Recombination and chromatin landscapes in the wheat genome
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Q&A session

Presenter: Ian Henderson, Department of Plant Sciences, University of Cambridge, UK

The webinar recording is available on the IWGSC YouTube channel at: https://youtu.be/k7rNGoePF74

Q: Do you think we could promote recombination in lower-recombination regions in wheat? Maybe with histone modifications?

Yes, possibly via targeting something like H3K27me3, or possibly by removng heterochromatin (eg reducing DNA methylation or H3K9me2).
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Q: What is unique of Gypsy to make these hide in heterocromatin? One would imagine that transposons need expression to move and hence would accumulate in the more relax chromatin space

Unclear, but transposons of different families have quite different preferences in where they integrate - some prefer gene rich regions, whereas others prefer the centromere. Why or how this is achieved is not well understood.
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Q: You nicely showed correlations between recombination rates and ChIP seq signal across the chromosome, but there are very clear, localised deviations from this. Do you have a possible explanation for this?

Possibly due to structural rearrangements such as inversions or indels.
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Q: Are the recombination profiles of sub-genome relatives the same or is it more pronounced in the 3-subgenome collective?

The D genome may have slightly lower recombination rates due to smaller size, but overall trends were similar over the three subgenomes.
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Q: Does methylation causes the gene silencing every time? what about the location of methylation?

Certainly methylation in gene promoters will prevent transcription, but location is important. For example, gene body methylation is rather associated with high transcription
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Q: Do you see a how this information could be used to modify recombination ? either frequencies or positions?

It's possible that H3K27me3 could be targeted in a specific way (eg using dCAS9) to test if this mark is sufficient

Q: Do you think that increasing the recombination rate on the near centromeric region would have any effect on the stable inheritance of wheat?

It's hard to say - it could certainly break up some of the large linkage blocks in those regions. However, in some species centromere proximal crossovers can be associated with anueploidy, so there could be problems with this strategy.

Q: Are recombination rate are genotype dependant?

Overall recombination rate is quite stable within species, but the local recombination topology can be different depending on the two sets of chromosomes that are recombining.
can we manipulate recombination rate by applying external stimulation?

Q: Are the wheat chromosomes too long to recombine safely close to the centromere (what happens to the progeny of rare centromeric recombinants

Yes it's interesting to speculate whether the extreme distal recombination pattern is adaptive or not, or just a consequence of the large genome architecture.

Q: Did you investigate copy number variation potential effect on recombination rate?

We didn't have the data available to do this, but where we have looked in Arabidopsis, SVs and CNVs appear to associate with repressed crossover.

Q: One of his stated aims for studying recombination in wheat is possibly to manipulate it in order to facilitate selective breeding. Has manipulation been tried / demonstrated in Arabidopsis?

Yes we have found strategies in Arabidopsis that are sufficient to modify recombination, eg HEI10 overexpression can increase crossovers, and loss of DNA methylation can change centromere-proximal crossovers. Translating these findings into wheat has been challenging!