Fluorescence in situ hybridization and optical mapping to correct scaffold arrangement in the tomato genome
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Abstract
The order and orientation (arrangement) of all 91 sequenced scaffolds in the 12 pseudomolecules of the recently published tomato (Solanum lycopersicum, 2n = 2x = 24) genome sequence were positioned based on marker order in a high-density linkage map. Here, we report the arrangement of these scaffolds determined by two independent physical methods, bacterial artificial chromosome - fluorescence in situ hybridization (BAC-FISH) and optical mapping. By localizing BACs at the ends of scaffolds to spreads of tomato synaptonemal complexes (= pachytene chromosomes), we showed that 45 scaffolds, representing a third of the tomato genome, were arranged differently than predicted by the linkage map. These scaffolds occur mostly in pericentric heterochromatin where 77% of the tomato genome is located and where linkage mapping is less accurate due to reduced crossing over. Although useful for only part of the genome, optical mapping results were in complete agreement with scaffold arrangement by FISH, while often disagreeing with scaffold arrangement based on the linkage map. The scaffold arrangement based on FISH and optical mapping changes the positions of hundreds of markers in the linkage map, especially in heterochromatin. These results suggest that similar errors exist in pseudomolecules from other large genomes that have been assembled using only linkage maps to predict scaffold arrangement, and these errors can be corrected using FISH and/or optical mapping. Of note, BAC-FISH also permits estimates of the sizes of gaps between scaffolds, and unanchored BACs are often visualized by FISH in gaps between scaffolds and thus represent starting points for filling these gaps.