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Computational Prediction and Characterization of 3D Genome Organization in *Brassica napus*

ADDRESS

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Background: The recent development of Hi-C (and related methods) has allowed for unprecedented sequence-level investigations into the structure-function relationship of the genome. Briefly, Hi-C is able to detect regions of the genome that are in close 3D spatial proximity (or "interacting"). This has allowed for the identification of complex gene regulatory networks that involve distal (and potentially trans-chromosomal) regions of the genome. Many computational methods have since been developed that leverage Hi-C data to predict 3D genome organization. These methods have been extensively used to characterize 3D genome organization in various model organisms (such as yeast, fruit flies and humans). Unfortunately, the investigation of 3D genome prediction in allopolyploid organisms like *Brassica napus* is lacking. This is problematic since the research community has proposed many cross-species "hallmarks" of 3D genome organization (such as chromosome territories, distinct regions of the nucleus occupied by a single chromosome) without confirming their existence in allopolyploid genomes.

Objective: Investigate the existence of previously identified hallmarks of 3D genome organization in the allopolyploid *Brassica napus*.

Methodology: A Hi-C library was generated with leaf tissue from *Brassica napus* genotype DH12075. New and existing computational tools were utilized to trim, map and normalize the raw sequencing reads from the Hi-C library resulting in the generation of a normalized whole-genome contact map. This contact map was used to predict and characterize the 3D genome organization. Results of the prediction were compared to the proposed hallmarks of genome organization identified in other model organisms. Finally, additional datasets depicting epigenetic marks and transcriptional activity were combined with the predicted structure to identify 3D gene regulatory networks.

Results & Conclusion: The computational prediction and characterization of 3D genome organization in *Brassica napus* revealed close association and increased interaction among homoeologous chromosomes. These characteristics have the potential to disrupt previously proposed hallmarks of 3D genome organization such as chromosome territories. Furthermore, the 3D gene regulatory networks presented here may help understand the complex biological mechanisms underlying gene expression in *Brassica napus*. Overall, this research provides invaluable insight into the 3D organization of the allopolyploid *Brassica napus*.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS