

Recombination patterns reveal information about centromere location on linkage maps - DTU Orbit (09/11/2017)

Recombination patterns reveal information about centromere location on linkage maps

Linkage mapping is often used to identify genes associated with phenotypic traits and for aiding genome assemblies. Still, many emerging maps do not locate centromeres – an essential component of the genomic landscape. Here, we demonstrate that for genomes with strong chiasma interference, approximate centromere placement is possible by phasing the same data used to generate linkage maps. Assuming one obligate crossover per chromosome arm, information about centromere location can be revealed by tracking the accumulated recombination frequency along linkage groups, similar to half-tetrad analyses. We validate the method on a linkage map for sockeye salmon (*Oncorhynchus nerka*) with known centromeric regions. Further tests suggest that the method will work well in other salmonids and other eukaryotes. However, the method performed weakly when applied to a male linkage map (rainbow trout; *O. mykiss*) characterized by low and unevenly distributed recombination – a general feature of male meiosis in many species. Further, a high frequency of double crossovers along chromosome arms in barley reduced resolution for locating centromeric regions on most linkage groups. Despite these limitations, our method should work well for high-density maps in species with strong recombination interference and will enrich many existing and future mapping resources.

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