



Komisja d/s Współdziałania Nauk Chemiczno-Biologiczno-Medycznych przy Łódzkim Oddziale PAN

ul. Piotrkowska 137/139 90-434 Łódź tel.: 636 80 18 fax: 636 24 15

Łódź, dnia 21.09.2017 r.

ZAPROSZENIE

W dniach 6-8 października 2017 r. gościem Łódzkiego Oddziału PAN i Centrum Badań Molekularnych i Makromolekularnych PAN w Łodzi będzie **Prof. ERIC WESTHOF** (Institute of Molecular and Cellular Biology CNRS, University of Strasbourg, France). Zapraszam Państwa do wzięcia udziału w posiedzeniu Komisji ds. Współdziałania Nauk Chemiczno-Biologiczno-Medycznych przy Łódzkim Oddziale PAN, w ramach którego

Prof. ERIC WESTHOF

wygłosi wykład pt.

The third genetic code

Posiedzenie odbędzie się dnia **6 października 2017 r. (piątek)** o godz. 12:00 w Centrum Badań Molekularnych i Makromolekularnych PAN w Łodzi, ul. Sienkiewicza 112, Budynek A, Sala Konferencyjna 08/09 (parter).

Profesor E. Westhof jest światowej sławy autorytetem w zakresie biologii strukturalnej kwasów nukleinowych i w poznawaniu molekularnych podstaw procesu przekazywania informacji genetycznej (oddziaływania tRNA – mRNA – rRNA). Jest członkiem EMBO, Akademii Europejskiej, Francuskiej Akademii Nauk i Niemieckiej Akademii Nauk LEOPOLDINA. Pełni funkcję Edytora dwóch prestiżowych czasopism dedykowanych chemii i biologii kwasów nukleinowych, *Nucleic Acids Research* i *RNA Journal* (CV w załączeniu).

Ponieważ wykład będzie dotyczył fundamentalnych zagadnień biologii, do jego wysłuchania serdecznie zapraszam nie tylko Członków Komisji, ale także Państwa współpracowników, doktorantów i studentów.

Z poważaniem,

Prof. dr hab. Barbara Nawrot
Przewodnicząca Komisji

The third genetic code

Eric Westhof

ARN, IBMC-CNRS, University of Strasbourg, France.

An integrative view of all the complex interaction networks between mRNA, tRNA, and rRNA is described: the stability of codon-anticodon trimers, the conformation of the anticodon stem-loop of tRNA, the modified nucleotides, and the interactions with bases of rRNA at the decoding site. An information-rich, alternative representation of the codon table is derived. The new organization of the 64 codons is circular with an asymmetric distribution of codons that leads to a clear segregation between GC-rich 4-codon boxes and AU-rich 2:2-codon and 3:1-codon boxes. The advantage of integrating data in this circular decoding system is that all tRNA sequence variations can be visualized, within an internal structural and energy framework, for each organism and anticodon. Within this new representation, the multiplicity and complexity of nucleotide modifications, especially at positions 34 and 37 of the anticodon loop, segregate meaningfully and correlate well with the necessity to stabilize AU-rich codon-anticodon pairs and to avoid miscoding in split codon boxes. Modifications of U34 are critical to decode purine-ending codons in split codon boxes. This allows for diversity in codon usage depending on genomic GC content as well as on the number and types of isoacceptor tRNAs. Although universal, the genetic code is not translated identically and several differences exist between organisms in the three kingdoms of life. To decipher diversely but efficiently the genetic code, cells developed sophisticated arrays between tRNA pools and tRNA modifications, anchored in the cellular metabolic enzymatic pathways and guaranteeing protein homeostasis. We suggest that, beyond the table of the first genetic code and the second genetic code made of the recognition rules between aminoacyl-tRNA synthetases and their tRNA substrates, these integrating metabolic networks constitute a third genetic code.

Curriculum vitae

Eric WESTHOF

Born 25 July 1948 in Uccle (Belgium)

French nationality.

12, rue de Copenhague, 67000 Strasbourg.



Architecture et Réactivité de l'ARN, Université de Strasbourg,

Institut de biologie moléculaire et cellulaire du CNRS

15 rue René Descartes, 67084 Strasbourg.

