IPHC-2020-RAB021-08

Sex identification of commercial landings

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Purpose

To provide an update regarding the status of studies designed to provide information regarding sex ratios in commercial landings of Pacific halibut.

BACKGROUND

Declining size-at-age of Pacific halibut in recent decades, in conjunction with larger size-at-age in females and a constant minimum size limit, have led to the expectation that directed Pacific halibut harvests have become increasingly composed of females. Understanding the sex ratio of commercial landings is critical for accurate estimation of parameters such as female spawning stock biomass. However, sex data cannot be obtained from commercial landings due to the requirement that Pacific halibut be dressed at sea, and other strategies for sex identification must be pursued. In 2014, the IPHC initiated a program to generate commercial sex-ratio data that included: 1) the development of at-sea sex-marking protocols for commercial vessels, 2) testing of sex-marking methods suitable for use on commercial vessels; first in a single port (Homer, 2015), then a single regulatory area (2B, 2016), and finally coastwide (2017), and 3) the development of a genetic sex assay.

DISCUSSION

At-sea sex marking

At-sea sex marking was accomplished by marking individual Pacific halibut during dressing, as follows: for females, two knife cuts made in the dorsal (upper) fin; for males, a single cut through the white-side gill plate. At-sea sex-mark data were voluntarily obtained from two vessels in 2015 resulting in 288 fish sampled, from 16 sampled offloads (317 samples) in Regulatory Area 2B in 2016, and from 84 offloads (929 samples) coastwide in 2017. To date, the data from the marking program have suggested that commercial vessels may capture Pacific halibut that are larger at age than are encountered in the IPHC's fishery-independent setline survey, resulting in a higher proportion of female catch that would be predicted using those survey data.

Fin clip samples from at-sea sex marked fish collected during the 2016 and 2017 fishing seasons were analyzed (i.e., genotyped) using the developed genetic tests (see next section) in order to validate the individual sexes as determined by at-sea sex marking.

Genetic assay

Genetic assay development employed restriction-site associated DNA sequencing (RADseq) to identify single nucleotide polymorphisms (SNPs) that are linked to sex in Pacific halibut. Three genetic markers limited to females were investigated for use in sexing Pacific halibut and two were developed into TaqMan genotyping assays that are currently conducted at the IPHC's Biological Laboratory in Seattle. Genetic analyses from tissue samples from at-sea sex marked fish in 2016 revealed that the marking accuracy was 79%. Subsequently, genetic analyses from

tissue samples from the larger set of samples of at-sea sex marked fish in 2017 revealed that the marking accuracy was 94.2%. Although at-sea sex marking accuracy appeared to be high when large sets of samples are analyzed, the low cost and almost complete accuracy of the genetic assays, combined with the current technical capabilities of the IPHC Biological Laboratory, strongly suggest that genetic sexing of Pacific halibut constitutes the best approach for determining the sex ratio of the commercial landings. Therefore, the IPHC has now conducted in-house genetic sexing of approximately 10,000 fish landed coastwide in 2017 and a similar number in 2018 from fin clips collected by IPHC's port specialists. The results of genetic sexing have provided sex ratio information for the first time from the commercial Pacific halibut landings and this information has informed the 2019 stock assessment. Plans are underway to continue with genetic sexing with samples from the 2019 commercial landings.

RECOMMENDATION

That the RAB:

1) **NOTE** paper IPHC-2020-RAB021-08, which outlined the completion of the at-sea sex marking project and the application of genetic assays for sex identification in the commercial landings.