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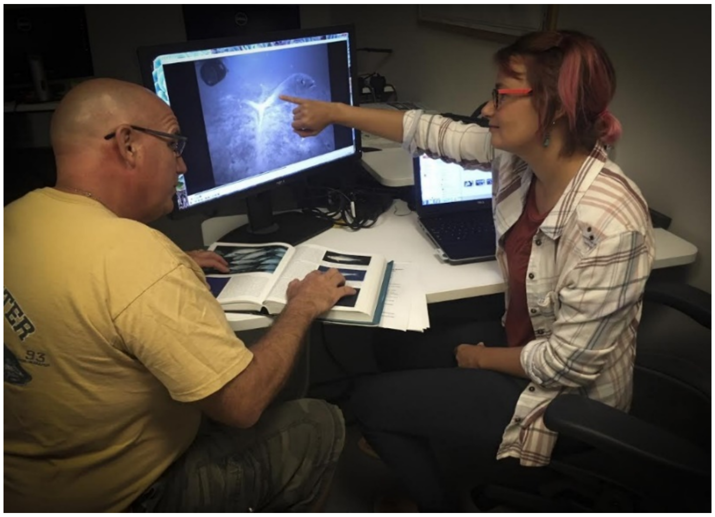

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Executive Summary

The Pacific Islands Fisheries Science Center (PIFSC) of the National Oceanic and Atmospheric Administration (NOAA) National Marine Fisheries Service (NMFS) designed and conducted a study to optimize a **B**ottomfish **F**ishery-**I**ndependent **S**urvey for the **H**awaii Deep 7 stock (BFISH) to produce accurate, precise, and cost-effective estimates of population length-structured abundance and biomass for use in stock assessment. Fishery-independent surveys can be used to obtain abundance-at-length data for estimating population indices without many of the biases associated with fishery-dependent catch and effort data. Development of this survey was noted as a top priority in recent Main Hawaiian Islands Bottomfish Research Coordination workshops (Yau and Oram, 2016).

Novel principles of statistical design were applied to improve survey stratification and efficiency. A geo-rectified (GIS) database of primary biophysical variables obtained from fishery-independent experimental studies and pilot surveys was used to spatially partition Deep 7 densities and variances from these studies into survey strata of similar properties. From these data, a full-scale survey was implemented, with sample allocation among strata based on estimated densities and variances from the pilot surveys.

A total of 540 primary sampling units (PSU) from the 2016 survey were analyzed. Coefficients of variation (CV) ranged from 15-24% for the more abundant of the Deep 7 species. Opakapaka showed the highest relative abundance (mean number per PSU) followed by ehu, kalekale, and onaga. Mean biomass per unit area of opakapaka was highest in shallow, hardbottom, high slope environments followed by mid-depth softbottom environments.

Absolute abundance and biomass estimates were derived by starting with a feasible range of effective sampling area for the reference survey gear and scaling the relative abundance and biomass estimates. These absolute estimates were validated by using a length-based modeling approach that incorporated life history demography to match observed length-structure and catch. Effective area sampled by the reference camera gear based on known area swept by diver surveys likely ranges from 354 m^2 (360° x 10.6 m) to 2827 m^2 (360° x 30 m) and was validated at 1281m^2 (360° x 20.2m). This yielded a Main Hawaiian Islands (MHI) absolute biomass estimate of approximately 10 million pounds for the Deep 7 complex as a whole and nearly 7 million pounds of opakapaka, one of the prime commercial fishery targets.

Future research should focus on methods that more precisely define effective sampling area and which can more accurately quantify relative abundance estimates from video footage.

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Introduction

Commercial and recreational fishing are extremely important to the economy and culture of Hawaii (Haight, Kobayashi, and Kawamoto, 1993). The Hawaiian deep-slope (100-400 m) fishery, representing more than 50% of the total insular commercial catch and valued in the millions of dollars (Western Pacific Regional Fishery Management Council, 2010), consists of seven high value bottomfish species (i.e., six snappers and one grouper), hereafter referred to as Deep 7 (Figure 1) (Western Pacific Regional Fishery Management Council, 2010). Bottomfish have been targeted throughout the eighteen islands of the Hawaiian archipelago by native Hawaiians for hundreds of years. They have been under a formal federal fishery management plan since 2005, when it was determined that the stock was experiencing overfishing (Moffitt, Kobayashi, and DiNardo, 2006). With the designation of the Papahānaumokuākea Marine National Monument in 2006, fishing became restricted to the eight Main Hawaiian Islands.

