



Universität
Basel

Research Project

Daphnia Functional Genomics Resource

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Project title Daphnia Functional Genomics Resource

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Organisation / Research unit

Departement Umweltwissenschaften / Evolutionary Biology (Ebert)

Department

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Daphnia Functional Genomics Resource

Understanding the interaction of the genome and the environment is an important public health consideration since many human disorders with complex genetic architectures are highly influenced by interactions between genetic and environmental factors. A critical need is the development of study systems with well advanced genomic infrastructures that also have tractable and well understood ecological contexts. Daphnia is a logical candidate study system for further development to fill this gap. Daphnia has long been considered one of the premiere systems for ecological study and recent advances have lead to a rapidly expanding genomic infrastructure including a complete genome sequence and gene expression arrays. To advance Daphnia as a model for understanding the interplay between genome structure/function and environmental factors in the development of complex phenotypes, we propose to establish mapped QTL panels and a SNP database as a shared resource for the research community. Since unique genotypes of Daphnia can be maintained indefinitely through clonal reproduction, mapped QTL panels will provide a sustainable resource enabling multiple researchers to capitalize on the rapidly advancing genomic infrastructure of Daphnia. Increasingly, research on complex phenotypes utilizes a combination of QTL analysis and microarray expression profiles (eQTLs). The application of these two methods, referred to as

genetical genomics, in a model system in which environmental conditions can be accurately and systematically manipulated will significantly advance our understanding of the relationship between the phenotype and the underlying genotypic and environmental effects.

Specifically we will: (1) Establish QTL mapping panels of F2 recombinant lines from relevant strains of Daphnia. (2) Develop a SNP database to facilitate fine-scale mapping. (3) Generate a high-density genetic map for each panel using a combination of microsatellite loci and SNP markers. (4) Establish the bioinformatics infrastructure to integrate genetic and phenotypic data from these panels with existing genomic data. (5) Maintain and distribute live cultures of the recombinant lines to enable QTL studies relevant to a wide range of research areas and provide bioinformatics support for this resource.

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