CMLS, Cell. Mol. Life Sci. 62 (2005) 1529–1531
1420-682X/05/141529-03
DOI 10.1007/s00018-005-5000-z

CMLS Cellular and Molecular Life Sciences

Announcement of the Editor-in-chief

Once a year (in July) we have decided to publish the names of the authors and the titles of the two most read (by internet) research papers and reviews published in CMLS the previous year. Thus we have the pleasure to provide you with the results of 2004.

Research Articles

1) An extensive microarray analysis of AAL-toxin-induced cell death in *Arabidopsis thaliana* brings new insights into the complexity of programmed cell death in plants

T. S. Gechev, I. Z. Gadjev and J. Hille

Department Molecular Biology of Plants, Researchschool GBB, University of Groningen, Kerklaan 30, 9751 NN Haren (The Netherlands)

Abstract. A T-DNA knockout of the *Arabidopsis* homologue of the tomato disease resistance gene Asc was obtained. The asc gene renders plants sensitive to programmed cell death (PCD) triggered by the fungal AAL toxin. To obtain more insights into the nature of AAL-toxin-induced cell death and to identify genes of potential importance for PCD, we carried out transcription profiling of AAL-toxin-induced cell death in this knockout with an oligonucleotide array representing 21,500 *Arabidopsis* genes. Genes responsive to reactive oxygen species (ROS) and ethylene were among the earliest to be upregulated, suggesting that an oxidative burst and production of ethylene played a role in the activation of the cell death. This notion was corroborated by induction of several genes encoding ROS-generating proteins, including a respiratory burst oxidase and germin oxalate oxidase. Cytochemical studies confirmed the oxidative burst and, in addition, showed synthesis of callose, a feature of the hypersensitive response. A diverse group of transcription factors was also induced. These events were followed by repression of most of the auxin-regulated genes known to be involved in growth and developmental responses. All photosynthesis-related genes were repressed. Blocking the synthesis of ethylene or NO significantly compromised cell death. In addition, we identified a heterogeneous group of early-induced genes, some of them never before associated with PCD. The group of early-induced genes included a number of proteases that were previously implicated in developmentally regulated types of PCD, suggesting a more principal role for these proteases in the PCD process. These findings provide new insights into the molecular mechanisms of plant PCD.

May 2004, Volume 61, Number 10, pp. 1185–1197

2) Nucleotide-binding domains of human cystic fibrosis transmembrane conductance regulator: detailed sequence analysis and three-dimensional modeling of the heterodimer

I. Callebaut[a], R. Eudes[a], J.-P. Mornon[a] and P. Lehn[b]

[a] Systèmes moléculaires & Biologie structurale, LMCP, CNRS UMR7590, Universités Paris 6 & Paris 7, 4 place Jussieu, 75252 Paris (France)
[b] INSERM U458, Hôpital Robert Debré, 49 blvd Sérurier, 75019 Paris (France)

Abstract. The cystic fibrosis transmembrane conductance regulator (CFTR) protein is encoded by the gene that is defective in cystic fibrosis, the most common lethal inherited disease among the Caucasian population. CFTR belongs to the ABC transporter superfamily, whose members form macromolecular architectures composed of two membrane-spanning domains and two nucleotide-binding domains (NBDs). The experimental structures of NBDs from several ABC transporters have recently been solved, opening new avenues for understanding the structure/function relationships and the consequences of some disease-causing mutations of CFTR. Based on a detailed sequence/structure analysis, we propose here a three-dimensional model of the human CFTR NBD heterodimer. This model, which is in agreement with recent experimental data, highlights the specific features of the CFTR asymmetric active sites located at the interface between the two NBDs. Moreover, additional CFTR-specific features can be identified at the subunit interface, which may play critical roles in active site interdependence and are uncommon in other NBD dimers.

January 2004, Volume 61, Number 2, pp. 230–242

Reviews

1) Ubiquitin-proteasome system A field guide to ubiquitylation

S. Fang[a] and A. M. Weissman[b]

[a] Medical Biotechnology Center, University of Maryland Biotechnology Institute, 725 W. Lombard Street, 21201 Baltimore, Maryland (USA)
[b] Center for Cancer Research, Laboratory of Protein Dynamics and Signaling, National Cancer Institute, 1050 Boyles Street, 21702 Frederick, Maryland (USA)

Abstract. The capacity for exquisite regulation of ubiquitylation provides eukaryotic cells with a means to fine-tune both protein function and levels. This complex set of processes affects myriad proteins and potentially impacts all cellular processes. Ubiquitylation is brought about through multienzyme processes, with specificity conferred primarily by interactions of substrates with specific ubiquitin protein ligases (E3s) in association with ubiquitin conjugating enzymes (E2s). Regulation of ubiquitylation occurs at multiple levels, including E2-E3 interactions, substrate recognition, chain elongation, binding of ubiquitin to conserved motifs and deubiquityation. This review presents the fundamentals of the ubiquitin conjugating system.

June 2004, Volume 61, Number 13, pp. 1546–1561

2) Peroxisome proliferator-activated receptor α target genes

S. Mandard, M. Müller and S. Kersten

Nutrition, Metabolism and Genomics Group, Wageningen University, 6700 Wageningen (The Netherlands)

Abstract. Peroxisome proliferator-activated receptors (PPARs) are nuclear proteins that belong to the superfamily of nuclear hormone receptors. They mediate the effects of small lipophilic compounds such as long-chain fatty acids and their derivatives on transcription of genes commonly called PPAR target genes. Here we review the involvement of PPARα in peroxisomal and mitochondrial fatty acid oxidation, microsomal fatty acid hydroxylation, lipoprotein, bile and amino acid metabolism, glucose homeostasis, biotransformation, inflammation control, hepato-carcinogenesis and other pathways, through a detailed analysis of the different known or putative PPARα target genes.

February 2004, Volume 61, Number 4, pp. 393–416

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