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The Pacific Islands Fisheries Science Center (PIFSC) of the National Oceanic and Atmospheric Administration's (NOAA) National Marine Fisheries Service (NMFS) is responsible for conducting assessments of the Deep 7 complex. These assessments are used by NOAA to determine stock status and by the Western Pacific Regional Fishery Management Council (WPRFMC) to recommend annual commercial fishery catch limits. The stock assessment process requires reliable time-series of catches, fishing effort, and life history demographics to estimate stock abundance trends and evaluate sustainability benchmarks (Quinn and Deriso, 1999). Until recently, the Deep 7 assessment relied exclusively on trends in fishery-dependent catch per unit effort (CPUE) as the sole abundance index (Brodziak et al., 2014). It is not clear whether these data are truly proportional to stock abundance, given factors including the non-random effort distribution pattern of the fishery. Fishery-dependent CPUE data may also be biased when used as an abundance index due to imposed length and catch limits, variable gear types, market forces, and fishers behavior (Hilborn and Walters, 1992; Maunder and Punt, 2004; Ault et al., 2014). Quantitative assessments to determine whether reef-fish stocks are being fished in a sustainable manner benefit from inclusion of population abundance indices (e.g., relative abundance, average length) estimated from fishery-dependent catch sampling and/or fishery-independent (FI) surveys (Aultet al., 2005; Ault et al., 2014). A key advantage of FI surveys is that they obtain similar abundance-at-length data for estimating population indices as fishery-dependent catch sampling programs but with greater statistical rigor (Ault et al., 1999; Smith et al., 2011). Another advantage is that FI surveys can be designed to estimate total population abundance, providing an important independent estimate of stock abundance for assessment models.

In 2011, the PIFSC NOAA Pacific Islands Fisheries Science Center (PIFSC) began developing a multi-gear, fishery-independent survey for the Main Hawaiian Islands Deep 7 stock (Richards et al., 2016) in an effort to continue improvements in the data used for stock assessment. Development of this survey was considered a top priority in recent Main Hawaiian Islands Bottomfish Research Coordination workshops (Yau and Oram, 2016). In this paper, we present a new method for estimating biomass for the Deep 7 complex derived from the first MHI-wide FI Deep 7 survey. Relative abundance and biomass are calculated, and estimated total abundance and biomass based on feasible effective sampling areas are validated using a length-based modeling approach for the principal survey gear.

