Exploring the dynamic relationship between gene expression and chromosome organisation during X-chromosome inactivation

X-chromosome inactivation during early female development is an essential epigenetic process that is required to achieve appropriate dosage for X-linked gene products. We are interested in understanding how the differential treatment of the two X chromosomes in the same nucleus is set up during development and how this differential expression is then maintained, or reversed in certain circumstances, either normally or in a disease context such as cancer. The establishment of X inactivation involves the non-coding Xist RNA that triggers chromosome-wide chromatin re-organisation and gene silencing. Recent insights have been made into the nature of these chromosome-wide changes, including the global loss of topologically associated domains (TADs)\(^1,2,3\). However little is known about the underlying mechanisms and the precise relationship between 3D chromosome structure and altered gene expression states on the X chromosome. Results of our recent studies, using a combination of single-cell chromosome-conformation capture technologies and high-resolution microscopy in differentiating embryonic stem cells and in vivo mouse embryos, will be presented and the implications for development and disease will be discussed.