Rubel

Virginia Merrill Bloedell Hearing Research Center,
University of Washington, Box 357923,
Seattle, WA. 98195 (USA).

Aviva M. Tolkovsky

Department of Biochemistry, University of Cambridge,
Tennis Court Road, Cambridge (U.K.)

James W. Truman

Department of Zoology, University of Washington,
Box 351800, Seattle, WA. 98195 (USA).

Kristin White

Cutaneous Biology Research Center, Massachusetts General
Hospital, Charlestown, MA. 02129 (USA).

LIST OF PARTICIPANTS

Mimoun Azzouz

Département d'Immunologie, Immunopharmacologie et Pathologie, Centre de Recherches Pharmaceutiques, BP 24, 74 Route du Rhin, F-67401 Illkirch, Cedex (France).

Tiziana Borsello

Istituto di Neurobiologia CNR, Viale Marx 15. Roma (Italy).

Michael J. Burek

Department of Neurobiology and Anatomy, Bowman Gray School of Medicine, Winston-Salem, NC. 27157 (USA).

Jordi Calderó

Unitat de Neurobiologia Cel.lular, Departament de Ciències Mèdiques Bàsiques, Facultat de Medicina, Universitat de Lleida, Av. Rovira Roure 44, 25198 Lleida, Catalonia (Spain).

Pilar Cazorla

Departamento de Biología Molecular, Centro de Biología Molecular "Severo Ochoa" Facultad de Ciencias, Universidad Autónoma, 28049 Madrid (Spain).

Valentín Ceña

Departamento de Farmacología y Terapéutica, Facultad de Medicina, Universidad de Alicante, Apdo. 374, 03080 Alicante (Spain).

Miguel A. Cuadros

Departamento de Biología Celular, Facultad de Ciencias, Universidad de Granada, 18071 Granada (Spain).

Javier Díaz-Nido

Departamento de Biología Molecular CX-470, Centro de Biología Molecular "Severo Ochoa", Facultad de Ciencias, Universidad Autónoma, 28049 Madrid (Spain).

Josep E. Esquerda

Universitat de Lleida, Dpt. Ciències Mèdiques Bàsiques, Unitat de Neurobiologia Cel.lular, Avda. Rovira Roure 44, 25198 Lleida (Spain).

Isidro Ferrer

Unidad de Neuropatología, Servicio de Anatomía Patológica, Hospital Príncipes de España, Universidad de Barcelona, Feixa Llarga s/nº, 08907 Hospitalet de Llobregat (Spain).

José María Frade

Department of Neurobiochemistry, Max-Planck Institut für
Psychiatrie, Am. Klopferspitz 18a,
D-82152 Martinsried (Germany).

Christian Gaiddon

CNRS URA 1446, IPCB, 21 rue R. Descartes,
67084 Strasbourg, Cedex (France).

Frank Gillardon

Physiologisches Institut, Universität Heidelberg, Im
Neuenheimer Feld 326, D-69120 Heidelberg (Germany).

Michal Hetman

Nencki Institute of Experimental Biology, Tissue Culture
Unit, Pasteura 3, 02-093 Warsaw (Poland).

Joaquín Jordán

Department of Pharmacological and Physiological Sciences,
University of Chicago, 947 East 58th Street,
Chicago, IL. 60637 (USA).

Susan Koester

Neuron, Editorial Offices, 1050 Massachusetts Avenue,
Cambridge, MA.02138 (USA).

Enca Martín-Rendón

Department of Biochemistry, University of Oxford,
South Parks Road, Oxford OX1 3QU (U.K.).

Dionisio Martín-Zanca

Instituto de Microbiología Bioquímica, CSIC, Dpt. de
Microbiología y Genética, Universidad de Salamanca,
Avda. del Campo Charro s/n, 37007 Salamanca (Spain).

Theologos Michaelidis

Department of Neurochemistry, Max-Planck-Institute for
Psychiatry, 8033 Planegg-Martinsried (Germany).

Aixa V. Morales

Department of Cellular and Developmental Biology, Centro
de Investigaciones Biológicas, CSIC, Velázquez 144, E
28006 Madrid (Spain).

Flora de Pablo

Department of Cellular and Developmental Biology, Centro
de Investigaciones Biológicas, CSIC, Velázquez 144,
28006 Madrid (Spain).

Luzia G. P. Pinon

School of Biological and Medical Science, Bute Medical
Buildings, University of St. Andrews,
Fife KY16 9AT, Scotland (U.K.).

Grisha Pirianov

National Centre of Oncology, Medical Academy Bulgaria,
Department of Anticarcinogenesis, 6 Plovdivsko pole
Street, 1756 Sofia (Bulgaria).

Anna M. Planas

Department of Pharmacology & Toxicology, Instituto de
Investigaciones Biomédicas de Barcelona, CSIC, Jordi
Girona 18-26, 08034 Barcelona (Spain).

Alberto Portera

Servicio de Neurología, Hospital Universitario «12 de
Octubre», Ctra. de Andalucía Km. 5,4, 28041 Madrid (Spain).

Diego Pulido

Centro de Biología Molecular «Severo Ochoa», CSIC-UAM,
Cantoblanco, 28049 Madrid (Spain).

Angeles Rodríguez-Peña

Instituto de Investigaciones Biomédicas, CSIC,
Arturo Duperier 8, 28029 Madrid (Spain).

Remy Sadoul

Glaxo Institute for Molecular Biology, 14 chemin des Aulx,
1228 Plan-Les-Ouates, Genève (Switzerland).

Leonidas Stefanis

Department of Pathology, College of Physicians & Surgeons
of Columbia University, 630 West 168th Street,
New York, NY. 10032 (USA).

Montserrat Vendrell

Departamento de Farmacología y Toxicología, Instituto de
Investigaciones Biomédicas de Barcelona,
Jordi Girona 18-26, 08034 Barcelona (Spain).

Zhengui Xia

Division of Neuroscience, Children's Hospital, John F.
Enders-2, Rm 250, 300 Longwood Ave.,
Boston, MA. 02115 (USA).

Daniel Zamanillo

ZMBH, Universität Heidelberg, Im Neuenheimer Feld 282,
69120 Heidelberg (Germany).

**NF- κ B/I κ B Proteins. Their Role in Cell Growth,
Differentiation and Development**

Organized by
R. Bravo and P. S. Lazo
8th-10th July, 1996

Ten years ago the first paper reporting the existence of a kappa immunoglobulin enhancer binding protein was published and called NF- κ B. This binding function presented a stage specific pattern of activation in B cells which led to a model that included an inhibitory protein (I κ B) which could retain NF- κ B in the cytoplasm. Upon activation of the cell, the inhibitor would be inactivated and NF- κ B translocated to the nucleus to activate gene transcription.

Since then, NF- κ B has been found to be an ubiquitous transcription factor composed of dimers and several homologous proteins have been identified, e.g., p50, p52, c-Rel, RelB, RelA (p65). The term Rel/NF- κ B now refers to a family of closely related dimeric complexes which are able to regulate specific gene transcription. In the last six years, emphasis has been placed on isolating and cloning the various members of the Rel/NF- κ B family, characterizing their structure and their interaction with DNA.

The family of inhibitory proteins, which includes the proto-oncogene Bcl-3, has also been the subject of active research as well as the study of the mechanisms by which different activators trigger NF- κ B activation. It is now clear that phosphorylation and ubiquitin mediated proteolysis are implicated in the mechanism of activation of NF- κ B. However, it remains unclear which kinases and proteases are responsible for these processes.

The important role of NF- κ B/I κ B proteins in growth regulation and differentiation can be deduced from their involvement in the transcriptional activation by growth factors, the oncogenic activities of some of the family members, and their activation by mitogens. However, the role of each individual protein has not been clearly established probably because of the ability of NF- κ B proteins to substitute for each other in the heterodimeric complexes.

The workshop dealt with the most recent advances in this active field of research, from the molecular level to the most complex biological models. Thus, it was discussed the characterization of the molecular interaction between DNA and NF- κ B proteins using crystallography data as well as biochemical studies on the interaction of the different NF- κ B proteins and their inhibitors, including the new inhibitor I κ B ϵ .

From the data presented at the workshop, it is apparent that signal transduction from the cell membrane to NF- κ B is rather complex, with different pathways being implicated.

It also appears that different kinases may be involved in the phosphorylation of I κ B proteins and that these inhibitory proteins play different roles in the activation process of NF- κ B.

Michael J. Lenardo

Laboratory of Immunology, National Institute of Allergy
and Infectious Diseases, NIH, 9000 Rockville Pike,
10/11N311, Bethesda, MD. 20892-1892 (USA).

Nancy Rice

ABL-Basic Research Program, NCI-Frederick Cancer Research
and Development Center, Frederick, MA. 21702-1201 (USA).

Pedro S. Lazo

Departamento de Bioquímica y Biología Molecular, Facultad
de Medicina, Universidad de Oviedo, 33071 Oviedo (Spain).

Claus Scheidereit

Max-Delbrück Center for Molecular Medicine, MDC,
Robert Rössle Strasse 10, 13122 Berlin (Germany).

Ulrich Siebenlist

NIH, Section on Immune Activation, Bldg. 10,
Room 11B16, Bethesda, MD. 20892-1876 (USA).

Paul B. Sigler

Howard Hughes Medical Institute, Department of Molecular
Biophysics & Biochemistry, Yale University, 260 Whitney
Ave. / JWG 423, P.O. Box 208114, New Haven, CT. 06520-8114
(USA).

Ruth Steward

The Waksman Institute, Department of Molecular Biology and
Biochemistry, Rutgers University, P.O. Box 759,
Piscataway, NJ. 08855-0759 (USA).

Inder M. Verma

The Salk Institute, Laboratory of Genetics,
P.O. Box 85800, La Jolla, CA. 92186 (USA).

Steven A. Wasserman

The University of Texas, Southwestern Medical Center,
Department of Biochemistry, 5323 Harry Hines Boulevard,
Dallas, TX. 75235-9038 (USA).

Thomas Wirth

Zentrum für Molekulare Biologie, Universität Heidelberg,
Im Neuenheimer Feld 282, 69120 Heidelberg (Germany).

LIST OF PARTICIPANTS

José Alcamí

Servicio de Microbiología, Centro de Investigación,
Hospital 12 de Octubre, Ctra. de Andalucía Km. 5.400,
28041 Madrid (Spain).

Vincent Bours

Departments of Medical Oncology and Medical Chemistry,
University of Liège, 4000 Liège (Belgium).

Jorge H. Caamaño

Bristol-Myers Squibb Pharmaceutical Research Institute,
Department of Oncology, PO Box 4000,
Princeton, NJ 08543-4000 (USA).

Haini Cai

Department of Biology, Pacific Hall, UCSD, 9500 Gilman
Drive, La Jolla, CA. 92093 (USA).

Anatoly Dritschilo

Georgetown University Medical Center, Department of
Radiation Medicine, 3800 Reservoir Road,
NW Washington, DC. 20007-2197 (USA).

Enric Espel

Laboratorio de Inmunología, Departamento de Fisiología,
Facultad de Biología, Universidad de Barcelona,
Diagonal 645, 08028 Barcelona (Spain).

Manuel Fresno

Centro de Biología Molecular «Severo Ochoa», CSIC,
Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Steve Gerondakis

The Walter and Eliza Hall Institute of Medical Research,
P.O. Box, The Royal Melbourne Hospital, Parkville,
Victoria 3050 (Australia).

Christelle Huguet

Laboratoire d'Oncologie Moléculaire, CNRS, URA 1160,
Institut Pasteur de Lille, 1 rue Calmette,
59019 Lille Cedex (France).

Chromosome Behaviour: The Structure and Function of Telomeres and Centromeres

Organized by
**B. J. Trask, C. Tyler-Smith, F. Azorín
and A. Villasante.**

23rd-25th September, 1996

As previously mentioned, results presented focused on several organisms including ciliated protozoa and *Drosophila*. Most eukaryotic telomeres are made by G-rich repeats which are generated by telomerase. A contrast is represented by *Drosophila*, where telomeres do not have those simple repeats; instead telomere-specific transposable elements are found. Data on telomerase-independent mechanisms for telomere maintenance in *Drosophila* were presented.

Interest was shown not only on the very end of chromosomes, but also on several structural and functional aspects of the subtelomeric regions. Results presented at the meeting indicate that DNA near end of human chromosomes has large blocks of duplicated material and is highly polymorphic. Furthermore, the large-scale polymorphic duplications can contain genes, such as members of the olfactory receptor gene family.

Unlike telomeres, where functional sequences are well conserved, the repeated sequences found at many centromeres vary widely between species. The identity of the functional sequence has been well characterized only in yeast.

There has been debate about whether the small centromere of *S. cerevisiae* provides a model for the larger centromeres of most other organisms: are *cerevisiae*-like "magic sequences" embedded in the centromeric repeats of other organisms?. In his summary of the meeting, John Carbon identified the demise of the "magic sequence" hypothesis as one of its major conclusions. New evidence presented at the workshop suggested that repeated sequences alone are sufficient to form the centromeres of multicellular eukaryotes.

Schizosaccharomyces pombe can be seen as providing a model for the centromeric DNA of higher eukaryotes, and the identification of the *S. pombe* centromere binding protein Abp1 with extensive homology to the mammalian centromere protein CENP-B allows the model to be extended to include proteins as well. The centromeric DNA of a *Drosophila* minichromosome has now been characterised: only satellite DNAs and transposons were found. None of these sequences were detected at all other *Drosophila* centromeres and each sequence had non-centromeric locations. These findings, together with the observation that deleted minichromosomes lacking the centromeric DNA can show surprising stability, led to the thought-provoking suggestion that there may be nothing at all special about the centromeric DNA: perhaps, after suitable epigenetic activation, any sequence whatsoever can show centromeric activity.

The relevance of some structural features of *Drosophila* centromeric satellites and the functions of specific proteins that interact with mammalian centromeres were also discussed. Workers on mammalian chromosomes have been trying for years to emulate the success of those working with yeast, and create mammalian artificial chromosomes starting

from DNA elements. The first reports of success from this approach provided some of the highlights of the meeting. Evidence is mounting that alphoid satellite DNA introduced into a cell may be sufficient to form a human centromere. Although more work is still required, the techniques are now at hand to create functioning human minichromosomes. Chromosome based vectors will allow the cis-acting DNA requirements for mammalian chromosome function to be rigorously defined. Furthermore, synthetic chromosomes could be extremely useful tools in the field of gene therapy.

In conclusion, findings reported at the workshop provided new insights into this dynamic field, giving a stimulating overview on the structure and function of two essential chromosomal structures. Undoubtedly, detailed function and structure may vary considerably from system to system; however, the workshop provided a wonderful opportunity to learn and to reflect about the possible links of chromosome behaviour among species, from yeast to human.

LIST OF INVITED SPEAKERS

Fernando Azorín

Centre d'Investigació i Desenvolupament, Departament de
Biologia Molecular i Cel·lular, CSIC, Jordi Girona 18-26,
08034 Barcelona (Spain).

William R.A. Brown

Biochemistry Department, CRC Chromosome Molecular Biology
Group, Oxford University, Oxford OX1 3QU (U.K.)

John Carbon

Department of Molecular, Cellular and Developmental
Biology, University of California,
Santa Barbara, CA. 93106-9610 (USA).

Louise Clarke

Department of Molecular, Cellular and Developmental
Biology, University of California,
Santa Barbara, CA. 93106-9610. (USA).

Howard Cooke

Western General Hospital, MRC Human Genetics Unit,
Crewe Road, Edinburgh EH4 2XU (U.K.).

Olga N. Danilevskaya

Department of Biology, Massachusetts Institute of
Technology, 77 Massachusetts Avenue,
Cambridge, MA. 02139-4307 (USA).

Susan M. Gasser

Swiss Institute for Experimental Cancer Research, ISREC,
155 chemin des Boveresses, CH-1066 Epalinges/ Lausanne
(Switzerland).

Clare Huxley

Department of Biochemistry and Molecular Genetics,
Imperial College School of Medicine at St. Mary's, London
W2 1PG (U.K.).

Gary Karpen

The Salk Institute, (MBVL), 10010 North Torrey Pines Road,
La Jolla, CA. 92037 (USA).

David M.J. Lilley

CRC Nucleic Acid Structure Research Group, Biochemistry
Department, University of Dundee, Dundee DD1 4HN (U.K.).

Hans J. Lipps

Institut für Zellbiologie, Universität Witten/Herdecke,
Stockumer Straße 10, D-58448 Witten (Germany).

Daniela Rhodes

MRC Laboratory of Molecular Biology, Hills Road,
Cambridge, CB2 2QH (U.K.).

Barbara J. Trask

Department of Molecular Biotechnology, University of
Washington, 1705 NE Pacific Ave,
Seattle, WA. 98195-2145 (USA).

Chris Tyler-Smith

CRC Chromosome Molecular Biology Group, Department of
Biochemistry, University of Oxford, South Parks Road,
Oxford OX1 3QU (U.K.).

Alfredo Villasante

Centro de Biología Molecular «Severo Ochoa», Facultad de
Ciencias, (CSIC-UAM), Cantoblanco, 28049 Madrid (Spain).

Huntington F. Willard

Department of Genetics, Center for Human Genetics, Case
Western Reserve University, School of Medicine,
2109 Adelbert Avenue, Cleveland, OH. 44106 (USA).

Tim J. Yen

The Fox Chase Cancer Center, 7701 Burholme Avenue,
Philadelphia, PA. 19111 (USA).

Virginia A. Zakian

Department of Molecular Biology, Princeton University,
Princeton, NJ. 08544 (USA).

LIST OF PARTICIPANTS

Marta Agudo

Centro de Biología Molecular «Severo Ochoa», CSIC,
Universidad Autónoma, Cantoblanco, 28049 Madrid (Spain).

Pilar Arana

Departamento de Genética, Facultad de Ciencias Biológicas,
Universidad Complutense, 28040 Madrid (Spain).

Rosario Armas-Portela

Departamento de Biología, Facultad de Ciencias,
Universidad Autónoma, 29049 Madrid (Spain).

Nicanor R. Austriaco

Department of Biology, Massachusetts Institute of
Technology, 77 Massachusetts Ave. Cambridge, MA. 02139
(USA).

Casimiro C-López

Department of Molecular Genetics, University of Lund,
Sölvegatan 29, S-223 62 Lund (Sweden).

Aarti Chand

Biochemistry Department, University of Oxford, South Parks
Road, Oxford OX1 3QU (U.K.).

Alfred Cortés

Departamento de Biología Molecular y Celular, Centro de
Investigación y Desarrollo, CSIC, Jordi Girona
Salgado 18-26, 08034 Barcelona (Spain).

Rosario Esteban

Centro de Investigaciones Biológicas, CSIC, Velázquez 144,
28006 Madrid (Spain)

Jiří Fajkus

Institute of Biophysics, Academy of Sciences of the Czech
Republic, Královopolská 135, 612 65 Brno (Czech Republic).

Elena Fernández-Ruiz

Servicio de Inmunología, Hospital de la Princesa,
Diego de León 62, 28006 Madrid (Spain).

Eric Gilson

Laboratoire de Biologie Moléculaire et Cellulaire de
l'Ecole Normale Supérieure de Lyon, 46 allé d'Italie,
69364 Lyon, Cedex 07 (France).

Rafael Giraldo

Departamento de Microbiología Molecular, Centro de
Investigaciones Biológicas, (CSIC), c/ Velázquez 144,
28006 Madrid (Spain).

Clara Goday

Department of Cell Biology and Development, Centro de
Investigaciones Biológicas, (CSIC), Velázquez 144,
28006 Madrid (Spain).

Philip W. Hammond

Howard Hughes Medical Institute, Department of Chemistry
and Biochemistry, University of Colorado,
Boulder, CO. 80309-0215 (USA).

Dori Huertas

Department of Biochemistry and Molecular Genetics,
Imperial College School of Medicine at St. Mary's,
London W2 1PG (U.K.).

Manuel Jamilena

Departamento de Biología Aplicada, Escuela Técnica
Superior, Universidad de Almería, La Cañada de San Urbano,
04120 Almería (Spain).

Ana Losada

Centro de Biología Molecular «Severo Ochoa», (CSIC-
UAM), Facultad de Ciencias, Universidad Autónoma,
Cantoblanco, 28049 Madrid (Spain).

Antonia Martín-Gallardo

Unidad de Estructura de Cromosomas, Departamento de
Estructura de Macromoléculas, Centro Nacional de
Biotecnología, CSIC, Campus Universidad Autónoma,
Cantoblanco, 28049 Madrid (Spain).

Manuel Martínez Valdivia

Bioquímica y Biología Molecular, Facultad de Ciencias,
Universidad de Cádiz, Apdo. 40,
11510 Puerto Real, Cádiz (Spain).

Jaqui Mason

Microbiology Unit, Department of Biochemistry, University
of Oxford, South Parks Rd., Oxford OW1 3QU (U.K.)

Jean-Louis Mergny

Laboratoire de Biophysique, Muséum National d'Histoire
Naturelle INSERM U201, CNRS UA481, 43 rue Cuvier,
75005 Paris (France).

Benjamín Piña

Centre d'Investigació i Desenvolupament, CSIC,
Jordi Girona 18, 08034 Barcelona (Spain).

J. Suso Platero

Howard Hughes Medical Institute, Fred Hutchinson Cancer
Research Center, 1124 Columbia St.,
Seattle, WA. 98104 (USA).

Julia Promisel Cooper

Department of Chemistry and Biochemistry, University of
Colorado, Campus Box 215, Boulder, CO. 80309-0215 (USA).

Aránzazu de la Puente

Instituto de Investigaciones Biomédicas, CSIC,
Arturo Duperier 4, 28029 Madrid (Spain).

José-A. Suja

Unidad de Biología Celular, Departamento de Biología,
Edificio de Ciencias Biológicas, Universidad Autónoma,
28049 Madrid (Spain).

Beth A. Sullivan

MRC Human Genetics Unit, Western General Hospital,
Crewe Road, Edinburgh EH4 2XU (U.K.).

Miguel A. Vega-Palas

Dipartimento di Genetica e Biologia Molecolare, Università
di Roma «La Sapienza», Piazzale Aldo Moro 5,
00185 Rome (Italy).

Lori L. Wallrath

Department of Biology, Washington University, Box 1229,
St. Louis, MI.63130 (USA).

RNA Viral Quasispecies

Organized by

S. Wain-Hobson, C. López Galíndez and E. Domingo

7th-9th October, 1996

The workshop on RNA viral quasispecies gathered a number of experts on topics related to RNA virus evolution. It was indeed a broad scope of topics ranging from the molecular basis of copying fidelity of viral polymerases to the contribution of virus variation to pathogenesis and to the emergence of new viruses. As is often the case in a gathering of stout scientists with long personal histories in unique environments, agreement in some issues paralleled disagreement in many others.

