

## **Visualization of orthology-based plant genome zipper seeding using circular diagrams**

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### **Abstract**

Building plant genome zippers is a critical step for construction of physical maps of newly sequenced genomes. Typically, blocks of conserved orthologs in evolutionary related plant species are calculated and used to seed genome zippers, which are further sorted based on a set of experimentally derived markers.

While traditional visualization techniques for genome zippers include color bars connected with lines, here we present a mechanism that generates a circular diagram plot representing conserved orthology blocks among the three selected plant species. The information underlining the plot is inferred via an automatic algorithm that starts with a set of query sequences with unknown physical mapping and two sets of genes in related plant species with available physical maps.

The algorithm calculates orthology relationships and conserved blocks among unmapped sequences from the newly sequenced species and the two mapped plant species and produces a circular diagram of the genome zipper seeding, which can be later enhanced with markers to extrapolate valid physical maps. In the near future, our visualization method can easily scale up and allow simultaneous analysis of mapping similarities and differences of up to 10 plant species – a feat that cannot be achieved with current visualization methods.

This approach is currently developed as part of a Canadian Wheat Alliance comparative genomics project to infer and improve physical maps for staple crops such as wheat and other related plant species.