2021 Steelhead Environmental Epigenetics

May 2021

Publication

Nilsson E, Sadler-Riggleman I, Beck D, Skinner MK (2021) Differential DNA Methylation in Somatic and Sperm cells of Hatchery versus Wild (Natural-Origin) Steelhead Trout Population. Environmental Epigenetics. 7(1):1-17, dvab002.
PMID: 34040807, PMCID: PMC8132314, DOI: 10.1093/eep/dvab002

Summary

Environmental factors such as nutrition, stress, and toxicants can influence epigenetic programming and phenotypes of a wide variety of species from plants to humans. The current study was designed to investigate the impacts of hatchery spawning and rearing on steelhead trout (*Oncorhynchus mykiss*) vs the wild fish on a molecular level. Additionally, epigenetic differences between feeding practices that allow slow growth (2 years) and fast growth (1 year) hatchery trout were investigated. The sperm and red blood cells (RBC) from adult male slow growth/maturation hatchery steelhead, fast growth/maturation hatchery steelhead, and wild (natural-origin) steelhead were collected for DNA preparation to investigate potential alterations in differential DNA methylation regions (DMRs) and genetic mutations, involving copy number variations (CNVs). The sperm and RBC DNA both had a large number of DMRs when comparing the hatchery vs wild steelhead trout populations. The DMRs were cell type specific with negligible overlap. Slow growth/maturation compared to fast growth/maturation steelhead also had a larger number of DMRs in the RBC samples. A number of the DMRs had associated genes that were correlated to various biological processes and pathologies. Observations demonstrate a major epigenetic programming difference between the hatchery and wild natural-origin fish populations, but negligible genetic differences. Therefore, hatchery conditions and growth/maturation rate can alter the epigenetic developmental programming of the steelhead trout. Interestingly, epigenetic alterations in the sperm allow for potential epigenetic transgenerational inheritance of phenotypic variation to future generations. The impacts of hatchery exposures are not only important to consider on the fish exposed, but also on future generations and evolutionary trajectory of fish in the river populations.

Keywords: epigenetic inheritance; fish; generational; genomics; hatchery; phenotypic variation; rearing conditions; sperm; steelhead.