Few virologists would now question that the quasispecies model of molecular evolution of macromolecules, proposed by M. Eigen a quarter of a century ago, is exerting a great influence in our current understanding of RNA viruses. Several examples were identified that document that specific mutations arising during viral replication are directly associated to new pathogenic potential of the evolved genomes. It is not yet possible to design experiments involving infections with viruses replicating with very high copying fidelity to test the effect of replication errors on virus pathogenesis. In spite of this, it is becoming increasingly clear that adaptability, measured as the ability to gain fitness, or the ability to cope with environmental changes (presence of antibodies, drugs) are directly related to the high mutation rates and quasispecies structure of viral populations.

There was much less agreement on the limits of applicability of the quasispecies concept. Are human populations quasispecies? And retrotransposons? Fortunately Eigen himself was there to clarify the origins of the concept, as also emphasized in several of his recent papers: Quasispecies implies a related set of simple replicons subjected to competitive selection. The main departure from previous models of population genetics is the consideration of the wild type as an ensemble of genomes instead of one genome with a defined nucleotide sequence. It is this mutant swarm - the preferred word of H. Temin- that offers sufficient plasticity for the ensemble to become an easy prey of selective forces and genetic drift.

The process of mutant generation, competition and selection can be analyzed in a controlled fashion in the replication of short-chained RNA species derived from bacteriophage Q β . Several more complex model systems were discussed. The classical influenza viruses -which preceded other viral systems in defining concepts of structural and evolutionary virology- poliovirus, foot-and-mouth disease virus, vesicular stomatitis virus, hepatitis C virus, human respiratory syncytial virus, retrotransposons and, of course, the human immunodeficiency viruses and their chimeric simian/human versions, among other animal and plant RNA viruses and genetic elements. Although several important concepts are emerging from these studies (limitations in the cloud of mutant swarms, multiple mutational pathways associated to escape from antibodies or to resistance to antiviral inhibitors, identification of mutations associated to deep fitness losses, the effect of viral population size on selective dominance of some classes of mutants, etc.) it was also quite

clear that additional input from population genetics would be of great help to virology. Some connexions between classical population biology theory and quasispecies have already been established but more are needed to assess the value of viruses to approach evolutionary problems.

New possibilities of antiviral intervention based on the error prone replication of viruses were also discussed. Copying fidelity of reverse transcriptase can be modified by structural alterations of the enzyme and the manipulation of fidelity to drive viral replication into error catastrophe is no longer a dream. An elegant exploitation of error-prone replication is the generation of heavily substituted nucleic acids and proteins. *In vitro* hypermutagenesis constitutes an impressive tool to explore the functional space of enzymes, and a means to generate molecules with new biological properties.

In conclusion, the meeting offered a lot to most and, fortunately, there were sufficient points of disagreement to lend ourselves to believing that Fundación Juan March may consider a similar meeting some years from now.

E. Domingo.

LIST OF INVITED SPEAKERS

Christof K. Biebricher

Max-Planck-Institute for Biophysical Chemistry,
Am Fassberg 11, D-37077 Göttingen (Germany).

John M. Coffin

Department of Molecular Biology and Microbiology, Tufts
University, 136 Harrison Avenue, Boston, MA. 02111 (USA).

Esteban Domingo

Centro de Biología Molecular «Severo Ochoa», Universidad
Autónoma, Cantoblanco, 28049 Madrid (Spain).

Manfred Eigen

Max-Planck-Institut für Biophysikalische Chemie, Karl-
Friedrich-Bonhoeffer-Institut, Am Fassberg, Postfach 2841,
D-37077 Göttingen-Nikolausberg (Germany).

John Holland

Department of Biology, 0116, University of California, San
Diego, 9500 Gilman Drive, La Jolla, CA. 92093-0116 (USA).

Norman L. Letvin

Beth Israel Hospital, Harvard Medical School,
330 Brookline Avenue, Boston, MA. 02215 (USA).

Lawrence A. Loeb

Joseph Gottstein Memorial Laboratory, Department of
Pathology, Box 357705, School of Medicine, University of
Washington, Seattle, WA. 98195-7705 (USA).

Cecilio López Galíndez

Centro Nacional de Biología Celular y Retrovirus,
Instituto de Salud Carlos III, Ctra. Majadahonda-Pozuelo
Km. 2, 28220 Majadahonda, Madrid (Spain).

Brian W.J. Mahy

Division of Viral and Rickettsial Diseases, National
Center for Infectious Diseases, (CDC), 1600 Clifton Rd.
N.E., Atlanta, GA. 30333 (USA).

José A. Melero

Centro Nacional de Biología Fundamental, Instituto de
Salud Carlos III, Ctra. Majadahonda-Pozuelo Km. 2, 28220
Majadahonda, Madrid (Spain).

Andreas Meyerhans

Department of Virology, University of Freiburg, Hermann-Herderstr. 11, D-79104 Freiburg (Germany).

Philip D. Minor

National Institute for Biological Standards and Control, Blanche Lane, South Mimms, Potters Bar, Hertfordshire, EN6 3QG (U.K.).

Andrés Moya

Departamento de Genética, Facultad de Biología, Universidad de Valencia, c/Dr. Moliner 50, 46100 Burjassot, Valencia (Spain).

Stuart T. Nichol

Centers for Disease Control and Prevention, (CDC), Special Pathogens Branch, Division of Viral and Rickettsial Diseases, 1600 Clifton Rd. N.E., Atlanta, GA. 30333 (USA).

Douglas D. Richman

University of California, San Diego, Dpts. of Pathology & Medicine, 0679, 9500 Gilman Drive, and San Diego Veterans Affairs Medical Center, La Jolla, CA. 92093-0679 (USA).

John J. Skehel

MRC, National Institute for Medical Research, Division of Virology, The Ridgeway, Mill Hill, London NW7 1AA (U.K.).

Simon Wain-Hobson

Institut Pasteur, Unité de Rétrovirologie Moléculaire, 28 rue du Dr. Roux, 75724 Paris (France).

Robert G. Webster

St. Jude Children's Research Hospital, Department of Virology/Molecular Biology, 332N. Lauderdale, P.O. Box 318, Memphis, TN. 38101 (USA).

Eckard Wimmer

Department of Molecular Genetics and Microbiology, School of Medicine, State University of New York at Stony Brook, Stony Brook, N.Y. 11794-5222 (USA).

LIST OF PARTICIPANTS

Ben Berkhout

Department of Human Retrovirology, University of
Amsterdam, Academic Medical Center, Meibergdreef 15,
1105 AZ Amsterdam (The Netherlands).

Hervé Bourhy

Rabies Unit, Institut Pasteur, 28 rue Dr. Roux,
75724 Paris (France).

Patricia A. Cane

Department of Biological Sciences, University of Warwick,
Coventry CV4 7AL (U.K.).

Josep M. Casacuberta

Departament Genètica Molecular, CID (CSIC),
c/ Jordi Girona 18-26, 08034 Barcelona (Spain).

Concepción Casado

Centro Nacional de Biología Celular y Retrovirus,
Instituto de Salud Carlos III, Ctra. Majadahonda-Pozuelo
Km. 2, 28220 Majadahonda, Madrid (Spain).

Cristina Escarmís

Centro de Biología Molecular «Severo Ochoa», CSIC, Facultad
de Ciencias, Universidad Autónoma, Cantoblanco,
28049 Madrid (Spain).

Fernando García-Arenal

Departamento de Biotecnología, E.T.S.I. Agrónomos,
Universidad Politécnica, Ciudad Universitaria,
28040 Madrid (Spain).

Jordi Gómez

Liver Unit, Department of Medicine, Hospital General
Universitari Vall d'Hebron, Universitat Autònoma, Passeig
Vall d'Hebron s/n, 08025 Barcelona (Spain).

Jaap Goudsmit

Department of Human Retrovirology, AMC, University of
Amsterdam, Meibergdreef 15, 1105 AZ Amsterdam
(The Netherlands).

Ulrich Kettling

Max-Planck-Institute for Biophysical Chemistry, Department
081, Am Faßberg 11, D-37077 Göttingen (Germany).

Pedro R. Lowenstein

Department of Medicine, Molecular Medicine Unit,
University of Manchester, Oxford Road,
Manchester M13 9PT (U.K.).

José Antonio Martínez-Izquierdo

Departamento de Genética Molecular, CID-CSIC,
Jordi Girona 18, 08034 Barcelona (Spain).

Miguel A. Martínez de la Sierra

Centro de Biología Molecular «Severo Ochoa», CSIC, Facultad
de Ciencias, Universidad Autónoma, Cantoblanco,
28049 Madrid (Spain).

Marcella A. McClure

Department of Biological Sciences, University of
Nevada, 4505 Maryland Parkway, Box 454004,
Las Vegas, NV. 89154-4004 (USA).

Luis Menéndez-Arias

Centro de Biología Molecular «Severo Ochoa», CSIC, Facultad
de Ciencias, Universidad Autónoma, Cantoblanco,
28049 Madrid (Spain).

Frank Oehlenschläger

Max-Planck-Institute for Biophysical Chemistry, Department
081, Am Faßberg 11, D-37077 Göttingen (Germany).

Ernst Peterhans

Institute of Veterinary Virology, University of Berne,
Länggass-Straße 122, CH-3001 Berne (Switzerland).

Valérie Pezo

Institut Pasteur, Unité de Rétrovirologie Moléculaire,
28 rue du Dr. Roux, 75724 Paris (France).

Alexander Plyusnin

Haartman Institute, Department of Virology, P.O. Box 21,
(Haartmaninkatu 3), FIN-00014 University of Helsinki
(Finland).

Josep Quer

Recerca Medicina Interna II, Area d'Investigació B,
Hospital Vall d'Hebron, Pg. Vall d'Hebron 119-129,
08035 Barcelona (Spain).

Miguel E. Quiñones-Mateu

Centro de Biología Molecular «Severo Ochoa», CSIC, Facultad
de Ciencias, Universidad Autónoma, Cantoblanco,
28049 Madrid (Spain).

Marilyn J. Roossinck

The S.R. Noble Foundation, PO Box 2180, 2510 Sam Noble
Parkway, Ardmore, OK. 73402 (USA).

Laurent Roux

Department of Genetics and Microbiology, University of
Geneva Medical School, CMU, 9 avenue de Champel,
1211 Genève 4 (Switzerland).

Lidia Ruiz Tabuenca

Laboratorio de Retrovirología «irsiCaixa» y Unidad de SIDA,
Hospital Universitario Germans Trias i Pujol,
Badalona, Barcelona (Spain).

Christophe Terzian

Centre de Génétique Moléculaire, CNRS,
91198 Gif sur Yvette (France).

Noël Tordo

Institut Pasteur, Laboratoire des Lyssavirus,
25 rue du Dr. Roux, 75724 Paris (France).

Antti Vaheri

Haartman Institute, Department of Virology, P.O. Box 21,
(Haartmaninkatu 3), FIN-00014 University of Helsinki
(Finland).

Alfonso Valencia

Protein Design Group, Centro Nacional de Biotecnología,
CSIC, Universidad Autónoma, Cantoblanco,
28049 Madrid (Spain).

Jean-Pierre Vartanian

Unité de Rétrovirologie Moléculaire, Institut Pasteur,
28 rue du Dr. Roux, 75724 Paris (France).

