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Title: Estimating effective population size of Delta Smelt using RAD-seq.

Abstract: Recently there has been discussion over whether or not the population decline of Delta Smelt (*Hypomesus transpacificus*) has affected its genetic diversity. Genetic effective population size (Ne) is one useful parameter to quantify the number of breeding individuals in an idealized population to result in the degree of genetic drift as observed in the wild Delta Smelt population. Currently, there are several approaches available to estimate Ne including temporal methods (Ne_T), which use samples from different generations, and a linkage disequilibrium method (Ne_{LD}), which samples individuals from a single generation. Previous studies have estimated the Ne_T and Ne_{LD} of the wild Delta Smelt population using 12-15 microsatellite markers but these estimates had wide confidence intervals and the sparsity of markers leaves entire portions of the genome unexamined. It is possible that with genomic data generated using next generation sequencing we may gain significant power and be able to more precisely estimate the Ne of the wild Delta Smelt population. Here we describe the development of a bioinformatics pipeline to estimate Ne values using RAD sequencing data. By utilizing thousands of loci in our estimation of Ne, we hope to develop a pipeline that sensitively and accurately estimates Ne_T across 23 generations and utilize an established linkage map to estimate Ne_{LD} within a single generation.