Title of Project	Investigating the role of centromeric RNA transcripts for centromere function and inheritance
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Summary of project
The centromere is a unique chromatin domain important for proper segregation of chromosomes during mitosis. In most organisms, the position of the centromere is determined epigenetically by the centromere-specific incorporation of the H3-variant CENP-A. Transcription at centromeres has been linked to the deposition of new CENP-A, although it is unclear whether transcription or the produced RNA are equally important. We and others have recently found that several components of the transcriptional machinery including RNA Polymerase II (RNAPII) and centromere-associated RNA transcripts temporally coincides with CENP-A loading in mitosis to G1. While we have evidence that the transcriptional process itself is required for CENP-A deposition at the centromere, this does not rule out a role for the centromeric transcripts themselves. To start we will identify the underlying DNA of *Drosophila* centromeres by deep-sequencing dCENP-A associated DNA fragments using the Oxford Nanopore technology (ONT). The assembly of large fragments will be achieved with the help of Alastair Kerr at the centre. Once assembly has taken place, we will purify the non-coding nascent centromeric RNA transcripts. With ultra long read sequencing (ONT and/or PacBio) we will map these transcripts to their underlying DNA templates. We will then seek to dissect the roles of transcription and RNA transcripts by identifying transcriptional start sites, potential promoters and transcription factor binding sites. Specifically targeting transcriptional repressors or RNases to centromeric loci will help to investigate the role of transcription in centromere inheritance and function. This work will be performed using Drosophila tissue culture cells as our model system.