

Publication

An SNP-based second-generation genetic map of *Daphnia magna* and its application to QTL analysis of phenotypic traits**JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 2827147**Author(s)** Routtu, J.; Hall, M. D.; Albere, B.; Beisel, C.; Bergeron, R. D.; Chaturvedi, A.; Choi, J. H.; Colbourne, J.; De Meester, L.; Stephens, M. T.; Stelzer, C. P.; Solorzano, E.; Thomas, W. K.; Pfrender, M. E.; Ebert, Dieter**Author(s) at UniBasel** [Ebert, Dieter](#) ; [Routtu, Jarkko](#) ;**Year** 2014**Title** An SNP-based second-generation genetic map of *Daphnia magna* and its application to QTL analysis of phenotypic traits**Journal** BMC genomics**Volume** 15**Number** 1**Pages / Article-Number** 1033**Keywords** life-history; local adaptation; phototactic behavior; introduced predators; adaptive evolution; genome size; linkage map; fresh-water; zooplankton; plasticity**Mesh terms** Animals; Chromosome Mapping; Cluster Analysis; *Daphnia*, genetics; Female; Gene Frequency; Genetic Association Studies; Genetic Linkage; Genetic Markers; Genome; Genome Size; Genotype; Lod Score; Male; Phenotype; Polymorphism, Single Nucleotide; Quantitative Trait Loci; Quantitative Trait, Heritable

Background: Although *Daphnia* is increasingly recognized as a model for ecological genomics and biomedical research, there is, as of yet, no high-resolution genetic map for the genus. Such a map would provide an important tool for mapping phenotypes and assembling the genome. Here we estimate the genome size of *Daphnia magna* and describe the construction of an SNP array based linkage map. We then test the suitability of the map for life history and behavioural trait mapping. The two parent genotypes used to produce the map derived from *D. magna* populations with and without fish predation, respectively and are therefore expected to show divergent behaviour and life-histories. Results: Using flow cytometry we estimated the genome size of *D. magna* to be about 238 mb. We developed an SNP array tailored to type SNPs in a *D. magna* F2 panel and used it to construct a *D. magna* linkage map, which included 1,324 informative markers. The map produced ten linkage groups ranging from 108.9 to 203.6 cM, with an average distance between markers of 1.13 cM and a total map length of 1,483.6 cM (Kosambi corrected). The physical length per cM is estimated to be 160 kb. Mapping infertility genes, life history traits and behavioural traits on this map revealed several significant QTL peaks and showed a complex pattern of underlying genetics, with different traits showing strongly different genetic architectures. Conclusions: The new linkage map of *D. magna* constructed here allowed us to characterize genetic differences among parent genotypes from populations with ecological differences. The QTL effect plots are partially consistent with our expectation of local adaptation under contrasting predation regimes. Furthermore, the new genetic map will be an important tool for the *Daphnia* research community and will contribute to the physical map of the *D. magna* genome project and the further mapping of phenotypic traits. The clones used to produce the linkage map are maintained in a stock collection and can be used for mapping QTLs of traits that show variance among the F2 clones.

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