Douglas L. Crawford, PhD

Director, Marine Genomics Laboratory

Associate Professor, Marine Biology & Fisheries

NSF-NIEHS Oceans & Human Health Center Role: Co-PI Genomic HABs, Co-PI Genomic Core

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Education

- 1980 - B.S. University of Washington, Seattle, WA
- 1983 - M.S. University of Kansas, Lawrence, KS
- 1989 - Ph.D. Johns Hopkins University, Baltimore, MD
- 1991 - Post. Doc. Hopkins Marine Station, Stanford University, Monterey, CA

Research Interests

My research seeks to define and understand evolutionary adaptation by integrating different levels of biological understanding: behavior, physiology, enzyme functions, DNA sequence variation and genomics. My first publications were on behavioral ecology (ant communications, optimal patch use in birds and army ants, thermal regulation). Since then my research has focused on biochemical and molecular traits in order to gain a finer resolution of how animals evolve. Importantly, evolutionary analyses also provide a better understanding of molecular and biochemical processes. This duality: using evolution to understand molecular physiology and using molecular traits to investigate evolutionary processes is the foundations of my research.

My primary research focus is the study of variation in gene expression and its physiological and evolutionary importance. To better understand the biological importance of gene expression, we are developing Functional Genomics tools for the teleost fish Fundulus. These tools include greater than 8,000 unique *Fundulus* cDNAs for microarray studies, bioinformatics to annotate and investigate these genes, and statistical capabilities to analyze large microarray datasets. Microarrays are thousands of micro-formatted DNA samples printed onto microscope slides in a precise and known pattern. Each DNA spot represents a single gene that is used to measure mRNA expression by hybridizing to fluorescently labeled mRNA. Thus, microarrays can be used to determine the patterns of mRNA expression for virtually all expressed genes in an organism, organ, or cell type. Our initial microarrays studies have examined the magnitude of variation and biological parameters that affect gene expression. Thus, similar to protein polymorphisms, our microarray analyses revealed that approximately 18% of genes differ significantly between healthy individuals within a population. Typically, this difference among individuals for a gene is 1.5 fold but often exceeds 2.5 fold. Differences among populations increase this variation. The majority of the variation among populations is most parsimoniously described as random because it correlates with the variation within populations. Some genes have unexpected patterns of expression: changes in gene expression unrelated to evolutionary distance. These data indicating substantial variation in gene expression, provide evidence that quantitative variation is important for evolution and that this variation within and between populations needs to be considered in medically relevant studies. To better understand the meaning of the variation in gene expression, we are investigating the relationship between how changes in mRNAs relate to changes in protein concentration, physiological performance, ecological setting and evolutionary divergence. This broad approach requires a diversity of research methods and critical thought.

Representative Publications

Anchordoguy, T.J., **D.L. Crawford**, I. Hardewig, and S.C. Hand. 1996. Heterogeneity of DNA binding to membranes used in quantitative dot blots. **Biotechniques** 20:754-755.

Artigues, A., **D.L. Crawford**, A. Iriate, and M. Martinez-Carrion. 1998. Divergent Hsc70 binding properties of mitochondrial and cytosolic asparate aminotransferase: implications for their segragation to different cellular compartments. **Journal of Biological Chemistry** 273:33130-33134.

Artigues, A., M.T. Bengoechea-Alonso, **D.L. Crawford**., A. Iriate, and M. Martinez-Carrion. 2000. Biological implication of the different Hsc70 binding properties of mitochondrial and cytosolic aspartate aminotransferase, p 33130-33134. In M. Martinez-Carrion, A. Iriate, and H. Kagan (ed.), Vitamin B6 Dependent Proteins, PQQ and Quinoproteins, vol. 273. Birhauser Verlag, Basel, Switzerland.

Clark, M.S., **D.L. Crawford**, and A. Cossins. 2003. Worldwide genomic resources for non-model fish species. **Comparative and Functional Genomics** 4:502-508.

Crawford, D.L. , A.R. Place, and D.A. Powers. 1990. Clinal variation in the specific activity of lactate dehydrogenase-B. **Journal of Experimental Zoology** 255:110-113.

Crawford, D.L. 1995. Nuclear genes from the copepod *Calanus finmarchicus*. **Molecular Marine Biology & Biotechnology** 4:241-247.

Crawford, D.L. 2001. Functional genomics does not have to be limited to a few select organisms. **Genome Biology** 2:INTERACTIONS1001.

Crawford, D.L. 2002. Evolution of physiological adaptation. In K.B. Storey and J.M. Storey (ed.), Cell and Molecular Responses to Stress, vol 3. Elsevier Publishing, NY.

More Info:

http://crawford.rsmas.miami.edu/Doug/dougcrawford.htm