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# 2018
# Faculty Candidate Seminar
# Rare Disease Genetics and Genomics

## *Inter*-chromosomal architecture of the non-coding genome in health and disease

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**Tuesday January 23, 2018**
4PM
Robert B Salter Auditorium
Peter Gilgan Centre for Research and Learning
686 Bay St.

*Determining how contacts between chromosomes (inter-chromosomal) are formed is critical to understand the spatiotemporal genome organization that impacts the biology and aetiology of disease. Studying translocation patients with the congenital cartilage malformation brachydactyly revealed that the long non-coding RNA (lncRNA) locus CISTR-ACT was part of inter-chromosomal contacts. Remarkably, the chromosomal translocations misplaced CISTR-ACT in the three-dimensional genomic architecture, thereby causing brachydactyly. So far, probing loci or allele positioning to study heterozygous disease states has been infeasible in living cells. Thus, Dr. Maass has established CRISPR-mediated live-cell imaging (CLING) techniques to provide the first spatiotemporal insights into loci and allelic positioning in living cells. Collectively, he addresses the mechanistic principles of non-coding loci and lncRNAs forming inter-chromosomal contacts by combining state-of-the-art approaches, such as high-throughput genomic techniques, 4D-imaging, murine in vivo models and patient samples. His interdisciplinary research explores how inter-chromosomal genome organization impacts development and disease mechanisms in a systems biology approach.*

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Summary

Dr. Maass has developed a live 4D-imaging technique to view inter-chromosomal interactions, implicating the misplacement of inter-chromosomal long non-coding RNA loci in human diseases that affect skeletal development

Proper spatiotemporal genome organization is crucial for gene regulation and developmental processes. While contacts on the same chromosome are well characterized, regulatory interactions between chromosomes (*inter*-chromosomal) also exist, but their molecular mechanisms remain elusive. Thus, determining how *inter*-chromosomal contacts are formed and impact normal and disease states is critical to better understand biology and aetiology of disease. Studying translocation patients with the congenital cartilage malformation brachydactyly revealed that the long non-coding RNA (lncRNA) locus *CISTR-ACT* was part of *inter*-chromosomal contacts. Remarkably, the chromosomal translocations misplaced *CISTR-ACT* in the three-dimensional genomic architecture, thereby causing brachydactyly. So far, probing loci or allele positioning to study heterozygous disease states has been infeasible in living cells. Thus, Dr. Maass has established CRISPR-mediated live-cell imaging (CLING) techniques to provide the first spatiotemporal insights into loci and allelic positioning in living cells. Collectively, he addresses the mechanistic principles of non-coding loci and lncRNAs forming *inter*-chromosomal contacts by combining state-of-the-art approaches, such as high-throughput genomic techniques**, 4D-imaging**, murine *in vivo* models and patient samples. His interdisciplinary research explores how *inter*-chromosomal genome organization impacts development and disease mechanisms in a systems biology approach.