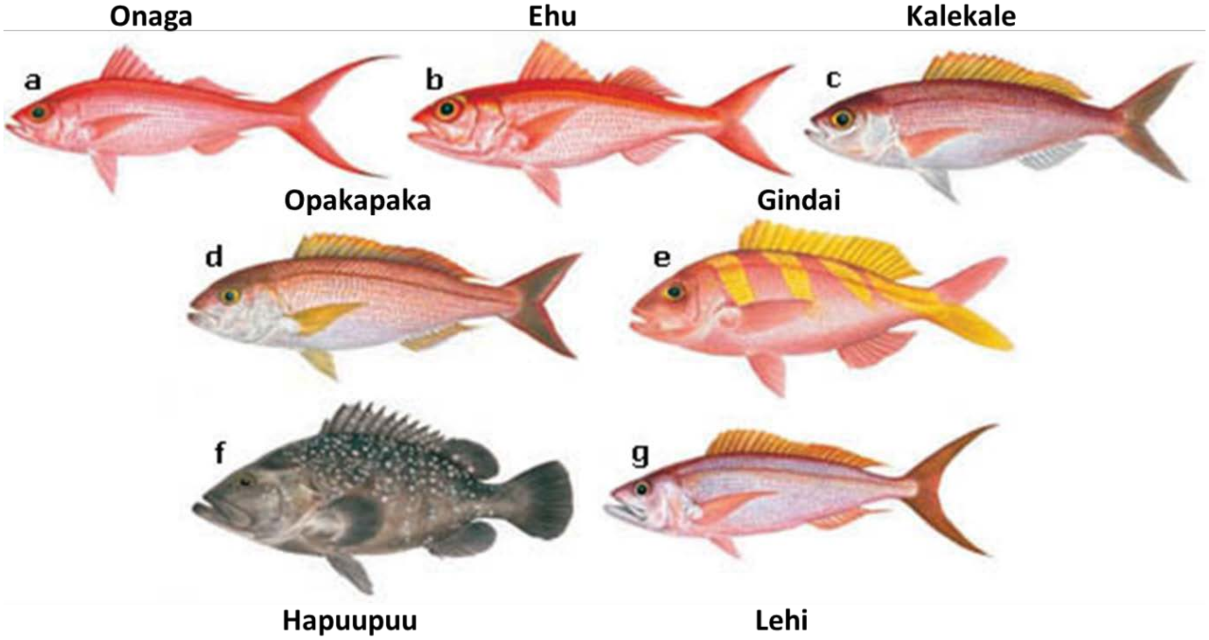

Figure 1. Members of the Hawaiian Deep 7 bottomfish (i.e., deepwater snappers and grouper) community: (A) onaga (Etelis coruscans); (B) ehu (Etelis carbunculus); (C) kalekale (Pristipomoides sieboldii); (D) opakapaka (Pristipomoides filamentosus); (E) gindai (Pristipomoides zonatus); (F) hapu’upu’u (Hyporthodus quernus); and, (G) lehi (Aphareus rutilans). Artwork by Les Hata (Hawaii DAR/DLNR).

Methods and Materials

Fishery Independent Survey

A Bottomfish Fishery-Independent Survey (BFISH) in the Main Hawaiian Islands (MHI) was conducted in 2016 to estimate key population metrics for the Deep 7 stock. Development of the stratified-random sampling methods and statistical design for the survey are detailed in Richards et al. (2016). The survey domain encompassed the full extent of mapped bottomfish habitats from 75 to 400 m depths, extending 600 km from the Big Island of Hawaii to the island of Kauai (Figure 2). The survey frame comprised 25,892 primary sample units (PSUs), each measuring 500 x 500 m, and was stratified according to depth category (75-200 m, 200-300 m, 300-400 m), substrate composition (softbottom, hardbottom), and substrate complexity (low slope, high slope) (Figure 2, Table 1). Stratification was based on five-meter resolution multibeam bathymetry and backscatter synthesis data outlined in Richards et al. (in review). Analyses of pilot survey data collected from 2011 to 2015 in the Maui-Nui region showed that this stratification scheme effectively partitioned the spatial variation in density for Deep 7 species (Richards et al., 2016). Samples were allocated among strata following a Neyman scheme (Cochran, 1977), and PSUs within strata were randomly selected without replacement from a discrete uniform probability distribution to ensure equal probability of selection (Law, 2007).

At a selected PSU, Deep 7 numbers and length composition by species were obtained from two principal survey gears: hook-line fishing and stationary stereo-video camera stations (Richards et al., 2016). A standard hook-line sample was 30 minutes of active fishing within a PSU by one vessel using two lines, each with four hooks and two bait types. Each captured fish was identified to species, and fork length was measured to the nearest cm. Two, replicate, randomized, 15-minute camera deployments were conducted at distinct locations within each PSU. In-situ footage was analyzed to generate species-level counts by the MaxN method (Cappo et al., 2006) and to measure fork lengths to the nearest mm. The MaxN method enumerates species within a video sequence by recording the number of individuals of a given species present within the single video frame containing the highest density of that species. This method prevents double-counting and yields a conservative estimate of abundance. Sample unit species counts for hook-line fishing were standardized in terms of drop cameras using gear calibration factors outlined in Richards et al. (2016). Estimation of Deep 7 relative abundance followed standard procedures for stratified random sampling (Cochran, 1977; Ault et al., 1999; Lohr, 2010; Smith et al., 2011). The number of fish per primary sample unit U_N was the principal metric used to develop the statistical sampling design. Computational formulae for estimating the mean number of fish $\overline{U}_N$, a relative index of population abundance, and associated variance at both the stratum and survey frame levels are provided in Table 2. Survey design estimation was carried out using the SAS (SAS Institute, v 9.4) and [R] (R Development Core Team, v 3.1.3) statistical software packages.