Tél 03 88 417046 ; Fax 03 88 602218 –

Mail: E.Westhof@ibmc-cnrs.unistra.fr

University courses

- July 1971 : Licence en Sciences Physiques, (Université de Liège, Belgium).
- December 1974 : Docteur en Sciences, (Université de Liège, Belgium).

Professional courses

- September 1971 - August 1977 : PhD Grant from EURATOM (Commission à l'Energie Atomique Européenne) at Regensburg Universität (Germany) then "Wissenschaftlicher Assistent" at Regensburg Universität.
- August 1977 - January 1980 : "FULBRIGHT-HAYS Research Fellow" with M. SUNDARALINGAM (Department of Biochemistry, University of Wisconsin, Madison, USA) then "Postdoctoral Fellow".
- February 1980 - December 1980 : "Wissenschaftlicher Mitarbeiter" (Institut für Strahlenchemie, Max Planck Institut in Mülheim an der Ruhr, Allemagne).
- January 1981 - August 1981 : "Research Associate" (Department of Biochemistry, University of Wisconsin, Madison, USA).
- September 1981 - September 1983 : Post-doctoral fellowship EMBO (Organisation Européenne de Biologie Moléculaire) à de l'Institut de Biologie Moléculaire et Cellulaire (IBMC) of CNRS at Strasbourg (J.P.EBEL et D.MORAS).
- October 1983 – September 1984 : Associate Professor at Université Louis Pasteur (ULP).
- October 1984 -September 1988 : Chargé de recherches (CR1) du CNRS.
- Since October 1988 : Professor Structural Biochemistry at ULP.
- 1995-2005 : Chair in Structural Biology at the Institut Universitaire de France.
- January 2005 – September 2016 : Director of the Research Unit UPR9002 of the CNRS 'Architecture et réactivité de l'ARN' à l'IBMC (110 researches, technicians, students and PhDs).
- January 2006 – September 2016 : Director of the IBMC (more than 210 members).
- September 2016 : Emeritus Professor at the University of Strasbourg.
- Since 2016 : Delegate for teaching and formation at the French Academy of Sciences.

Member of

- European Molecular Biology Organization, EMBO (1998).
- Corresponding member of the Académie des Sciences (1999).
- Deutsche Akademie der Naturforscher LEOPOLDINA (2000).
- Academia Europaea (2001).
- Fellow of the American Association for the Advancement of Science (2001)
- Fellow of the Institute of Physics, London, U.K. (2004).
- Société française de Biochimie et de Biologie Moléculaire (President 2004-2009)
- RNA Society (Director 2000-2004; President-elect 2004; President 2005; Past President 2006).
- French Academy of Sciences, Académie des Sciences (2011).

University activities

- President of the Research commission of the Faculty of life sciences at the ULP (2003-2007).
- Elected member of the Scientific Council of the ULP (2002-2006).
- Vice-president for Research and Doctoral Studies of the Université Louis Pasteur (2007-2008)
- Vice-president for Research and Doctoral Studies of the Université de Strasbourg (2009-2012).

Editorial activities

- Associate editor of RNA, Cold Spring Harbor Laboratory.
- Executive editor of Nucleic Acids Research, Oxford University Press.
- Executive editor of Journal of Molecular Recognition, Wiley.

Prizes and Distinctions

- Prize Jacques MONOD (Institut Pasteur, 1992).
- Prize Charles-Léopold Mayer de l'Académie des sciences (2007).
- Medal Feodor Lynen, Gesellschaft für Biochemie und Molekulare Biologie (2011).
- Medal of the French Society for Biochemistry and Molecular Biology, SFBBM (2014).
- Chevalier de l'Ordre du mérite (2015).
- Lifetime Achievement Award, International RNA Society, Kyoto (2016).

Publications

437 publications in ISI Web of Knowledge (> 25 000 citations, h-index=83).

- Michel, F., and Westhof, E. (1990). Modelling of the three-dimensional architecture of group I catalytic introns based on comparative sequence analysis. Journal of molecular biology 216, 585-610.

