Researchers provide detailed genetic information on fish commonly used in environmental toxicology studies

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The fathead minnow (Pimephales promelas) has long been a premier animal model for research and regulation related to environmental toxins. Unfortunately, however, genetic information about this species is incomplete. The lack of genome sequence information for the species has limited scientists' ability to dissect complex traits, evaluate genetic markers, identify gene regulatory sequences, and elucidate biological pathways.

Now investigators have addressed the need for genome-scale information for the fathead minnow by generating in-depth sequence information using next generation sequencing methods and making both the sequence data and two draft genome assemblies publicly available.

The information will enhance the utility of the fathead minnow as a model organism for studying the mechanisms of environmental toxins. "This research will help build the scientific foundation for greater use of predictive ecotoxicology and illustrates the collaborative synergy among industry, academia, and regulatory agency researchers," said Dr. Robert Hoke, lead author of the Environmental Toxicology & Chemistry study.

More information: Frank R. Burns et al. Sequencing and de novo draft assemblies of a fathead minnow ( ) reference genome , *Environmental Toxicology and Chemistry* (2015). DOI: 10.1002/etc.3186

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