

Keynote seminar "Biologie & Clinique"

Dr Bertie Göttgens

Cambridge Institute for Medical Research, UK

Le Dr Göttgens étudie les réseaux de facteurs de transcriptions responsables du développement des cellules souches hématopoïétiques et des cellules endothéliales et leurs dérégulations dans les cellules leucémiques.

Regulatory Networks and Transcriptional Landscapes of Normal and Malignant Haematopoiesis

Invitation : Estelle Duprez - Centre de Recherche en Cancérologie de Marseille

Mardi 3 Juillet 2018 à 11h - *Accès libre*

Salle de Conférence du Centre d'Information, de Prévention et de Consultation en Cancérologie de l'Institut Paoli-Calmettes, entrée et parking 15 Bd Lei Roure - 13009 Marseille

Renseignements

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Centre de Recherche en Cancérologie de Marseille

Unité Mixte de Recherche

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Regulatory Networks and Transcriptional Landscapes of Normal and Malignant Haematopoiesis



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The long term research goal of the Göttgens group is to decipher the molecular hierarchy of regulatory transcriptional networks responsible for blood stem cell and endothelial development. To this end, the group uses complementary state-of-the-art approaches including embryonic stem cell and transgenic assays, bioinformatics, high throughput sequencing and mathematical modelling. The cumulative output of more than 40 research papers over the last 4 years has been the development of the most comprehensive network model for any adult stem cell type with over 40 transcription factors and more than 100 in vivo validated direct functional interactions. This integrated approach has resulted in the discovery of previously unrecognized combinatorial interactions between key regulators of blood stem cells with important implications for the transcriptional control of stem cell development and differentiation.

The importance of transcriptional control in both normal and leukemic cells is underlined by the large number of transcription factor genes that cause leukemia when disrupted or mutated. Future work will address how transcriptional programs are perturbed in specific subtypes of leukemia and may thus open up new avenues for the development of targeted therapies.

Retour
Cliquez Ici

Selected publications:

Single-cell analysis reveals the continuum of human lympho-myeloid progenitor cells.

Karamitros D, Stoilova B, Aboukhalil Z, Hamey F, Reinisch A, Samitsch M, Quek L, Otto G, Repapi E, Doondeea J, Usukhbayar B, Calvo J, Taylor S, Goardon N, Six E, Pflumio F, Porcher C, Majeti R, [Göttgens B](#), Vyas P
Nat Immunol. 2017 Nov 21. PMID:29167569.

Reconstructing blood stem cell regulatory network models from single-cell molecular profiles.

Hamey FK, Nestorowa S, Kinston SJ, Kent DG, Wilson NK, [Göttgens B](#).
Proc Natl Acad Sci U S A. 2017 Jun 6;114(23):5822-5829.

Blood: Education for stem cells.

Guibentif C, [Göttgens B](#).
Nature. 2017 May 25;545(7655):415-417.

Mammalian Transcription Factor Networks:

Recent Advances in Interrogating Biological Complexity

Wilkinson AC, Nakauchi H, [Göttgens B](#).
Cell Syst. 2017 Oct 25;5(4):319-331.

Resolving early mesoderm diversification through single-cell expression profiling.

Scialdone A, Tanaka Y, Jawaid W, Moignard V, Wilson NK, Macaulay IC, Marioni JC, [Göttgens B](#).
Nature. 2016 Jul 14;535(7611):289-293. doi: 10.1038/nature18633. Epub 2016 Jul 6. PMID:27383781

Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations.

Wilson NK, Kent DG, Buettner F, Shehata M, Macaulay IC, Calero-Nieto FJ, Sánchez Castillo M, Oedekoven CA, Diamanti E, Schulte R, Ponting CP, Voet T, Caldas C, Stingl J, Green AR, Theis FJ, [Göttgens B](#).
Cell Stem Cell. 2015 Jun 4;16(6):712-24. doi: 10.1016/j.stem.2015.04.004. Epub 2015 May 21. PMID:26004780

The JAK-STAT signaling pathway is differentially activated in CALR-positive compared with JAK2V617F-positive ET patients.

Lau WW, Hannah R, Green AR, [Göttgens B](#).
Blood. 2015 Mar 5;125(10):1679-81.

Growth factor independence 1 antagonizes a p53-induced DNA damage response pathway in lymphoblastic leukemia.

Khandanpour C, Phelan JD, Vassen L, Schütte J, Chen R, Horman SR, Gaudreau MC, Krongold J, Zhu J, Paul WE, Dührsen U, [Göttgens B](#), Grimes HL, Möröy T.
Cancer Cell. 2013 Feb 11;23(2):200-14.

RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis.

Lichtinger M, Ingram R, Hannah R, Müller D, Clarke D, Assi SA, Lie-A-Ling M, Noailles L, Vijayabaskar MS, Wu M, Tenen DG, Westhead DR, Kouskoff V, Lacaud G, [Göttgens B](#), Bonifer C.
EMBO J. 2012 Nov 14;31(22):4318-33.

LIF-independent JAK signalling to chromatin in embryonic stem cells uncovered from an adult stem cell disease.

Griffiths DS, Li J, Dawson MA, Trotter MW, Cheng YH, Smith AM, Mansfield W, Liu P, Kouzarides T, Nichols J, Bannister AJ, Green AR, [Göttgens B](#).
Nat Cell Biol. 2011 Jan;13(1):13-21.

Combinatorial transcriptional control in blood stem/progenitor cells: genome-wide analysis of ten major transcriptional regulators.

Wilson NK, Foster SD, Wang X, Knezevic K, Schütte J, Kaimakis P, Chilarska PM, Kinston S, Ouwehand WH, Dzierzak E, Pimanda JE, de Bruijn MF, [Göttgens B](#).
Cell Stem Cell. 2010 Oct 8;7(4):532-44.

Reprogramming of T cells to natural killer-like cells upon Bcl11b deletion.

Li P, Burke S, Wang J, Chen X, Ortiz M, Lee SC, Lu D, Campos L, Goulding D, Ng BL, Dougan G, Huntly B, [Göttgens B](#), Jenkins NA, Copeland NG, Colucci F, Liu P.
Science. 2010 Jul 2;329(5987):85-9.