Zhibing Yun

Division of Clinical Virology, Karolinska Institute at
Huddinge, University Hospital, F68, Huddinge (Sweden).

Eloisa Yuste

Centro Nacional de Biología Celular y Retrovirus,
Instituto de Salud Carlos III, Ctra. Majadahonda-Pozuelo
Km. 2, 28220 Majadahonda, Madrid (Spain).

Absciscic Acid Signal Transduction in Plants

Organized by
R. Quatrano and M. Pagès
28th-30th October, 1996

The mechanism(s) by which phytohormones trigger physiological responses have long eluded plant physiologists. How these relatively small and simple molecules can elicit such major responses that differ from tissue to tissue during plant development has been a very difficult question to approach. However, through the use of molecular and genetic approaches, tremendous strides have been made within the last decade to elucidate the molecular basis of phytohormone action. These advances have been most notable with responses elicited by the phytohormones ethylene, auxin and abscisic acid. Overall progress in this important area of plant science research is represented in this meeting that focuses on one of these phytohormones, abscisic acid (ABA). It is clear that the data accumulated from recent research has led to considerable progress in our understanding of the ABA response pathway; from perception of the ABA signal, through the expression and function of specific genes in a given physiological response. Future research, using the approaches outlined in this workshop, will undoubtedly lead to the further clarification of the role of ABA in plant development and serve as paradigm by which the modes of action of other phytohormones and plant signals can be better understood.

The role of ABA in the typical life cycle of a higher plant is mostly confined to the development of the seed, and in response to environmental stresses in vegetative tissue. Levels of endogenous ABA increase during the development of the seed, and is part of a developmental pathway which promotes maturation of the seed and the acquisition of desiccation tolerance, as well as prevents precocious germination. Evidence from genetic and molecular data, as well as from embryo culture indicates that this pathway is an integral component of the developmental program within all higher plants. An early response of vegetative plant tissue to environmental stresses, such as osmotic and temperature extremes, involves increases in the endogenous levels of ABA and or in the sensitivity of cells to ABA, as an internal signal to trigger a set of responses to protect immobile plants from these perturbations. Although the signaling pathway from ABA to gene expression may be similar in seeds and in vegetative tissue, it is clear that different sets of genes are expressed in the different tissues. Hence, the importance of understanding the molecular and genetic basis of the ABA response pathway has enormous implications in agricultural practices and in engineering crops in the future with improved traits in seeds and in tolerance of environmental stresses.

Genetic approaches using the model plant *Arabidopsis* have identified mutants whose phenotypes are defective in ABA responses in both vegetative and reproductive tissues. Since one can easily map these mutant loci in *Arabidopsis*, which consists of an extremely small genome, positional cloning techniques are available to isolate the mutated genes. Also, insertional mutagenesis in *Arabidopsis*, as well as in maize, has also led to the further isolation and characterization of genes active in the ABA response pathway. Studies of two such ABA-insensitive mutants, *abi1* and *abi3(vp1)*, have resulted in the isolation of genes

that have been identified as a phosphatase and a transcriptional activator, respectively. The identification of other genes that interact with each of these gene products, as well as the substrates for their action, is the subject of intense genetic and biochemical research and study. More biochemical/cytological approaches have identified the ionic intermediates and the membrane channels responsible for these ionic fluxes that transduce the ABA signal (e.g. Ca) and drive various physiological responses to ABA (e.g. stomatal closure).

Direct microinjection techniques have identified unique intermediates (e.g. cyclic ADP-ribose) that are responsible for specific gene expression at the level of ABA-responsive promoters. Furthermore, molecular approaches have detailed the cis-elements and several transacting factors (including VP1) that are critical for the transcription of ABA-responsive genes. Although the initial receptor of ABA has not been identified, new approaches are being targeted to this major unknown. Likewise, although the function of ABA-responsive genes in various physiological processes (e.g. desiccation tolerance) are not known in molecular terms, considerable progress has been made on the molecular structure and important domains of these proteins.

It is clear from these recent studies outlined in this workshop, that our knowledge of the ABA signal transduction pathway has progressed greatly in the last several years, but major gaps still exist in our understanding. For example, what is the nature of the ABA receptor, what are the critical changes that occur in response to the ABA signal at the level of transcription resulting in ABA-dependent gene expression, and, what is the link between the proteins that appear in response to ABA and the tissue-specific physiological responses ?

Ralph S. Quatrano
Montserrat Pagès

LIST OF INVITED SPEAKERS

Dorothea Bartels

Max-Planck-Institut für Züchtungsforschung,
Carl-von-Linné-Weg 10, D-50829 Köln (Germany).

Michael R. Blatt

Laboratory of Plant Physiology and Biophysics, Wye
College, University of London, Wye, Kent TN25 5AH (U.K.).

Elizabeth A. Bray

Department of Botany and Plant Sciences, University of
California, Riverside, CA. 92521 (USA).

Nam-Hai Chua

Laboratory of Plant Molecular Biology, The Rockefeller
University, 1230 York Avenue, New York, NY. 10021-6399
(USA).

Timothy J. Close

Department of Botany Plant Sciences, University of
California, Riverside, CA. 92521-0124 (USA).

Michel Delseny

University of Perpignan, Laboratoire de Physiologie et
Biologie Moléculaire des Plantes, UMR 5545 CNRS,
52 Avenue de Villeneuve, 66860 Perpignan (France).

Jérôme Giraudat

Institut des Sciences Végétales, Centre National de la
Recherche Scientifique, Avenue de la Terrasse-Bat 23,
91198 Gif sur Yvette Cedex (France).

Erwin Grill

Department of Botany, Technical University of Munich,
Arcisstr. 16, 80333 München (Germany)

Alistair Hetherington

Lancaster University, Division of Biology,
Lancaster LA1 4YQ (U.K.).

David Ho

Plant Biology Program, Department of Biology, Division of
Biology and Biomedical Sciences, Washington University,
St. Louis, MI. 63130 (USA).

Maarten Koornneef

Department of Genetics, Wageningen Agricultural
University, Dreijenlaan 2, 6703 HA, Wageningen
(The Netherlands).

Antonella Leone

Research Centre for Vegetable Breeding, National Research Council, I-80055 Portici-Napoli (Italy).

Donald R. McCarty

Plant Molecular and Cellular Biology Program, Horticultural Sciences Department, University of Florida, Gainesville, FL. 32605 (USA).

John Mundy

Molecular Biology Institute, Copenhagen University, Øster Farimagsgade 2A, 1353 Copenhagen K, (D.K.).

Montserrat Pagès

Departament de Genètica Molecular C.I.D. (C.S.I.C.), Jordi Girona 18-26, 08034 Barcelona (Spain).

Ralph Quatrano

Department of Biology, University of North Carolina, Coker Hall, South Road, Chapel Hill, NC. 27599-3280 (USA).

Julio Salinas

Area de Biología Molecular y Virología Vegetal, CIT-INIA, Carretera de la Coruña Km.7, 28040 Madrid (Spain).

Julian I. Schroeder

Department of Biology and Center for Molecular Genetics, University of California, San Diego, La Jolla, CA. 92093-0116 (USA).

Terry L. Thomas

Department of Biology, Texas A&M University, College Station, TX. 77843 (USA).

Kazuko Yamaguchi-Shinozaki

Biological Resources Division, Japan International Research Center for Agricultural Sciences (JIRCAS), 2-1 Ohwashi, Tsukuba 305 (Japan).

LIST OF PARTICIPANTS

Suzanne R. Abrams

Plant Biotechnology Institute, National Research Council of
Canada, 110 Gymnasium Place, Saskatoon, SK. S7N 0W9
(Canada).

Natacha Bies

Laboratory of Plant Physiology and Molecular Biology, (UMR
4555), University of Perpignan, 66860 Perpignan-Cedex
(France).

Peter K. Busk

Departamento de Genética Molecular, Centro de Investigación
y Desarrollo, (C.S.I.C.), Jorge Girona 18-26,
08034 Barcelona (Spain).

Pilar Carbonero

Laboratorio Bioquímica y Biología Molecular, Departamento de
Biotecnología, UPM, E.T.S. Ingenieros Agrónomos,
28040 Madrid (Spain).

Francisco J. Cejudo

Instituto de Bioquímica Vegetal y Fotosíntesis, Facultad de
Químicas, Universidad de Sevilla, CSIC, Apdo. 553,
41080 Sevilla (Spain).

Françoise Cellier

Biochimie et Physiologie Végétales, UMII-CNRS URA 573-INRA-
ENSAM, Place Viala, 34060 Montpellier, Cedex 1, (France).

Francisco A. Culiáñez-Macià

Instituto de Biología Molecular y Celular de Plantas,
Universidad Politécnica de Valencia, C.S.I.C.,
Camino de Vera s/n, 46002 Valencia (Spain).

Peter Engström

Department of Physiological Botany, Uppsala University,
Villavägen 6, S-752 36 Uppsala (Sweden).

Mercè Figueras

Departament Genètica Molecular, Centre d'Investigació i
Desenvolupament, CSIC, c/Jordi Girona 18-26,
08034 Barcelona (Spain).

Adela Goday

Departament Genètica Molecular, Centre d'Investigació i
Desenvolupament, CSIC, c/Jordi Girona 18-26,
08034 Barcelona (Spain).

Aurelio Gómez-Cadenas

Departamento Citricultura, IVIA, 46113 Moncada,
Valencia (Spain).

Stefania Grillo

Research Center for Vegetable Breeding, CNR,
Via Università 133, 80055 Portici (Italy).

Tsukaho Hattori

Center for Molecular Biology and Genetics, Mie University,
1515 Kamihama-cho, Tsu 514 (Japan).

Juan Jordano

Instituto de Recursos Naturales y Agrobiología, (CSIC),
Apartado 1052, 41080 Sevilla (Spain).

Matilde José-Estanyol

Dpto. Genètica Molecular, Centre d'Investigació i
Desenvolupament, CSIC, c/ Jordi Girona Salgado 18-26, 08034
Barcelona (Spain).

Maya Kicheva

Bulgarian Academy of Sciences, Acad. M. Popov Institute of
Plant Physiology, Acad. G. Bonchev St. Bldg. 21, Sofia 1113
(Bulgaria).

Jennifer Kuzma

Laboratory of Plant Molecular Biology, The Rockefeller
University, 1230 York Avenue, New York, NY. 10021-6399
(USA).

Barbara Leyman

Laboratory of Plant Physiology and Biophysics, Wye College,
University of London, Wye, Kent TN25 5AH (U.K.).

Elena Marín

Département d'Ecophysiologie Végétale et de Microbiologie,
Centre de Cadarache, 13108 Saint Paul lez Durance (France).

Annie Marion-Poll

Laboratoire de Biologie Cellulaire, INRA, 78026 Versailles,
Cedex (France).

José A. Martínez-Izquierdo

Departamento de Genética Molecular, CID-CSIC,
Jordi Girona 18, 08034 Barcelona (Spain).

José M. Martínez-Zapater

Instituto Nacional de Investigaciones Agrarias, Laboratorio
de Biología Molecular y Virología Vegetal,
Ctra. de La Coruña Km 7,5, 28040 Madrid (Spain).

Montaña Mena

Laboratorio de Bioquímica y Biología Molecular, Departamento
de Biotecnología, UPM, ETS de Ingenieros Agrónomos,
28040 Madrid (Spain).

Carlos Nicolás

Departamento de Biología Vegetal, Facultad de Biología,
Universidad de Salamanca, Avda. Campo Charro s/n,
37007 Salamanca (Spain).

