



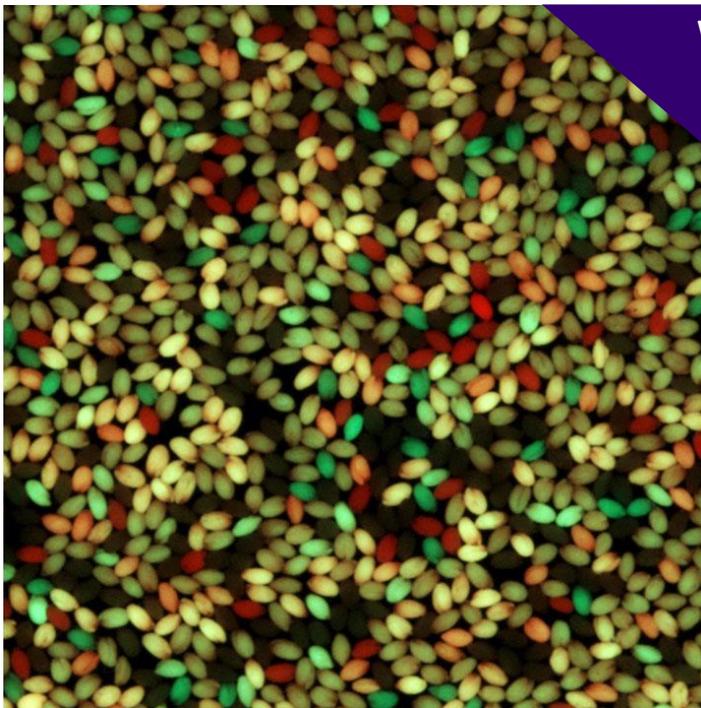
Biology Seminar

By: Dr. Ian Henderson

University of Cambridge | Reader in Genetics and Epigenetics, Department of Plant Sciences

<https://www.plantsci.cam.ac.uk/research/ianhenderson>

Genetic and epigenetic control of meiotic recombination in plant genomes



Wednesday, April 08, 2020 | 09:30am

Zoom Seminar:

<https://washington.zoom.us/j/532849333>

Meiosis is a highly conserved eukaryotic cell division that produces gametes required for sexual reproduction. During meiosis, homologous chromosomes undergo recombination, which can result in reciprocal crossover and gene conversion. Meiosis and recombination have a profound effect on natural genetic variation and genome evolution, which in turn has strategic importance for crop breeding. I will present our work using genome-wide methods to map meiotic recombination, primarily in the model plant *Arabidopsis thaliana*.

We have investigated the role of chromatin and epigenetic information on recombination, which has revealed hotspots of recombination associated with nucleosome-free regions in gene promoters and terminators. Surprisingly, we also observe recombination hotspots in specific classes of

transposons, including Helitrons. We have demonstrated the importance of chromatin by using RNA-directed DNA methylation to epigenetically silence a crossover hotspot.

Most recently, we have been studying the centromeres, which are some of the least understood, and typically unassembled, regions of chromosomes - despite playing a critical role in segregation and spindle attachment. The *Arabidopsis* centromeres are composed of megabase scale arrays of ~178 bp satellite repeats, interspersed with retrotransposons. From our maps of recombination it is clear that centromeric regions are suppressed for meiotic crossovers. Paradoxically, the satellite arrays bear abundant signatures of recombination, which must occur in order to generate these heavily duplicated sequences. Therefore, major questions remain concerning how these satellite arrays are generated and evolve.

Recently, new possibilities have emerged with the advent of long read sequencing technologies (e.g. PacBio and Nanopore). We are actively using these approaches to assemble the satellite arrays. We are combining these technologies with classical genetics in order to ask, (i) which recombination pathways mediate changes to centromere satellite arrays, (ii) to what extent is mitotic versus meiotic recombination involved, and (iii) what are the roles of epigenetic marks? Ultimately, I hope this work will provide new insights into the evolution of centromere satellite arrays generally across eukaryotes.

Seminar Speaker Host: Takato Imaizumi

