Conservation Units for steelhead trout in BC.

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A major impediment to the conservation of genetic variation within species is the absence of a systematic approach identifying rare and unusual populations.   The problem is particularly acute in the North temperate freshwater fish fauna.   Many of these species consist of large numbers of semi-independent population units, often called stocks, which are widely recognized by management agencies. Like species, stocks have independent gene pools but gene flow among stocks is typically greater, and morphological and ecological differences smaller, than that among species. The current approach to defining stock structure is an ad hoc process that using demographic data, combined with genetic and phenotypic differences, which are evaluated using expert opinion. We have developed a more systematic approach to the classifying intraspecific diversity, which strives to identify unique and threatened steelhead populations by incorporating current genetic, demographic and distributional information to build a database that includes all British Columbia steelhead populations. Our system integrates three types of genetic differentiation. Small differences in neutral markers are used to define independent population units that are the fundamental classification unit within the species. Adaptive similarity and differentiation among these populations is inferred from habitat characteristics, such as gradient, that have previously been associated with local adaptation. Superimposed on this mosaic of locally adapted populations are major phylogenetic groups that represent ancient lineages that have been isolated from each other for much longer time periods. Sharp clines in gene frequencies among populations are used to define the boundaries of these phylogenetic groups.   The output will be released as a database in the WLAP data warehouse.