Tapio Palva

Division of Genetics, Department of Biosciences, University
of Helsinki, P.O. Box 56 (Viikinkaari 5),
FIN-00014 Helsinki (Finland).

Salomé Prat

Centro de Investigación y Desarrollo, CSIC,
Jorge Girona 18-26, 08034 Barcelona (Spain).

M^a Jesús Rodrigo

Instituto de Biología Molecular y Celular de Plantas, CSIC,
Universidad Politécnica de Valencia, Camino de Vera 14,
46022 Valencia (Spain).

Pedro Luis Rodríguez Egea

Technische Universität, Lehrstuhl für Botanik,
Arcisstrasse 16,4 Stock, D-80333 München (Germany).

M.K. Walker-Simmons

United States Department of Agriculture, Agriculture
Research Service, 209 Johnson Hall, Washington State
University, Pullman, WA. 99164-6420 (USA).

Mei Wang

Department of Plant Biotechnology, Center for
Phytotechnology, Leiden University/Netherlands Organization
for Applied Research, Wassenaarseweg 64, 2333 AL Leiden
(The Netherlands).

Oxygen Regulation of Ion Channels and Gene Expression

Organized by
E. Kenneth Weir and J. López Barneo
24th-26th November, 1996

This workshop concentrated on a relatively new but rapidly growing research field. The influence of O₂ sensing on cellular functions is an emergent topic that in the coming years will certainly have a broad impact in biomedicine. The initial progress in the field has been achieved independently by researchers with different background and technical expertise, without much communication among them. Thus, we thought that the gathering of a selection of scientists, representative of the various disciplines with interest in the subject, would render an enormous conceptual enrichment and could lead to a breakthrough in the maturation and development of the field. This was among the first international workshops on the subject aimed at the interchange of ideas and concepts among scientists from areas as diverse as molecular biology, biochemistry, physiology, pharmacology and clinical research.

Oxygen, one of the most abundant elements in the biosphere, is crucial for the maintenance of most life forms on earth. It has a major biological role as acceptor of the electrons in the mitochondrial respiratory chain and in doing so enables the synthesis of ATP by phosphorylative oxidation. Despite its paramount importance, little is known about how organisms are capable of sensing O₂ availability and adjusting the gas uptake to their changing needs, in different habitats or physiological situations. Because, in mammals, O₂ is taken up in the respiratory system and transported to the tissues by the blood, the most immediate adaptative response to the lack of environmental O₂ is an increase in the frequency of breathing. Acute hypoxia also produces dilatation in most arteries, which is an important mechanism participating in the local regulation of vascular tone. Besides these fast physiological responses, long-term hypoxia can induce in specific cells modifications in gene expression and enzymatic activity. Well-known examples of these chronic adaptations to the lack of O₂ are the induction of erythropoietin, the hormone that stimulates the production of red blood cells, and of vascular endothelial growth factor, which may mediate hypoxia-initiated angiogenesis.

Research in recent years has begun to shed light on the basic cellular and molecular mechanisms underlying acute and chronic adaptations to low O₂ tension. The cardiorespiratory responses to hypoxia seem to be mediated by O₂-sensitive ion channels, expressed in glomus cells of the carotid body (the primary O₂-sensitive arterial chemoreceptors), arterial smooth muscle cells, neuroepithelial bodies of the lung, pheochromocytoma and brain cells. The molecular nature of the intrinsic O₂-sensors associated with ion channels, or those O₂-sensitive molecules capable of triggering the signal pathway(s) regulating transcription, although unknown, is currently being investigated in several laboratories. The molecular characterization of the O₂ sensitive molecules will surely lead to a better understanding of many pathophysiological processes (such as hypertension or the responses of brain and heart cells to ischemia) and will generate new strategies for the pharmacological treatment of human diseases.

E. Kenneth Weir and José López-Barneo.

LIST OF INVITED SPEAKERS

Helmut Acker

Max-Planck-Institut für Molekulare Physiologie,
Rheinlanddamm 201, D-44139 Dortmund (Germany).

Stephen L. Archer

Veterans Affairs Medical Center and University of
Minnesota, Minneapolis, MN. (USA)

Pierre Boistard

Laboratoire de Biologie Moléculaire des Relations
Plantes-Microorganismes CNRS-INRA, BP 27,
31326 Castanet Tolosan Cedex (France).

Jaime Caro

Thomas Jefferson University, Jefferson Medical College,
Department of Medicine, Cardeza Foundation for Hematologic
Research, 1015 Walnut Street,
Philadelphia, PA. 19107-5099 (USA).

Maria F. Czyzyk-Krzeska

Department of Molecular and Cellular Physiology,
University of Cincinnati, PO Box 670576,
Cincinnati, OH. 45267-0576 (USA).

Laura L. Dugan

Center for the Study of the Nervous System Injury,
Washington University in St. Louis, Department of
Neurology, Box 8111, 660 S. Euclid Ave,
St. Louis, MO. 63110 (USA).

Alfredo Franco-Obregón

Department of Cardiology, Children's Hospital Medical
Center, Harvard Medical School, 1309 Enders Building,
320 Longwood Avenue, Boston, MA. 02115 (USA)

Constancio González

Departamento de Bioquímica y Biología Molecular y
Fisiología, Facultad de Medicina, Universidad de
Valladolid, 47005 Valladolid (Spain).

Gabriel G. Haddad

Department of Pediatrics & Cellular & Molecular
Physiology, Section of Respiratory Medicine, Yale
University School of Medicine, 333 Cedar Street,
Fitkin Bldg. RM. 506, New Haven, CT. 06520-8064 (USA).

José López-Barneo

Departamento de Fisiología Médica y Biofísica, Facultad de Medicina, Universidad de Sevilla, Avda. Sánchez Pizjuán 4, 41009 Sevilla (Spain).

Colin A. Nurse

Department of Biology, McMaster University, 1280 Main Street West, Hamilton, ON. Canada L8S 4K1.

Chris Peers

Institute for Cardiovascular Research, University of Leeds
Leeds LS2 9JT (U.K.).

Olaf Pongs

Institut für Neurale Signalverarbeitung, Zentrum für Molekulare Neurobiologie, University of Hamburg, Martinistr. 52 - Haus 42, D-20246 Hamburg (Germany).

Peter J. Ratcliffe

Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX39DU (U.K.).

Helmut Sies

Institut für Physiologische Chemie I, Heinrich-Heine-Universität Düsseldorf, Postfach 101007, D-40001-Düsseldorf (Germany).

Nicholas B. Standen

Ion Channel Group, Department of Cell Physiology and Pharmacology, University of Leicester, P.O. Box 138, Leicester LE1 9HN (U.K.).

E. Kenneth Weir

VA Medical Center IIIC, University of Minnesota, 1 Veterans Drive, Minneapolis, MN. 55417 (USA).

Xiao-Jian Yuan

Department of Medicine, Division of Pulmonary and Critical Care Medicine and Department of Physiology, University of Maryland School of Medicine, Baltimore, MD. 21201 (USA).

LIST OF PARTICIPANTS

Laura Almaraz

Departamento de Bioquímica y Biología Molecular y Fisiología, Facultad de Medicina, Universidad de Valladolid, c/Ramón y Cajal s/nº, 47005 Valladolid (Spain).

Julián Aragonés

Servicios de Inmunología y Biología Molecular, Hospital de la Princesa, Universidad Autónoma, c/Diego de León 62, 28006 Madrid (Spain).

Matías A. Ávila

Instituto de Investigaciones Biomédicas, CSIC, Arturo Duperier 4, 28029 Madrid (Spain).

Keith J. Buckler

University Laboratory of Physiology, Parks Road, Oxford OX1 3PT (U.K.).

Elisabeth Carpenter

Institute for Cardiovascular Research, University of Leeds, Leeds LS2 9JT (U.K.).

Emilio Cervantes

Departamento de Biología Vegetal, Facultad de Biología, Universidad de Salamanca, 37007 Salamanca (Spain).

Mª Dolores Chiara

Dpt. Fisiología Médica y Biofísica, Facultad de Medicina, Universidad de Sevilla, Avda. Sánchez Pizjuán 4, 41009 Sevilla (Spain).

Laura Conforti

Department of Molecular and Cellular Physiology, College of Medicine, University of Cincinnati, 231 Bethesda Avenue, Cincinnati, OH. 45267-0576 (USA).

Emilio Geijo

Departamento de Fisiología, Facultad de Medicina, Universidad de Alicante, Apartado 374, 03080 Alicante (Spain).

Christopher J. Hatton

Institute for Cardiovascular Research, University of Leeds, Leeds LS2 9JT (U.K.).

Eric M. Horn

Department of Molecular and Integrative Physiology,
Neuroscience Program and College of Medicine, University
of Illinois, Urbana, IL. 61803 (USA).

L.Eric Huang

Hematology-Oncology Division, Brigham & Women's Hospital,
Harvard Medical School, Boston, MA. 02115 (USA).

Prem Kumar

Department of Physiology, Medical School, University of
Birmingham, Birmingham B15 2TT (U.K.).

José Ramón López-López

Departamento de Bioquímica y Biología Molecular y
Fisiología, Facultad de Medicina, Universidad de
Valladolid, 47005 Valladolid (Spain).

Gracia-P. Ortega-Sáenz

Departamento de Fisiología Médica y Biofísica, Facultad de
Medicina, Universidad de Sevilla, Avda. Sánchez Pizjuan 4,
41009 Sevilla (Spain).

Manuel O. de Landázuri

Servicio de Inmunología, Hospital de la Princesa,
Universidad Autónoma, c/ Diego de León 62, 28006 Madrid
(Spain).

Ricardo Pardal

Departamento de Fisiología Médica y Biofísica, Facultad de
Medicina, Universidad de Sevilla, Avda. Sánchez Pizjuán 4,
41009 Sevilla (Spain).

David R. Pepper

Department of Physiology, Medical School, University of
Birmingham, Birmingham B15 2TT (U.K.).

M^a Teresa Pérez-García

Departamento de Bioquímica y Biología Molecular y
Fisiología, Facultad de Medicina, Universidad de
Valladolid, 47005 Valladolid (Spain).

Ricardo Rigual

Departamento de Bioquímica y Biología Molecular y
Fisiología, Facultad de Medicina, Universidad de
Valladolid, 47005 Valladolid (Spain).

Hildgund Schrempf

Angewandte Genetik der Mikroorganismen,
FB Biologie/Chemie, Universität Osnabrück, Postfach 44 69,
49069 Osnabrück (Germany).

Barry L. Taylor

Department of Microbiology and Molecular Genetics and
Center for Molecular Biology and Gene Therapy, Loma Linda
University, Loma Linda, CA. 92350 (USA).

Pablo Wappner

The Weizmann Institute of Science, Department of Molecular
Genetics and Virology, Rehovot 76100 (Israel).

XV Juan March Lectures

The Juan March lectures were first organized in 1982, and since then have been held every year without interruption. The purpose of these lectures is to put Spanish students and professionals in the field of Biology in direct contact with some outstanding world figures in this field. The invited lecturers often take advantage of their visit to Spain to give additional seminars in different laboratories.

In 1996, the XV lectures series took place, with the general theme of **TRANSCRIPTION FACTORS**. The speakers and topics were as follows:

19 February

DAVID BALTIMORE

Department of Biology
Massachusetts Institute of Technology
Cambridge, MA (USA)
1975 Nobel Prize in Physiology or Medicine

The NF- κ B transcription factor and lymphoid cell activation.

