

Pierre MILLARD

Personal details

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Research experiences

Since 2013 **Manchester Center for Integrative Systems Biology, Manchester Institute of Biotech.**
University of Manchester, Manchester, UK

Visiting academic in Systems biology ("Young researcher fellowship award", INRA; AgreenSkills Fellowship)

Project: "Towards the digital *E. coli*"

- Development of a kinetic model of *Escherichia coli* including signaling, metabolism and gene regulation

2009-2012 **Metasys team, Laboratoire d'Ingénierie des Systèmes Biologiques et Procédés**
INSA, Toulouse, France

PhD in Microbiology ("Young researcher fellowship award", INRA)

Project: "Role of the post-transcriptional regulator Csr in the carbon nutrition of laboratory and commensal strains of *Escherichia coli*"

- Development and validation of a complete methodology for quantitative, system-level investigations of the metabolism of *Escherichia coli*
 - Development of IsoDesign, a software for *in silico* optimization of experimental design for ¹³C-fluxomics
 - Development of methods to collect intracellular metabolites of *E. coli* for stationary and unstationary ¹³C-fluxomics
 - Quantitative metabolomics (MS-based)
 - Quantitative isotopic analysis by mass spectrometry
 - Development of IsoCor, a software for the treatment of MS isotopic data
 - Development of influx_s, a software for ¹³C-flux calculation
- System-level investigations of the role of the post-transcriptional regulator Csr in the control of the metabolism of *E. coli* strains (wild-type and Csr mutants of strains K-12 MG1655 and Nissle 1917) on a set of physiologically-relevant carbon sources
 - Obtaining metabolic knowledge on two phylogenetically distinct strains of *E. coli*
 - Obtaining detailed quantitative metabolic knowledge on *E. coli* growing on physiologically-relevant carbon sources
 - Role of the Csr system on the central metabolism of these strains
- Analysis of the growth-rate dependency of the metabolome of *E. coli* K-12 MG1655 on glucose

2009 (7 months) **Metasys team, Laboratoire d'Ingénierie des Systèmes Biologiques et Procédés (LISBP)**
INSA, Toulouse, France

Master Thesis in Structural biochemistry, Proteomics and Metabolomics

Project: "¹³C-metabolic flux analysis of *Escherichia coli* cultivated on fucose and gluconate"

- Development and validation of a sampling method of intracellular metabolites for steady-state ¹³C-fluxomics in *E. coli*
- Determination of intracellular flux distribution of *E. coli* on fucose and gluconate

2008 (3 months) Metasys team, Laboratoire d'Ingénierie des Systèmes Biologiques et Procédés (LISBP)

INSA, Toulouse, France

Project: "Study of the methylglyoxal pathway in *Escherichia coli*"

- Identification of the *in vivo* topology of the central metabolic network of *E. coli* on fucose
- Comparison of fucose metabolism in two *E. coli* strains (K-12 MG1655 and Nissle 1917)

2008 (4 months) Laboratoire de Synthèse et Physico-Chimie des Molécules d'Intérêt Biologique (SPCMIB)

Université Paul Sabatier, Toulouse, France

Project: "Folding of nucleic acid – stabilization of 'hairpin' structure"

- Synthesis of oligonucleotides with a conformationally restricted neutral linkage into their unpaired moiety
- Effect of these modifications on their folding and stability into defined secondary structure

Academic formation

2009	Master degree in Structural biochemistry, Proteomics and Metabolomics	Université Paul Sabatier (Toulouse, France)
2008	M.S. in Biochemistry and Molecular biology	Université Paul Sabatier (Toulouse, France)
2007	B.S. in Biochemistry and Molecular biology	Université Paul Sabatier (Toulouse, France)
2002	French high-school diploma	Lycée Bernard Palissy (Agen, France)

