

8th World Congress on

PLANT GENOMICS AND PLANT SCIENCE

August 10-11, 2018 Osaka, Japan

The DNA landscape in *Avena*: Chromosome and genome evolution defined by major repetitive DNA classes in whole-genome sequence reads**Qing Liu**

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Cultivated oat (*Avena sativa*) was inferred to experience ancient allotetraploidy and subsequent recent allohexaploidy events involving C-, A-, and D-genome ancestors ($x=7$). Whole-genome sequencing followed by k-mer and RepeatExplorer clustering analyses enabled assessment of repetitive DNA composition in cultivated oat and its wild relatives' genomes. Fluorescence *In Situ* Hybridization (FISH)-based karyotypes were developed to understand chromosome and repetitive sequence evolution of cultivated oat. Repetitive DNA proportions were 71.962%-73.596% with the more abundant gypsy (42.882%-44.004%) than copia (15.938%-17.445%) retrotransposons in four *Avena* species genomes. FISH karyotype of cultivated oat was constructed by using twenty-five genome-specific probes, all chromosomes involved intergenomic translocations. The mean recombination rate varied from 0.0411 of chromosome pair number (cpn) 39/40 up to 0.2430 cM/Mbp of cpn 27/28 and the recombination rate of C-Genome Chromosomes (GC) is higher than that of A/D-GC. The results provide a molecular toolkit to characterize repeat abundance and sequence composition in *Avena* genomes, determine different maternal progenitors involved in multiple hybridization events of *Avena sativa* and facilitate genetic improvement of this vital crop. In addition, the study generated various data resources that are available for future exploration of the *Avena sativa* genome.

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