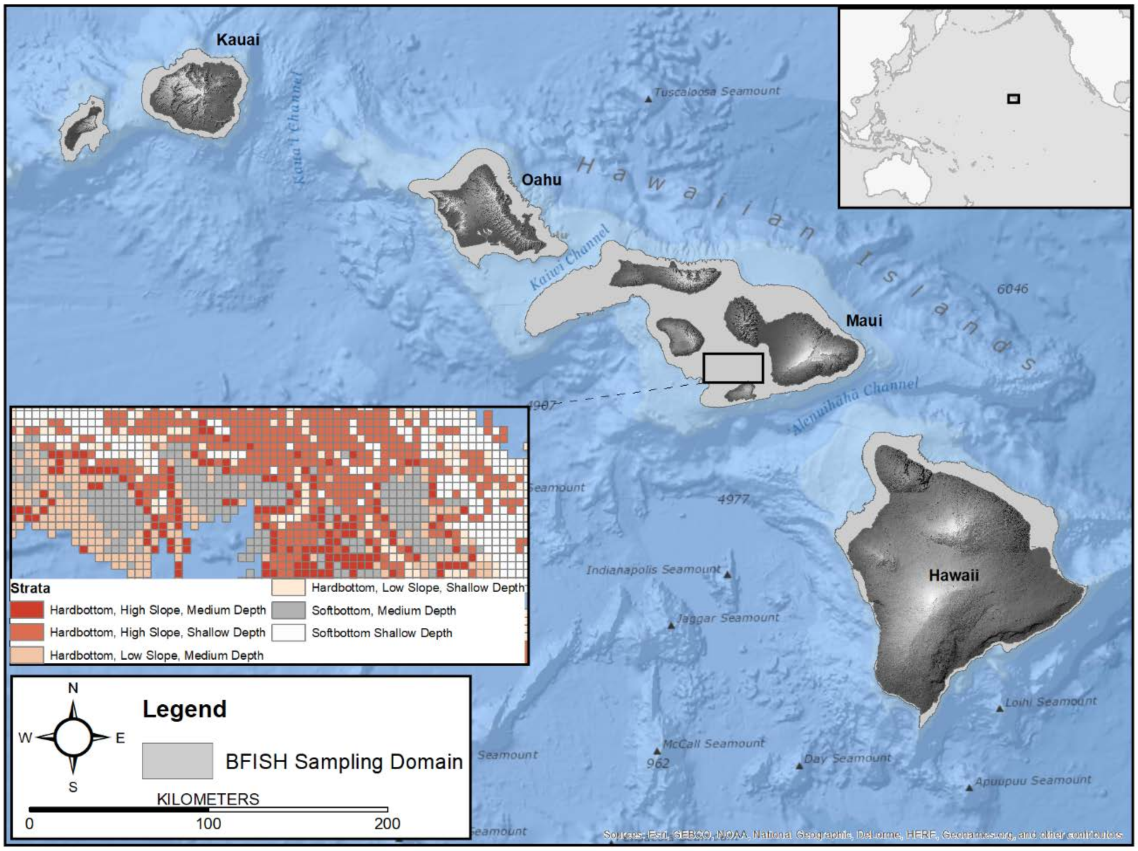

Figure 2. The spatial frame of the BFISH survey extending from Kauai in the northwest to the island of Hawaii in the southeast. Inset shows a section of the survey frame in the Maui-Nui region showing the 500 x 500 m grid cells classified by habitat-depth strata

Table 1. The total number of 500 x 500 m grid cells (primary sample units, PSUs) by substrate-slope-depth strata within the Main Hawaiian Islands bottomfish survey domain.

Substrate	Slope	Depth	Strata Code	PSUs
HB	H (high)	Shallow	HB_H_S	4777
HB (hardbottom)	L (low)	Shallow	HB_L_S	4562
HB	L	Deep	HB_L_D	3801
HB	H	Deep	HB_H_D	2749
HB	L	Mid-depth	HB_L_M	2688
HB	H	Mid-depth	HB_H_M	2412
SB (softbottom)	A (high and low slope)	Shallow (75-200 m)	SB_A_S	1863
SB	A	Deep (300-400 m)	SB_A_D	1591
SB	A	Mid-depth (200-300 m)	SB_A_M	1449
		Total		25892

Biomass Estimation

Estimating population total biomass entailed multiplying the mean biomass per unit $\overline{U}_B$ by the number of sample units in the survey frame. Biomass in a sample unit (Table 2, eq. T-3) was obtained by converting length to weight of each individual fish via an allometric weight-length function (Table 2, eq. T-4), then summing the weights for all observed fish by species. Allometric functions were developed for Deep 7 species using paired weight-length observations collected in the MHI by scientists at NOAA's PIFSC. Allometric model parameters (Table 2, eq. T-5) were estimated using the nonlinear least-squares procedure in [R] (R Development Core Team, v 3.1.3).