- Westhof, E., Altschuh, D., Moras, D., Bloomer, A.C., Mondragon, A., Klug, A., and Van Regenmortel, M.H. (1984). Correlation between segmental mobility and the location of antigenic determinants in proteins. *Nature* 311, 123-126.
- Westhof, E., Dumas, P., and Moras, D. (1985). Crystallographic refinement of yeast aspartic acid transfer RNA. *Journal of molecular biology* 184, 119-145.
- Leontis, N.B., and Westhof, E. (2001). Geometric nomenclature and classification of RNA base pairs. *RNA* 7, 499-512.
- Brion, P., and Westhof, E. (1997). Hierarchy and dynamics of RNA folding. *Annual review of biophysics and biomolecular structure* 26, 113-137.
- Vicens, Q., and Westhof, E. (2001). Crystal structure of paromomycin docked into the eubacterial ribosomal decoding A site. *Structure* 9, 647-658.
- Westhof, E. (1988). Water: an integral part of nucleic acid structure. *Annual review of biophysics and biophysical chemistry* 17, 125-144.
- Massire, C., Jaeger, L., and Westhof, E. (1998). Derivation of the three-dimensional architecture of bacterial ribonuclease P RNAs from comparative sequence analysis. *Journal of molecular biology* 279, 773-793.
- Lescoute, A., and Westhof, E. (2006). Topology of three-way junctions in folded RNAs. *RNA* 12, 83-93.
- Lescoute, A., Leontis, N.B., Massire, C., and Westhof, E. (2005). Recurrent structural RNA motifs, Isostericity Matrices and sequence alignments. *Nucleic acids research* 33, 2395-2409.
- Grosjean, H. and Westhof, E. (2016). An integrated, structure- and energy-based view of the genetic code. *Nucleic Acids Res.* 44, 8020-8040.
- Rozov, A., Demeshkina, N., Khusainov, I., Westhof, E., Yusupov, M. and Yusupova, G. (2016) Novel base-pairing interactions at the tRNA wobble position crucial for accurate reading of the genetic code. *Nat Commun*, 7, 10457.
- Rozov, A., Demeshkina, N., Westhof, E., Yusupov, M. and Yusupova, G. (2016) New Structural Insights into Translational Miscoding. *Trends Biochem Sci*, 41, 798-814.
- Rozov, A., Westhof, E., Yusupov, M. and Yusupova, G. (2016) The ribosome prohibits the G*U wobble geometry at the first position of the codon-anticodon helix. *Nucleic Acids Res*, 44, 6434-6441.
- Miao, Z. and Westhof, E. (2015) Prediction of nucleic acid binding probability in proteins: a neighboring residue network based score. *Nucleic Acids Res*, 43, 5340-5351.
- Miao, Z., Adamiak, R.W., Blanchet, M.F., Boniecki, M., Bujnicki, J.M., Chen, S.J., Cheng, C., Chojnowski, G., Chou, F.C., Cordero, P. et al. (2015) RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. *RNA*, 21, 1066-1084.
- Westhof, E., Yusupov, M. and Yusupova, G. (2014) Recognition of Watson-Crick base pairs: constraints and limits due to geometric selection and tautomerism. *F1000Prime Rep*, 6, 19.
- Westhof, E. (2014) Isostericity and tautomerism of base pairs in nucleic acids. *FEBS Lett*, 588, 2464-2469.
- Demeshkina, N., Jenner, L., Westhof, E., Yusupov, M., and Yusupova, G. (2012). A new understanding of the decoding principle on the ribosome. *Nature* 484, 256-259.
- Cruz, J.A., and Westhof, E. (2011). Sequence-based identification of 3D structural modules in RNA with RMDetect. *Nature methods* 8, 513-521.

Edited books

- E. Westhof, « Water and Biological Macromolecules », Ed. McMillan, London (1993)
- E. Westhof & N. Hardy, « Folding and Self-assembly of Biological Macromolecules », Ed. World Scientific, Singapore (2004)
- R.K. Hartmann, A. Bindereif, A. Schön, E. Westhof, « Handbook of RNA Biochemistry », Ed. Wiley-VCH, Weinheim (2005)
- N. Leontis & E. Westhof, « RNA 3D Structure Analysis and Prediction », Ed. Springer, Berlin Heidelberg 2012.