Skills

- **Biochemistry and microbial physiology**
 - Carbon and energy metabolism of *Escherichia coli*
 - Metabolic adaptation of *E. coli*
 - Role of post-transcriptional regulation in the control of *E. coli* physiology and metabolism
 - Metabolic diversity of *E. coli*
- **System-level approaches**
 - Microbial cultivation, high-throughput cultivation systems (microtiter plate reader, robotic platform)
 - ¹³C-metabolic flux analysis
 - Quantitative metabolomics (IDMS strategy) by MS and NMR
 - ¹³C-metabolomics
 - Quantitative isotopic analysis by MS and NMR
- **In silico tools & Modelling approaches**
 - Programming (Python and R programming languages, basic knowledge in C++ and Matlab)
 - Data processing (automated treatment of growth data, correction of MS data for naturally occurring isotopes, automated treatment of NMR spectra...)
 - Mathematical modelling of metabolic networks for ¹³C-fluxomics
 - Kinetic modelling of metabolic & gene regulatory networks
- **Analytical tools**
 - Liquid chromatography (anion exchange, strong cation exchange, reverse phase...)
 - Mass spectrometry (triple quadrupole – MRM, MIM, Scan modes... – and MALDI-TOF spectrometers)
 - LC-MS coupling
 - Nuclear magnetic resonance (¹H, ¹³C; 1D and 2D-NMR on a 500MHz and a 800MHz Bruker spectrometers equipped with cryoprobes)
 - Circular dichroism

Langages

French (mother tongue)
English (fluent)

Publications

Millard P., Letisse F., Sokol S., Portais J.C. (2013). IsoDesign : A software for optimizing the design of ^{13}C -metabolic flux analysis experiments. *Biotechnology and bioengineering*, DOI:10.1002/bit.24997.

Revelles O., **Millard P.**, Nougayrède J.P., Oswald E., Létisse F. and Portais J.C. (2013). The Carbon Storage Regulator (Csr) system exerts a nutrient-specific control over central metabolism in *Escherichia coli* strain Nissle 1917. *Plos One*, 8(6).

Millard P., Letisse F., Sokol S., Portais J.C. (2012). IsoCor: Correcting MS data in isotope labeling experiments. *Bioinformatics*, 28(9):1294-1296.

Sokol S., **Millard P.**, Portais J.C. (2012). influx_s: increasing numerical stability and precision for metabolic flux analysis in isotope labelling experiments. *Bioinformatics*, 28(5):687-693.

Boissonnet A., Dupouy C., **Millard P.**, Durrieu M.P., Tarrat N. et Escudier J.M. (2011). α,β -D-CNA featuring canonical and noncanonical α/β torsional angles behaviours within oligonucleotides. *New J. Chem*, 35, 1528-1530.

Dupouy C., **Millard P.**, Boissonnet A., Escudier J.M. (2010). α,β -D-CNA preorganization of unpaired loop moiety stabilizes DNA hairpin (2010). *Chem Commun*, 46(28):5142-5144.

Communications

- **Oral presentations**

ThEcoli: a kinetic model of *Escherichia coli* central metabolism. 30 August – 3 September 2013, 14th International Conference on System Biology, Copenhagen, Denmark

IsoCor and influx_s : Two bioinformatic tools for high-throughput ^{13}C -fluxomics. 21-23 May 2012, 6th scientific days of the French Network for Metabolomics and Fluxomics, Nantes, France

Mass spectrometry studies of metabolic systems: using the Pascal's triangle to probe the isotopologue space. 23-25 May 2011, 5th scientific days of the French Network for Metabolomics and Fluxomics, Paris, France

- **Posters**

Millard P., *et al.* (2012). IsoCor & influx_s: Bioinformatics tools for high-throughput ^{13}C -fluxomics. (25-28 June, Metabolomics Society 8th Annual Meeting, Washington, DC, USA)

Dubois M., **Millard P.**, *et al.* (2011). MetMS : identification software for global metabolomics. (23-25 May, 5th scientific days of the French Network for Metabolomics and Fluxomics, Paris, France)

Revelles O., **Millard P.**, *et al.* (2010). Role of Csr system in the metabolism and fitness of *Escherichia coli* Nissle 1917.

Millard P., Revelles O., *et al.* (2010). Systems biology of commensal and pathogenic *Escherichia coli* strains. (5-7 September, Current Opinion in Cellular Host-Pathogen Interactions, Amsterdam, The Netherlands)

Massou S., **Millard P.**, *et al.* (2009). High-accuracy LC-MS/MS quantification of isotopomer distribution in intracellular metabolites for ^{13}C -fluxomics. (30 August – 2 September, Fifth International Conference of The Metabolomics Society, Edmonton, Canada)

References

References available on request.