

Publication

A high-density genetic map reveals variation in recombination rate across the genome of *Daphnia magna***JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 3705177**Author(s)** Dukić, Marinela; Berner, Daniel; Roesti, Marius; Haag, Christoph R.; Ebert, Dieter**Author(s) at UniBasel** [Ebert, Dieter](#) ; [Dukic, Marinela](#) ; [Berner, Daniel](#) ; [Rösti, Marius](#) ;**Year** 2016**Title** A high-density genetic map reveals variation in recombination rate across the genome of *Daphnia magna***Journal** BMC genetics**Volume** 17**Number** 1**Pages / Article-Number** 137

Recombination rate is an essential parameter for many genetic analyses. Recombination rates are highly variable across species, populations, individuals and different genomic regions. Due to the profound influence that recombination can have on intraspecific diversity and interspecific divergence, characterization of recombination rate variation emerges as a key resource for population genomic studies and emphasises the importance of high-density genetic maps as tools for studying genome biology. Here we present such a high-density genetic map for *Daphnia magna*, and analyse patterns of recombination rate across the genome.; A F2 intercross panel was genotyped by Restriction-site Associated DNA sequencing to construct the third-generation linkage map of *D. magna*. The resulting high-density map included 4037 markers covering 813 scaffolds and contigs that sum up to 77% of the currently available genome draft sequence (v2.4) and 55% of the estimated genome size (238 Mb). Total genetic length of the map presented here is 1614.5 cM and the genome-wide recombination rate is estimated to 6.78 cM/Mb. Merging genetic and physical information we consistently found that recombination rate estimates are high towards the peripheral parts of the chromosomes, while chromosome centres, harbouring centromeres in *D. magna*, show very low recombination rate estimates.; Due to its high-density, the third-generation linkage map for *D. magna* can be coupled with the draft genome assembly, providing an essential tool for genome investigation in this model organism. Thus, our linkage map can be used for the on-going improvements of the genome assembly, but more importantly, it has enabled us to characterize variation in recombination rate across the genome of *D. magna* for the first time. These new insights can provide a valuable assistance in future studies of the genome evolution, mapping of quantitative traits and population genetic studies.

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