
ZOOLOGISCHES KOLLOQUIUM
des Zoologischen Institutes
im
HÖRSAAL DES BIOZENTRUMS

Mittwoch, den 30.06.2010 16 Uhr

„Environmental Gene
Regulation of an Expansive
Aquatic Arthropod Genome “

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Understanding the ecological context of genome structure, function and evolution begins by sequencing the genomes of species that are sentinels within ecosystems. The recent investigations by the /Daphnia /Genomics Consortium are uncovering how this micro-crustacean's gene inventory and regulation are products of the many challenges common in aquatic environments. A surprising result from the /D. pulex /genome annotation project is its impressive catalog of genes; more than 1/3 of genes have no detectable homologs in any other available proteome. The large gene count is due to numerous gene duplications that yield an abundance of tandem gene clusters that are specific to the /Daphnia /lineage.

Using tiling-path and multi-plex high-throughput microarrays that probe the entire sequenced genome, we conduct experiments that sample the transcriptome during development and reproduction, and during distinct ecological challenges. These experiments simultaneously annotate the boundaries of gene models, identify alternative transcripts, increase the gene count by over 40% and reveal the functional diversity of orphaned and expanded gene families. Our investigation of gene expression under varying environmental conditions shows that the lineage-specific genes are the most responsive to ecological challenges.

These studies contribute to and benefit from the Daphnia Genomics Consortium.
<http://daphnia.cgb.indiana.edu> <<http://daphnia.cgb.indiana.edu/>>

Gäste sind herzlich willkommen!

Die Mitarbeiter der Ökologie

→ bei Rückfragen: 470-8249 (Brabender)