



Title: Bridging genotype to phenotype: using rainbow trout as a model species

Organizer & Affiliation: Yangfan Zhang (yangfan@zoology.ubc.ca), University of British Columbia

Co-organizer & Affiliation: Anthony Farrell (tony.farrell@ubc.ca), University of British Columbia

Co-organizer & Affiliation: Patricia M. Schulte (pschulte@zoology.ubc.ca), University of British Columbia

Description:

Bridging from genotype to phenotype is key goal for the biological sciences, because building this connection provides a deep understanding of how an organism functions and can respond to environmental change. Rainbow trout are an ideal model fish species in which to bridge this gap because of the rich and long history of studying environmental impacts on the physiology of this species, and the recent development of genomic tools. In this symposium we will showcase this new bridging of genotypic and phenotypic knowledge for rainbow trout. Rainbow trout are indigenous to the northwest of North America, but humans have successfully introduced rainbow trout to all continents, except for the Antarctic, and hatchery stocking of some strains of rainbow trout is utilized extensively across both the native and introduced range. This clearly illustrates that this species has an impressive ability to adapt to different environments. Indeed, the ability of rainbow trout to succeed over a short evolutionary time in face of drastic environmental change makes rainbow trout a candidate model species to ask three key questions: What genotypic changes have occurred in populations of different habitats? Do these genotypic changes correspond to phenotypes that evolve differentially across geographic gradients? How does this genotypic diversity, variation in gene expression or an amalgamation of both contribute to phenotypic diversity? This symposium will feature recent advances in genomics, transcriptomics and phenotypic characterization in rainbow trout. Collectively, we aim to showcase how it is possible to bridge multiple levels of biological organization and advance the frontier of knowledge about how environments shape genotype and gene expression to form a phenotype.