Introduced by: **Manuel Fresno.**

Centro de Biología Molecular "Severo Ochoa"
Universidad Autónoma de Madrid (Spain)

26 February

MARK PTASHNE

Department of Molecular and Cellular Biology
Harvard University
Cambridge, MA (USA)

Molecular mechanisms of gene regulation.

Introduced by: **Ana Aranda.**

Instituto de Investigaciones Biomédicas
Madrid (Spain)

4 March

WALTER J. GEHRING

Biozentrum
University of Basel (Switzerland)

The role of *eyeless* as a master control gene in eye morphogenesis and evolution.

Introduced by: **Ginés Morata.**

Centro de Biología Molecular "Severo Ochoa"
Universidad Autónoma de Madrid (Spain)

11 March

FRANÇOIS JACOB

Institut Pasteur
Paris (France)
1965 Nobel Prize in Physiology or Medicine

Regulatory circuits in transcription.

Introduced by: **Antonio Garcia-Bellido.**

Centro de Biología Molecular "Severo Ochoa"
Universidad Autónoma de Madrid (Spain)

Sessions Open to the Public

In connection with some workshops, prominent invited speakers have also given additional lectures in sessions open to the public. In 1996, these were as follows:

During the workshop on **RNA Viral quasispecies** (7-9 October):

- JOHN HOLLAND

Department of Biology
University of California, San Diego
La Jolla, CA (USA)

**The population behaviour of RNA virus quasispecies and
significance for virus diseases.**



- SIMON WAIN-HOBSON

Unité de Rétrovirologie Moléculaire
Institut Pasteur
Paris (France)

**Genetic variation reveals the biology and dynamics of
retroviral infections.**

Introduced by: **Esteban Domingo.**

Centro de Biología Molecular "Severo Ochoa"
Universidad Autónoma de Madrid (Spain)

During the workshop on **Abscisic Acid signal transduction in plants** (28-30 October):

- NAM-HAI CHUA

Laboratory of Plant Molecular Biology
The Rockefeller University
New York (USA)

Phytochrome phototransduction pathways.

Introduced by: **Montserrat Pagès.**

Centro de Investigación y Desarrollo
C.S.I.C. Barcelona (Spain)

Reviews in Scientific Journals

During 1996 the meetings organized by the Centre have been reviewed in the following articles:

- **Neurobiology of Nociceptors** (1996). Eds. C. Belmonte and F. Cerveró. Oxford University Press (Oxford).
(Based on the workshop *What do nociceptors tell the brain?*, held in February 1992).
- Vicente, M. and Errington, J. (1996) Structure, Function and Controls in Microbial Division. **Molecular Microbiology** **20**(1): 1-7.
(On the workshop of the same title, held in May 1995)
- López-Botet, M., Moretta, L. and Strominger, J. (1996) NK-Cell Receptors and Recognition of MHC Class I Molecules. **Immunology Today** **17**: 214-217.
(On the workshop *NK-Cell Receptors and Recognition of the Major Histocompatibility Complex Antigens*, held in September 1995).
- Dreyfuss, G., Hentze, M. and Lamond, A.I. (1996) From Transcript to Protein. **Cell** **85**: 963-972.
(On the workshop of the same title, held in March 1996).
- Henderson, C.E. (1996) Programmed Cell Death in the Developing Nervous System. **Neuron** **17**: 579-585.
(On the workshop of the same title, held in July 1996).
- Baeuerle, P.A. and Baltimore, D. (1996). NF- κ B: Ten Years After. (Meeting Review). **Cell** **87**: 13-20.
(On the workshop on *NF- κ B/I κ B Proteins. Their Role in Cell Growth, Differentiation and Development*, held in July, 1996).
- Siebenlist, U. (1996). NF- κ B/I κ B Proteins. Their Role in Cell Growth, Differentiation and Development. **Biochimica et Biophysica Acta. (Reviews on Cancer)** **1332**(1): R7-R13.
(On the workshop of the same title, held in July, 1996).
- Nichol, S. (1996). RNA viruses. Life on the edge of catastrophe. **Nature** **384**:218-219.
(On the workshop on *RNA viral quasispecies*, held in October, 1996).
- Fresno, M., Kopf, M. and Rivas, L. Cytokines in Infectious Diseases. **Immunology Today**(In press).
(On the workshop of the same title, held in June, 1996).
- Barthels, D., Ho, T.H.D. and Quatrano, R. **Plant Cell**.(submitted)
(On the workshop on *Abscisic Acid Signal Transduction in Plants* held in October, 1996).

1997 Meetings Schedule

INSTITUTO JUAN MARCH

CENTRE FOR INTERNATIONAL MEETINGS ON BIOLOGY

1997 MEETINGS SCHEDULE

Date	Meeting Subject	Organizers
10-12 February	TGF- β Signalling in Development and Cell Cycle Control	J. Massagué. Howard Hughes Medical Institute. New York. C. Bernabeu. Centro de Investigaciones Biológicas. Madrid.
10-12 March	Novel Biocatalysts	S. J. Benkovic. The Pennsylvania State University. University Park. A. Ballesteros. Instituto de Catálisis y Petroleoquímica. Madrid.
21-23 April	Signal Transduction in Neuronal Development and Recognition	M. Barbacid. Bristol-Myers Squibb Pharmaceutical Research Institute. Princeton. D. Pulido. Centro de Biología Molecular "Severo Ochoa". Madrid.
12-13 May	100th Meeting: Biology at the Edge of the Next Century	Centre for International Meetings on Biology. Madrid.
26-28 May	Membrane Fusion	V. Malhotra. University of California, San Diego. La Jolla. A. Velasco. Facultad de Biología. Universidad de Sevilla.
9-11 June	DNA Repair and Genome Instability	T. Lindahl. Imperial Cancer Research Fund. Herts. C. Pueyo. Facultad de Ciencias. Universidad de Córdoba.
7-19 July *	Biochemistry and Molecular Biology of Non-conventional Yeasts	J. M. Cregg. Oregon Graduate Institute of Science and Technology. Portland. C. Gancedo. Instituto de Investigaciones Biomédicas. Madrid. J. M. Siverio. Facultad de Biología. Universidad de La Laguna.
22-24 September	Principles of Neural Integration	C. Gilbert. The Rockefeller University. New York. G. Gasic. Neuron Editorial Offices. Cell Press. Cambridge. C. Acuña. Facultad de Medicina. Universidad de Santiago de Compostela.
6-8 October	Programmed Gene Rearrangement: Site-Specific Recombination	N. D. F. Grindley. Yale University. New Haven. J. C. Alonso. Centro Nacional de Biotecnología. Madrid.
20-22 October	Plant Morphogenesis	M. Van Montagu. University of Gent. J. L. Micol. Facultad de Ciencias. Universidad de Alicante.
3-5 November	Development and Evolution	W. Gehring. Biozentrum. University of Basel. G. Morata. Centro de Biología Molecular "Severo Ochoa". Madrid.
1-3 December	Plant Viroids and Viroid-Like Satellite RNAs from Plants, Animals and Fungi	H. L. Sänger. Max-Planck-Institut für Biochemie. Martinsried. R. Flores. Instituto de Biología Molecular y Celular de Plantas. Valencia.

All meetings, with the exception marked *, will take place on the premises of the Instituto Juan March:

Castelló, 77
Telephone: 34 - 1 - 435 42 40
Fax: 34 - 1 - 576 34 20
28006 Madrid (Spain)

Individual advertisements for every meeting, with more detailed information, are published with sufficient anticipation.

The Scientific Council

The Scientific Council of the Centre comprises the following members:

Miguel Beato

Institut für Molekularbiologie und Tumorforschung. Marburg (Germany).

José A. Campos-Ortega

Institut für Entwicklungsbiologie. Köln (Germany).

Gregory Gasic

Neuron Editorial Offices. Cambridge (USA).

César Milstein

Medical Research Council. Cambridge. (United Kingdom).

Margarita Salas

Centro de Biología Molecular. CSIC - Universidad Autónoma de Madrid. (Spain).

The Scientific Council determines the priorities for the Centre's activities. It may put forward initiatives to be carried out in collaboration with Spanish or foreign laboratories. It also considers proposals of meetings submitted to the Centre by Spanish or foreign scientists, selecting and approving those it feels deserve support.

In general terms, the Scientific Council advises the Centre for International Meetings on Biology on any scientific subject or issue falling within the scope of the Center's activities.

Index of Personal Names

A

Aberdam, Daniel: 25
 Abrams, Suzanne R.: 137
 Acker, Helmut: 145
 Acuña, Carlos: 165
 Adorini, Luciano: 43
 Agudo, Marta: 117
 Akhurst, Rosemary J.: 83
 Alani, Rhoda M.: 85
 Albà, M.Mar: 35
 Alcamí, Antonio: 75
 Alcamí, José: 45, 105
 Alcorta, Itziar: 56
 Alitalo, Kari: 63
 Almaraz, Laura: 147
 Alonso, Juan C.: 53, 165
 Andrian, Ulrich H. von: 63
 Andrup, Lars: 56
 Anguita, Juan: 75
 Ansel, John C.: 83
 Aoufouchi, Said: 35
 Aparicio, Pedro: 65, 85
 Aragonés, Julián: 147
 Arana, Pilar: 117
 Aranda, Ana: 153
 Archer, Stephen L.: 145
 Armas-Portela, Rosario: 117
 Arroyo, Alicia G.: 65
 Arroyo, Javier: 45
 Austriaco, Nicanor R.: 117
 Avila, Pilar: 56
 Avila, Matías A.: 147
 Axelrod, Amy: 45
 Azorín, Fernando: 15, 109, 115
 Azzouz, Mimoun: 95

B

Bae, Youngmee: 45
 Bach-Elias, Montserrat: 33
 Baeuerle, Patrick A.: 5, 103, 161
 Bagutti, Claudia: 85
 Baker, Tania A.: 53
 Baltimore, David: 5, 103, 153, 161
 Ballard, Dean W.: 103
 Ballario, Paola: 25
 Ballesteros, Antonio: 165
 Barbacid, Mariano: 165
 Barrandon, Yann: 83
 Barres, Barbara A.: 93
 Bartels, Dorothea: 135, 161
 Basset, Paul: 83
 Beato, Miguel: 169
 Belasco, Joel G.: 33
 Belmonte, C: 161
 Belsham, Graham J.: 35
 Benkovic, S.J.: 165
 Beretta, Laura: 35
 Berkhout, Ben: 127

Bernabeu, Carmelo: 165
 Bernales, Irantzu: 56
 Bertoni, Giovanni: 25
 Biebricher, Christof K.: 125
 Bies, Natacha: 137
 Blatt, Michael R.: 135
 Blumenberg, Miroslav: 85
 Böck, August: 25
 Boeck, Ronald P.: 35
 Boistard, Pierre: 145
 Bolland, Silvia: 53
 Bonheyo, George: 56
 Borsello, Tiziana: 95
 Boss, Jeremy M.: 43
 Bourhy, Hervé: 127
 Bours, Vincent: 105
 Bouvet, Philippe: 35
 Bravo, Rodrigo: 15, 99, 102, 103
 Bray, Elizabeth A.: 135
 Bredesen, Dale E.: 93
 Breitreutz, Dirk: 85
 Brown, William R.A.: 115
 Buckler, Keith J.: 147
 Burek, Michael J.: 95
 Burgeson, Robert E.: 83
 Burns, Drusilla L.: 53
 Busk, Peter K.: 137

