COLLABORATIVE RESEARCH CENTER | SFB 680

Molecular Basis of Evolutionary Innovations

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Uncovering transcriptional regulatory principles of early human embryonic development

Distal regulatory elements, such as enhancers, play a preponderant role in the establishment of cell-type and developmental-stage specific gene expression profiles. However, these elements are difficult to identify, since they lack strong defining features and show limited sequence conservation. Using a combination of epigenomic approaches (ChIP-seq, RNA-seq) and ESC-based differentiation protocols, we have characterized the full enhancer repertoire of pluripotent (i.e. human embryonic stem cells (hESC)) and multipotent (i.e. human neural crest cells (hNCC)) human embryonic cell populations. In hESC, we uncovered a unique chromatin signature that identifies a novel class of enhancers, which are inactive but poised in hESC and that become active upon differentiation in a lineage-specific manner. Similarly, our epigenomic approach allowed us to characterize enhancers in hNCC, a hitherto largely inaccessible and biochemically intractable vertebrate-specific embryonic cell population. Importantly, NCC contribute to the formation of multiple tissues and organs, such as the peripheral nervous system and most of the facial bones and cartilages. Using the sequence information contained within hNCC enhancers, we uncovered NR2F1 and NR2F2, two orphan nuclear receptors, as novel neural crest and craniofacial regulators.

December 4 , 17:00

Institute for Genetics, Zülpicher Str. 47a,
New Seminar Room 0.46, Ground Floor

Host: Michael Lässig

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