The number of PSUs in the MHI survey frame was determined from the habitat maps (Figure 2, Table 1) (Richards et al, in review). However, a standard PSU sample likely did not cover the full area of the PSU (250,000 m^2), yielding a two-stage sampling process, with a standard sample treated as a second-stage unit (SSU) (Cochran, 1977; Smith et al., 2011). Estimation of population biomass was achieved by multiplying the mean biomass per sample unit $\overline{U}_B$ for the survey frame (Table 2, eq. T-9) by the number of SSUs in each PSU, then by the number of PSUs in the survey frame (Table 2, eq. T-10).

Camera sampling was carried out using a two-stage design, with two replicate camera deployments made at distinct locations within the PSU. Values from the two replicates were averaged as the sample value for a PSU. Most sampling was carried out using hook-and-line gear, with only one sample per PSU; hence, the sample variance among SSUs was not estimable. Thus, the computational equations for the relative abundance indices of mean number per sample unit $\overline{U}_N$, (Table 2, eqs. T-1 and T-8) and mean biomass per sample unit $\overline{U}_B$ (Table 2, eqs. T-2 and T-9) and their associated variances (Table 2, eqs. T-6 and T-7), simplify to single-stage design equations.

Table 2. Computational formulae for the stratified random sampling design used for bottomfish surveys.

Symbol	Definition	Computational Formula	Equation Number
$\overline{U}_{Nh}$	Mean number of fish per sample unit in stratum h	$\overline{U}_{Nh} = \frac{1}{n_h}\sum_i U_{Nhi}$	T-1
n_h	Number of units sampled in stratum h		
U_{Nhi}	Number of fish in sample unit i in stratum h		
$\overline{U}_{Bh}$	Mean biomass of fish per sample unit in stratum h	$\overline{U}_{Bh} = \frac{1}{n_h}\sum_i U_{Bhi}$	T-2
U_{Bhi}	Biomass in sample unit i in stratum h	$U_{Bhi} = \sum_j W_{hij}$	T-3
W_{hij}	Weight of fish j in sample unit i in stratum h	$W_{hij} = \alpha(L_{hij})^{\beta}$	T-4
L_{hij}	Length of fish j in sample unit i in stratum h		
α, β	Parameters of allometric weight-length function		T-5

$\mathrm{var}\left[\overline{U}_h\right]$	Variance of mean number or biomass per unit in stratum h	$\mathrm{var}\left[\overline{U}_h\right] = \left(1 - \frac{n_h}{PSUs_h}\right)\frac{s_h^2}{n_h}$	T-6
$PSUs_h$	Total number of primary sampling units (map grid cells) in stratum h		
s_h^2	Sample variance of number or biomass in stratum h	$s_h^2 = \frac{\sum_i \left(U_{hi} - \overline{U}_h\right)^2}{n_h - 1}$	T-7
$\overline{U}_N$	Mean number of fish per sample unit for the full survey frame	$\overline{U}_N = \sum_h w_h \overline{U}_{Nh}$	T-8
$\overline{U}_B$	Mean biomass per sample unit for the full survey frame	$\overline{U}_B = \sum_h w_h \overline{U}_{Bh}$	T-9
w_h	Stratum h weighting factor	$w_h = \frac{PSUs_h}{\sum_h PSUs_h}$	
$\mathrm{var}\left[\overline{U}\right]$	Variance of survey frame mean number or biomass per unit	$\mathrm{var}\left[\overline{U}\right] = \sum_h w_h^2 \,\mathrm{var}\left[\overline{U}_h\right]$	
$SE\left[\overline{U}\right]$	Standard error of survey frame mean number or biomass per unit	$SE\left[\overline{U}\right] = \sqrt{\mathrm{var}\left[\overline{U}\right]}$	
$CV\left[\overline{U}\right]$	Coefficient of variation of mean number or biomass per unit	$CV\left[\overline{U}\right] = \frac{SE\left[\overline{U}\right]}{\overline{U}}$	
$\overline{B}$	Mean total population biomass in survey frame	$\overline{B} = \overline{U}_B \times PSUs \times SSUs$	T-10

