

Taxonomic (r)evolutions in *Oncorhynchus clarkii* (Cutthroat Trout): The future starts now

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In the 1950s, Robert Behnke reexamined the Cutthroat Trout and identified 14 subspecies based on morphological traits, Pleistocene events, and modern geographic ranges. His designations became instrumental in recognizing and preserving the remaining diversity of cutthroat trout. Molecular techniques have reinforced Behnke's phylogenies, but, have also revealed inconsistencies. To further resolve these relationships, we generated *de novo* transcriptomes for nine cutthroat subspecies, as well as a Bear River Bonneville form and two Colorado River lineages (Blue and Green). We present phylogenies of these subspecies generated from 1983 orthologous genes identified in the transcriptomes. We confirm many of the relationships identified in previous morphological and molecular studies and discuss the importance of significant differences apparent in our phylogeny within a geological perspective. Specific findings include three distinct clades: 1) Bear River Bonneville form and Yellowstone Cutthroat Trout; 2) Bonneville Cutthroat Trout ; and 3) Greenback and Rio Grande Cutthroat Trout. These findings suggest that recent Unified Species Concept-based species elevations were premature, promote taxonomic instability, and do not accurately capture the overall diversity contained in Cutthroat Trout. This resulting confusion, within both management agencies and the public, risks disruption of the goals of population preservation and restoration of Cutthroat Trout.