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Draft Genome and Estimates of Effective Population Size of Hypomesus Transpacificus (Delta Smelt).

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Abstract Text:

The use of a reference genomes greatly improves bioinformatic analyses such as estimating demographic parameters. Here we will describe the sequencing and assembly of the first draft genome in the *Hypomesus* order, and then how we used it to more precisely estimate N_e and observe the decline of genetic diversity in Delta Smelt over the last two decades. To produce and assemble the genome, we sequenced a single individual to an ultra-high depth (180x coverage) using 10X Genomics sequencing, then merged separate 60x coverage assemblies from that individual. Thus far, we have estimated the size of the delta smelt genome to be 0.9Gb, and our draft genome has a scaffold N50 of 1.59Mb. The draft genome could then be used as a reference for mapping and aligning RAD-sequencing data for all RAD-sequencing projects for Delta Smelt. Our first analysis was on 2,605 individuals to estimate the long-term and short-term effective population sizes from 1994 to 2018. For both long-term and short-term N_e, we observed a trend of decreasing Ne from 1994 to 2018–one that mirrors the decline in the wild. Our results show that genetic diversity appears to be decreasing in this imperiled species.

Title: Draft Genome and Estimates of Effective Population Size of Hypomesus Transpacificus (Delta Smelt).

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Special Equipment Needs: I am a student member of AFS Northeastern Division, and wish to be considered for the NED Best Student Presentation/Poster award.

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