**Title:** Estimating the contemporary effective population size of *Hypomesus transpacificus* using RAD sequence data.

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**Body:** *Hypomesus transpacificus* (Delta Smelt) is a small (5-7cm), translucent, panmictic species of Osmeridae fish endemic to the San Francisco Estuary (Delta) in California. A once plentiful fish in the Delta, the species has been listed as federally threatened since 1993. Drought and anthropogenic effects are associated with the rapid collapse of the Delta Smelt population and it is now feared that stochastic processes could push the species to extinction. Management strategies include the maintenance of a conservation hatchery; restoration efforts to improve habitat conditions and vital rates; and monitoring Delta Smelt population size by conducting regular surveys to estimate census size via physical capture. An accurate estimation of effective population size (Ne) will provide a useful component for conservation efforts aimed at maintaining genetic diversity within the wild Delta Smelt population. Previous estimates of Ne used 12-15 microsatellite markers, have wide confidence intervals, and the small number of markers leaves entire linkage groups of the genome unexamined. Here, we capitalize on the recent reimplementation of NeEstimator to estimate Ne in a non-model organism. We use 17 generations (1993-2014) of restriction site-associated DNA sequencing (RAD sequencing) data cut with Sbf1 to estimate Ne using a two-generation temporal method (NeT) and a single-generation bias-corrected linkage disequilibrium method (NeLD). We believe these estimates to have greater power to more precisely estimate the effective population size of Delta Smelt to better inform the management and conservation practices in the Delta.