

Deborah Weighill (Jacobson lab)

Computational Systems Biology

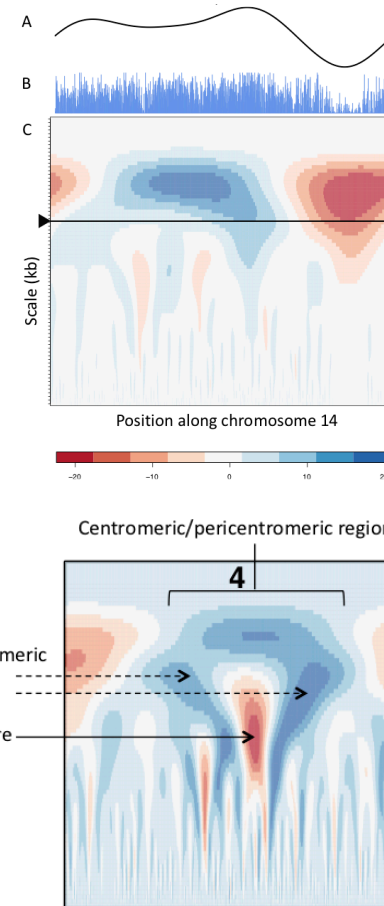


Novel approach: Wavelet-based Genomic Signal Processing for Centromere Identification and Hypothesis Generation. First ever genome-wide use of wavelet theory.

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| Objective | <ul style="list-style-type: none">Use wavelet-based signal processing to identify centromere positions in <i>Populus trichocarpa</i> from available multi-omic data. |
| New science | <ul style="list-style-type: none">Performed wavelet-based signal processing of density signals from variant and methylation data.Identified centromeric regions in <i>P. trichocarpa</i> from resulting wavelet coefficients.Co-evolution analysis identified concentrations of variants in the centromeric regions correlated with variants in a putative <i>P. trichocarpa</i> CENH3 protein, a centromere-specific histone. |
| Impact | <ul style="list-style-type: none">Centromere location is important in investigations involving recombination, such as genomic selection. CENH3 correlation analysis supports the hypothesis that the sequence of the centromere is co-evolving with the centromere-interacting CENH3. |

Wavelet-based Genomic Signal Processing for Centromere Identification and Hypothesis Generation.

Weighill D, Macaya-Sanz D, DiFazio S, Joubert W, Shah M, Schmutz J, Sreedasyam A, Tuskan G and Jacobson D (2019) Front. Genet. 10:417. doi: 10.3389/fgene.2019.00487



CWT and Smooth Peaks.

CWT landscape of the gene density profile of chromosome 14. (B) is the original gene density signal, (C) is the CWT coefficient landscape of the signal and (A) shows the vector of wavelet coefficients of the scale corresponding to the large scale valley, as shown by the arrow in C.

Methylation Wavelet Signature of Centromere.

“Tooth-x-ray” centromeric signature for SNP density consisting of a broad scale peak encompassing the centromeric/pericentromeric regions, and the lower scale valley within the large peak indicating the centromeric region.