C

C-López, Casimiro: 117
 Caamaño, Jorge H.: 105
 Cabañas, Carlos: 65
 Cabezón, Elena: 56
 Cai, Haini: 105
 Calderó, Jordi: 95
 Campos-Ortega, José A.: 169
 Cane, Patricia A.: 127
 Canosa, Inés: 56
 Capetti, Amedeo: 75
 Carbon, John: 112, 115
 Carbonero, Pilar: 137
 Carmona, Manuel: 25
 Caro, Jaime: 145
 Carpenter, Elisabeth: 147
 Carroll, Joseph M.: 85
 Casacuberta, Josep M.: 127
 Casadesús, Josep: 56
 Casado, Concepción: 127
 Casanova, Mª de los Llanos: 85
 Casasnovas, José M.: 65
 Cases, Ildefonso: 25
 Cazorla, Pilar: 95
 Cejudo, Francisco J.: 137
 Celada, Antonio: 15, 39, 42, 43
 Cellier, Françoise: 137
 Ceña, Valentín: 95
 Cervantes, Emilio: 147
 Cerveró, F.: 161
 Chand, Aarti: 117
 Chandler, Michael: 56

Chang, Cheong-Hee: 45
 Chiara, M^a Dolores: 147
 Chua, Nam-Hai: 135, 157
 Clarke, Louise: 115
 Clarke, Peter G.H.: 93
 Clerici, Mario: 73
 Close, Timothy J.: 135
 Coffin, John M.: 125
 Comella, Joan X.: 15, 89, 92, 93
 Compton, John: 85
 Conforti, Laura: 147
 Conti, Claudio J.: 85
 Cooke, Howard: 115
 Corces, Víctor G.: 23
 Corral, Ricardo: 75
 Cortés, Alfred: 117
 Cregg, J.M.: 165
 Cresswell, Peter: 43
 Cruz, Fernando de la: 15, 49, 52,
 53
 Cuadros, Miguel A.: 95
 Culiáñez-Maciá, Francisco A.: 137
 Cullen, Bryan R.: 35
 Czyzyk-Krzeska, Maria F.: 145

D

Danilevskaya, Olga N.: 115
 Davidson, Irwin: 25
 Davies, Alun M.: 93
 Débarbouillé, Michel: 23
 Dejana, Elisabetta: 63
 Delseny, Michel: 135
 Díaz Orejas, Ramón: 56
 Díaz-Nido, Javier: 95
 Diego, Juana Luisa de: 75
 Dixon, Ray: 23
 Djian, Philippe: 85
 Dlugosz, Andrzej A.: 83
 Domingo, Esteban: 15, 121, 124,
 125, 157
 Dornand, Jacques: 75
 Drenckhahn, Detlev: 63
 Dreyfuss, Gideon: 33, 161
 Driscoll, Monica: 93
 Dritschilo, Anatoly: 105
 Dugan, Laura L.: 145

E

Edwalds-Gilbert, Gretchen: 35
 Ehrlich, S. Dusko: 53
 Eigen, Manfred: 123, 125
 Elsen, Peter J. van den: 45
 Engel, Pablo: 65
 Engelhardt, Britta: 65
 Engström, Peter: 137
 Enjuanes, Luis: 35
 Errington, J.: 161
 Escarmis, Cristina: 127
 Espel, Enric: 45, 75, 105

Espuny Suarez, Ruth: 35
 Espinosa, Manuel: 53
 Esquerda, Josep E.: 95
 Esteban, Mariano: 73
 Esteban, Rosario: 117
 Ezquerria, Angel: 75

F

Fajkus, Jiří: 117
 Farrand, Stephen K.: 53
 Ferguson, Mark W.J.: 83
 Fernández-Ruiz, Elena: 117
 Ferrer, Isidro: 95
 Figueras, Mercè: 137
 Finkelman, Fred D.: 73
 Flavell, Richard A.: 43
 Flores, R.: 165
 Fortes, M^a Purificación: 36
 Frade, José María: 96
 Franco-Obregón, Alfredo: 145
 Freire-Picos, M^a Angeles: 35
 Frenette, Paul S.: 65
 Fresno, Manuel: 15, 69, 72, 73,
 105, 153, 161
 Frontelo, Pilar: 86
 Furie, Martha B.: 63

G

Gaiddon, Christian: 96
 Gallegos, M^a Trinidad: 25
 Gancedo, Carlos: 165
 Gandarillas, Alberto: 86
 García-Arenal, Fernando: 127
 García-Barcina, María: 65
 García-Bellido, Antonio: 153
 García-Blanco, Mariano A.: 36
 García-Pardo, Angeles: 65
 Gardan, Rozenn: 25
 Gasalla José Manuel: 66
 Gasic, Gregory: 165, 169
 Gasser, Susan M.: 115
 Gebauer, Fátima: 36
 Geiduschek, E. Peter: 23
 Geijo, Emilio: 147
 Gélina, Céline: 103
 Gehring, Walter J.: 153, 165
 Germain, Ronald N.: 43
 Gerondakis, Steve: 105
 Ghosh, Partho: 45
 Ghosh, Sankar: 103
 Gilmore, Thomas D.: 103
 Gilbert, C.: 165
 Gilson, Eric: 118
 Gillardon, Frank: 96
 Gimeno, Ramón: 75
 Giraldo, Rafael: 118
 Girard, Jean-Philippe: 66

Giraudat, Jérôme: 135
 Glimcher, Laurie H.: 43
 Goday, Clara: 118
 Goday, Adela: 138
 Gómez, Jordi: 127
 Gómez del Moral, Manuel: 75
 Gómez-Cadenas, Aurelio: 138
 González, Andrés: 11, 92
 González, Constancio: 145
 Gonzalo, Rosa María: 75
 Gofalons, Eduard: 45
 Goñi, Félix M.: 57
 Goudsmit, Jaap: 127
 Grahn, A. Marika: 57
 Gralla, Jay D.: 23
 Greene, Lloyd A.: 93
 Greene, Warner C.: 103
 Grill, Erwin: 135
 Grillo, Stefania: 138
 Grindley, N.D.F.: 165
 Grohmann, Elisabeth: 57
 Gubser, Charles C.: 36
 Güttler, Andrea: 57
 Guzmán, Leda: 57

H

Haase, Jana: 57
 Haddad, Gabriel G.: 145
 Haggård-Ljungkuist, Elisabeth: 53
 Halford, Stephen E.: 53
 Hämmerling, Günter J.: 43
 Hammond, Philip W.: 118
 Haraldsen, Guttorm: 66
 Harlan, John M.: 63
 Haro, César de: 36
 Hatton, Christopher J.: 147
 Hattori, Tsukaho: 138
 Havran, Wendy L.: 83
 Henderson, Christopher E.: 93, 161
 Hentze, Matthias W.: 33, 161
 Hetherington, Alistair: 135
 Hetman, Michal: 96
 Ho, David: 135, 161
 Hohl, D.: 83
 Hohn, Barbara: 54
 Holland, John: 125, 157
 Hooykaas, Paul J.J.: 54
 Horn, Eric M.: 148
 Horvitz, H. Robert: 93
 Hörz, Wolfram: 23
 Huang, L. Eric: 148
 Hübner, Griseldis: 86
 Huertas, Dori: 118
 Hugué, Christelle: 105
 Hultgren, Scott: 54
 Hultmark, Dan: 106
 Huxley, Clare: 115

I

Israël, Alain: 103
 Issekutz, Thomas B.: 63
 Izaurralde, Elisa: 33

J

Jacob, François: 153
 Jacobson, Michael D.: 94
 James, Stephanie: 76
 Jamilena, Manuel: 118
 Jaraquemada, Dolores: 45
 Jeon, Saewha: 86
 Johnson, Eugene M.: 15, 89, 92, 94
 Jorcano, José Luis: 15, 79, 82, 83
 Jordán, Joaquín: 96
 Jordano, Juan: 138
 José-Estanyol, Matilde: 138
 Juan, Manel: 66
 Juárez, Antonio: 57
 Jutila, Mark A.: 63

K

Kaiser, Sibylle: 86
 Karlsson, Lars: 43
 Karpen, Gary: 115
 Keller, Walter: 33
 Kerr, Ian M.: 44
 Kerr, Lawrence D.: 106
 Kettling, Ulrich: 127
 Khan, Saleem A.: 57
 Kicheva, Maya: 138
 Kim, Jin-Soo: 26
 Kima, Peter: 76
 Kimura, Tominori: 76
 Koester, Susan: 96
 Koornneef, Maarten: 135
 Kooyk, Yvette van: 66
 Kopf, Manfred: 73, 161
 Krainer, Adrian: 33
 Kropshofer, Harald: 45
 Küchenmeister, Jörg: 106
 Kumar, Prem: 148
 Kupper, Thomas S.: 83
 Kustu, Sydney: 23
 Kuzma, Jennifer: 138
 Kwiatkowski, Dominic: 73

L

Lafita, Alfredo: 11
 Laín de Lera, M^a Teresa: 106
 Lamas, Mónica: 26
 Lamond, Angus I.: 33, 161
 Landáuzuri, Manuel O. de: 15, 59, 62, 64, 148

Lane, E. Birgitte: 84
 Langhorne, Jean: 73
 Lanka, Erich: 15, 49, 52, 54
 Lara, Enrique: 76
 Larcher, Fernando: 86
 Launois, Pascal: 76
 Lazo, Pedro S.: 15, 99, 102, 104
 Lechner, Franziska: 76
 Lederberg, J.: 51
 Lee, Janet S.: 46
 Legrain, Pierre: 33
 Lenardo, Michael J.: 104
 Leone, Antonella: 136
 Letvin, Norman L.: 125
 Leyman, Barbara: 138
 Li, Qiao: 26
 Liew, F.Y.: 73
 Liljedahl, Monika: 46
 Lilley, David M.J.: 116
 Lin, Rongtuan: 106
 Lindahl, T.: 165
 Lipps, Hans J.: 116
 Lloberas, Jorge: 46
 Llosa, Matxalen: 54
 Lobb, Roy R.: 66
 Locksley, Richard M.: 73
 Loeb, Lawrence A.: 125
 López Galíndez, Cecilio: 15, 121, 125
 López Trascasa, Margarita: 66
 López-Barneo, José: 15, 141, 143, 146
 López-Botet, M.: 161
 López-Cabrera, Manuel: 106
 López-López, José Ramón: 148
 Loreni, Fabrizio: 36
 Lorenzo, Víctor de: 15, 17, 21, 23
 Losada, Ana: 118
 Louis, Jacques A.: 73
 Lowenstein, Pedro R.: 128
 Lu, Hong-Tao: 46
 Luca, Michele de: 86
 Lucas, Rudolf: 76
 Luque, Alfonso: 66
 Luque, Ignacio: 106
 Luscinskis, Francis W.: 63

M

MacDonald, H.R.: 44
 Mach, Bernard: 15, 39, 41, 44
 Mackay, Charles: 63
 Madruga, Jaime: 106
 Magasanik, Boris: 20, 23
 Maggi, Enrico: 74
 Mahy, Brian W.J.: 125
 Malhotra, V.: 165
 Mantovani, Roberto: 46
 March, Carlos: 11
 March, Juan: 11

March Ordinas, Juan: 11
 March, Leonor: 11
 Marín, Elena: 138
 Marión, Rosa M.: 36
 Marion-Poll, Annie: 138
 Marqués, Silvia: 26
 Martí, Mercè: 46
 Martín-Gallardo, Antonia: 118
 Martín-Rendón, Enca: 96
 Martín-Zanca, Dionisio: 96
 Martínez de la Sierra, M. A.: 128
 Martínez Laso, Jorge: 46
 Martínez Naves, Eduardo: 46
 Martínez-Salas, Encarnación: 36
 Martínez Valdivia, Manuel: 118
 Martínez-A., Carlos: 74
 Martínez-Izquierdo, José A.: 128, 139
 Martínez-Zapater, José M.: 139
 Mason, Jaqui: 119
 Massagué, Joan: 165
 Matson, Steven W.: 54
 Mattaj, I.: 15, 29, 31
 McCarty, Donald R.: 136
 McClure, Marcella A.: 128
 McDonald, Patrick P.: 106
 McEver, Rodger P.: 63
 Mebius, Reina E.: 66
 Melero, José A.: 76, 125
 Mena, Montaña: 139
 Meneguzzi, Guerrino: 86
 Menéndez-Arias, Luis: 128
 Mercurio, Frank: 106
 Mergny, Jean-Louis: 119
 Meyerhans, Andreas: 126
 Michaelidis, Theologos: 96
 Micol, José Luis: 165
 Milstein, César: 36, 169
 Minor, Philip D.: 126
 Mohanty, Bidyut K.: 26
 Moncalián, Gabriel: 57
 Monsalve, María: 26
 Montagu, M. van: 165
 Montaner, Silvia: 107
 Montoya, María C.: 66
 Morales, Aixa V.: 96
 Morata, Ginés: 153, 165
 Moreno, F. Javier: 76
 Moretta, L.: 161
 Morris, Rebecca J.: 86
 Moulon, Corinne: 46
 Moya, Andrés: 125
 Müller, Werner: 74
 Mundy, John: 136
 Muñoz-Cánoves, Pura: 36
 Muñoz-Fernández, Mª Angeles: 76
 Murillas, Rodolfo: 86

N

Naranjo José R.: 94
 Navarro, Pilar: 66
 Nicolás, Carlos: 139
 Nichol, Stuart T.: 126, 161
 Nieto, Amelia: 36
 Nixon, B. Tracy: 26
 Nock, Steffen: 37
 Nordeen, Ernie J.: 94
 Novick, Richard P.: 54
 Nurse, Colin A.: 146

O

Oehlschlager, Frank: 128
 Oguiza, José Antonio: 26
 Olmo, Marcel.11 del: 37
 Oppenheim, Ariella: 26
 Oppenheim, Amos B.: 26
 Oppenheim, Ronald W.: 15, 89, 92, 94
 Orian, Amir: 107
 Örn, Anders: 74
 Ortega-Sáenz, Gracia-P.: 148
 Ortín, Juan: 15, 29, 31, 34
 Oswald, Isabelle P.: 74
 Otten, Luc: 46

P

Pablo, Flora de: 97
 Pagès, Montserrat: 15, 131, 134, 136, 157
 Palva, Tapio: 139
 Paramio, Jesús M.: 86
 Pardal, Ricardo: 148
 Pareja, Eduardo: 46
 Parida, Shreemanta K.: 77
 Parker, Roy: 34
 Pascual, Esther: 87
 Pascual-Salcedo, M. Dora: 77
 Patarroyo, Manuel: 67
 Paya, Carlos V.: 107
 Peers, Chris: 146
 Pelicic, Vladimir: 57
 Pellegrini, Graziella: 87
 Peña, José: 47
 Peñalva, Miguel Angel: 23
 Pepper, David R.: 148
 Pérez-García, M^a Teresa: 148
 Pérez-Martín, José: 15, 17, 21, 24
 Perona, Rosario: 107
 Peterhans, Ernst: 128
 Petray, Patricia B.: 77
 Petterson, Sven: 107
 Peyron, Jean-François: 107
 Pezo, Valérie: 128
 Pinon, Luzia G. P.: 97

Piña, Benjamín: 119
 Piñel, Enrique: 11
 Pirianov, Grisha: 97
 Pirrotta, Vincenzo: 24
 Pizcueta, Pilar: 67
 Planas, Anna M.: 97
 Planta, Rudi J.: 24
 Platero, J. Suso: 119
 Plumbbridge, Jacqueline: 26
 Plyusnin, Alexander: 128
 Pongs, Olaf: 146
 Portera, Alberto: 97
 Pozo, Miguel A. del: 67
 Prat, Salomé: 139
 Prohens, Jaime: 11
 Promisel Cooper, Julia: 119
 Ptashne, Mark: 24, 153
 Puente, M^a Aránzazu de la: 119
 Pueyo, Carmen: 165
 Pugsley, Anthony P.: 54
 Puig, Susana: 87
 Pulido, Diego: 97, 165

Q

Quatrano, Ralph: 15, 131, 134, 136, 161
 Quer, Josep: 128
 Quintanilla, Miguel: 87
 Quifones-Mateu, Miguel E.: 129

R

Ramírez, Angel: 87
 Ramos, Juan Luis: 27
 Ratcliffe, Peter J.: 146
 Redondo, Juan Miguel: 67
 Regueiro, José R.: 47
 Reichelt, Julia: 87
 Reith, Walter: 44
 Rey Campos, Javier: 27
 Rhodes, Daniela: 116
 Rice, Nancy: 104
 Richman, Douglas D.: 126
 Richter, Joel D.: 34
 Rigual, Ricardo: 149
 Rine, Jasper D.: 24
 Ríos, Luis: 87, 161
 Rivas, Luis: 15, 69, 74
 Rivas, Susana: 58
 Rocha, Marian: 77
 Rodrigo, M^a Jesús: 139
 Rodríguez, Pedro Luis: 139
 Rodríguez-Medina, Manuel S.: 107
 Rodríguez-Peña, Angeles: 97
 Rodríguez Robles, Antonio: 11
 Rojo, Fernando: 27
 Romani, Luigina: 74
 Romero, M. Rosario: 87

Roop, Dennis R.: 15, 79, 82, 84
 Roossinck, Marilyn J.: 129
 Rosbash Michael: 34
 Roux, Laurent: 129
 Rubel, Edwin W.: 94
 Rudenko, Gloria: 27
 Ruiz Tabuenca, Lidia: 129
 Ruiz-Argüeso, Tomás: 27
 Russel, Marjorie: 54

S

Sabin, Elizabeth A.: 77
 Sadoul, Remy: 97
 Saenger, Wolfram: 54
 Salas, Margarita: 24, 169
 Salgado, Josefa: 37
 Salinas, Julio: 136
 Salz, Helen: 37
 Sammar, Marei: 67
 Sánchez-Madrid, Francisco: 64
 Sánchez-Pérez, Miguel: 47
 Sanger, H.L.: 165
 Sant, Andrea J.: 44
 Santamaria Babi, Luis F.: 67
 Santero, Eduardo: 27
 Sanz, María Jesús: 67
 Sassone-Corsi, Paolo: 24
 Scott, Phillip: 74
 Schaffner, Walter: 15, 17, 21, 24
 Scheidereit, Claus: 104
 Schleif, Robert: 20, 24
 Schreiber, Robert D.: 44
 Schrempf, Hildgund: 149
 Schroeder, Julian I.: 136
 Sen, Rajan: 107
 Séraphin, Bertand: 34
 Shachar, Idit: 47
 Sher, Alan: 15, 69, 72, 74
 Siebenlist, Ulrich: 104, 161
 Siegel, Vivian: 37
 Sies, Helmut: 146
 Sigler, Paul B.: 104
 Simon, Marcia: 87
 Sittler, Annie: 37
 Siverio, J.M.: 165
 Skehel, John J.: 126
 Smith, C. Wayne: 64
 Soler, Dulce: 67
 Soler, Concepción: 47
 Sonenberg, Nahum: 34
 Sonnenberg, Arnoud: 84
 Springer, Christoph: 37
 Springer, Timothy A.: 15, 59, 62, 64
 Standen, Nicholas B.: 146
 Stasiak, Andrzej: 58
 Stefanis, Leonidas: 97
 Steimle, Viktor: 44

Steinmetz, Eric J.: 37
 Steitz, Joan A.: 34
 Steward, Ruth: 104
 Strohmaier, Heimo M.: 58
 Strominger, J.: 161
 Su, Li: 37
 Suja, José-A.: 119
 Sullivan, Beth A.: 119
 Sun, Tung-Tien: 84

T

Tartakoff, Alan M.: 34
 Tatum, E.L.: 51
 Tauler, Albert: 37
 Taylor, Barry L.: 149
 Teixidó, Joaquín: 67
 Temin, H.M.: 123
 Terzian, Christophe: 129
 Thomas, C.M.: 51
 Thomas, Terry L.: 136
 Thyphronitis, George: 77
 Ting, Jenny P.-Y.: 44
 Tolkovsky, Aviva M.: 94
 Tordo, Noël: 129
 Tormo, José: 58
 Trask, Barbara J.: 15, 109, 116
 Trieu-Cuot, Patrick: 54
 Trinchieri, Giorgio: 74
 Trowsdale, John: 44
 Truman, James W.: 94
 Tyler-Smith, Chris: 15, 109, 116

U

Udalova, Irina: 77
 Uhlin, Bernt Eric: 24
 Uitto, Jouni: 84

V

Vaheri, Antti: 129
 Valcárcel, Juan: 15, 29, 31, 34
 Valencia, Alfonso: 129
 Vallbona, Pablo: 11
 Vartanian, Jean-Pierre: 129
 Vega-Palas, Miguel A.: 119
 Velasco, A.: 165
 Velasco, Marta: 77
 Vendrell, Montserrat: 97
 Verma, Inder M.: 104
 Vestweber, Dietmar: 64
 Vicente, M.: 161
 Vilella, Ramón: 77
 Villadangos, José A.: 47
 Villasante, Alfredo: 15, 109, 116
 Vogt, Anne B.: 47

W

Waal Malefyt, René de: 47
 Wain-Hobson, Simon: 15, 121,
 126,157
 Walker-Simmons, M.K.: 139
 Wallrath, Lori L: 119
 Wang, James C.: 55
 Wang, Mei: 140
 Wappner, Pablo: 149
 Wasserman, Steven A.: 104
 Watt, Fiona M.: 84
 Webster, Robert G.: 126
 Weir, E. Kenneth: 15, 141, 143,
 146
 Weiss, Verena: 27
 Weissman, Irving L.: 64
 Werner, Sabine: 84
 Westermann, Jürgen: 67
 White, Kristin: 94
 Whiteside, Simon T.: 107
 Willard, Huntington F.: 116
 Williams, Timothy J.: 64
 Wimmer, Eckard: 126
 Wirth, Thomas: 104
 Wissink, Sacha: 107

X

Xia, Zhengui: 98

Y

Yamaguchi-Shinozaki, Kazuko: 136
 Yaron, Avraham: 107
 Yen, Tim J.: 116
 Yuan, Xiao-Jian: 146
 Yun, Zhibing: 129
 Yuspa, Stuart H.: 84
 Yuste, Eloisa: 130
 Yuste, José Luis: 11

Z

Zachgo, Sabine: 47
 Zakian, Virginia A.: 116
 Zamanillo, Daniel: 98
 Zambryski, Patricia: 55
 Zechner, Ellen L.: 58

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Instituto Juan March de Estudios e Investigaciones
Castelló, 77 • 28006 Madrid (España)
Tel. 34 - 1 - 435 42 40 • Fax 34 - 1 - 576 34 20 • <http://www.march.es>