|  |  |
| --- | --- |
| ***School/Department:*** | ***Department of Cell Biology, Erasmus MC*** |
| ***Supervisor information:*** | * *Prof dr D. Huylebroeck,* [*d.huylebroeck@erasmusmc.nl*](mailto:d.huylebroeck@erasmusmc.nl) * ***Selected publications:***   Dries R et al. ***Stem Cells****, in press.*  Dobreva MP\*et al. (2018). ***Development*** 145, dev157222.  Stryjewska A et al. (2017)***Stem Cells***35:611-625.  Wu LM et al (2016). ***Nat Neurosci.*** 19:1060-1072.  Scott CL et al. (2016). ***J Exp Med****.* 213:897-911.  Gomes Fernandes M et al.. (2016). ***J Exp Med***. 212, 2015-2025.  Omilusik KD et al (2015). ***J Exp Med***. 212, 2027-2039.  van den Berghe V et al (2013). ***Neuron*** 77, 70-82. |
| ***Project Title:*** | **Systems/Omics approaches to study nuclear interpretation of BMP signaling in stem/progenitor cells** |
| ***Abstract:*** | BMP signaling controls multiple cellular processes during embryogenesis and its developmental actions are recapitulated during tissue/organ repair. We study how these signals are interpreted within cells via co-operation of Smads and Smad-binding proteins, including transcription factors (TFs), serving the fine-tuning of the signaling and mounting proper and precise transcriptional responses in cell differentiation/maturation. Our analysis of (primarily conditional) knockout (KO) mice combined with intense biochemistry/omics studies has revealed in vivo functions and action mechanisms of single components of the BMP system. However, cell-culture models are needed to study how the BMP system integrates into gene regulatory networks of cells, including stem/progenitor cells, and maintains cell-state or controls exit from (pluri)potency into entry/progression of differentiation, followed by cell maturation. An overview of such regulations, including at the single-cell level, is missing for the BMP system. We use perturbation (esiRNA, CRISPR) of a prioritized list of components and multi-omics read-out in stem cells, using mouse embryonic stem cells (mESCs) as main cell type. We integrate mRNA expression dynamics, gene-gene interactions inferred from perturbations and single-cell mRNA-profiling, and develop technologies enabling simultaneous analysis of at least two omics techniques. Individual (esi-RNA based) perturbations reveal that the majority of gene-gene interactions in our list display cell-stage specific behavior in adjacent stages, but also robustness. |
| ***Requirements of candidate:*** | * We are looking for highly motivated, talented students to join our international team. * Master degree or MD. * A fair scholarship that covers subsistence allowance and international air plane ticket. * Working in the lab requires that the student has good communication skills. * English language requirement:   *English speaking countries & Netherlands:* no requirement  *Other countries:* IELTS 7.0 *(min 6.0 for all subs)*, TOEFL 100 *(min 20 for all subs)* |

**2020 CSC-PhD programme information will be shared and updated online:** [**https://www.eur.nl/en/about-eur/erasmus-university-china-center-0/cscscholarship/prospectivephd-candidates**](https://www.eur.nl/en/about-eur/erasmus-university-china-center-0/cscscholarship/prospectivephd-candidates)

**Application to:** [**EuccChinaOffice@eur.nl**](mailto:EuccChinaOffice@eur.nl) **before March 10, 2020**