$PSUs$	Number of Primary Sampling Units (grid cells) in survey frame		
$SSUs$	Number of theoretical secondary sample units within each grid cell in survey frame		
$SE[\overline{B}]$	Standard error of population biomass	$SE[\overline{B}] = \sqrt{\mathrm{var}[\overline{U}_B](PSUs \times SSUs)^2}$	
$\overline{L}$	Mean length in exploited phase in survey frame	$\overline{L} = \frac{\overline{Y}}{\overline{X}}$	T-11
$\overline{X}$	Per unit mean number in exploited phase in survey frame	$\overline{X} = \sum_h w_h \overline{X}_h$	
$\overline{Y}$	Per unit mean sum of lengths in exploited phase in survey frame	$\overline{Y} = \sum_h w_h \overline{Y}_h$	
$\overline{X}_h$	Per unit mean number in exploited phase in stratum h	$\overline{X}_h = \frac{1}{n_h} \sum_i X_{hi}$	
X_{hi}	Number in exploited phase in sample unit i in stratum h		
$\overline{Y}_h$	Per unit mean sum of lengths in exploited phase in stratum h	$\overline{Y}_h = \frac{1}{n_h} \sum_i Y_{hi}$	
Y_{hi}	Sum of lengths in exploited phase in sample unit i in stratum h		

$\text{var}[\bar{L}_h]$	Variance of mean length in exploited phase in stratum h	$\text{var}[\bar{L}_h] = \left(1 - \frac{n_h}{PSUs_h}\right)\frac{s_h^2(Y \mid X)}{n_h \bar{X}_h^2}$	
$s_h^2(Y \mid X)$	Sample variance of Y conditioned on X in stratum h	$s_h^2(Y \mid X) = \frac{\sum_i (Y_{hi} - \bar{L}X_{hi})^2}{n_h - 1}$	
$SE[\bar{L}]$	Standard error of mean length in exploited phase in survey frame	$SE[\bar{L}] = \sqrt{\sum_h w_h^2 \text{var}[\bar{L}_h]}$	T-12

Estimation of Feasible Range for Camera Sampled Area

A principal uncertainty in the fishery-independent survey estimation of population biomass for Deep 7 species was the exact value for the number of SSUs in a PSU, derived from the sampled area of the SSU. For the reference camera gear,

Equation 1:

$$\text{SSUs} = \frac{\text{PSU area}}{\text{SSU area}}$$

where PSU area was 250,000 m^2 and SSU area was the effective area sampled. Stationary drop camera sampling was analogous to stationary point counts for shallow-water diver reef fish visual census surveys (Smith et al., 2011) in which the two-dimensional sampling area was considered to be a circle with radius *r*, thus

Equation 2

$$\text{SSU area} = \pi \cdot r^2 .$$

However, the effective sampling area is a three-dimensional volume, with the possibility of fish being attracted from outside the defined radius. The technical specifications of the cameras are an 82° field of vision with a 7.5 m radius (Amin et al. 2017), resulting in a 40.25 m2 minimum effective sampling area. However, it is likely that the effective sampling area is much larger than this, given a variety of factors. The camera provides a novel structure for inquisitive species and makes use of a small amount of bait to orient targets in front of the cameras for identification and measurement. The horizontal field of view can exceed 82° as the camera system swings slightly in the current. The sampling period is 15 minutes (Misa et al. 2016), which could allow fish to enter from beyond the 82° by 7.5 m area. For diver-based surveys of reef fishes (Bohnsack and Bannerot, 1986; Smith et al., 2011), the effective area sampled by a buddy team of two divers with no bait, each sampling 7.5 m cylinders in a 5- to 8-minute time period, is 354 m^2, which equates to a single cylinder with radius of 10.6 m. Given the conditions listed earlier, it is reasonable that the effective radius of the camera is greater than 15 m, with the upper feasible radius estimate unlikely to exceed 30 m (2,827 m^2).

A population modeling approach was developed to estimate the feasible range for effective camera sampling area in terms of radius distance. This approach entailed estimating a realistic range for opakapaka population biomass that corresponded with fishery catches and observed population length structure in the exploitable phase of the population, using equation T-10 to solve for SSUs, then using Equation 1 and Equation 2 to solve for radius distance *r*.

The length-based stochastic numerical cohort-structured model of Ault et al. (1998) was parameterized for opakapaka using empirical information from life history demographic studies, the BFISH survey, and the commercial fishery. Opakapaka data were used for model parameterization as requisite life-history data were not available for the other Deep 7 species. Parameters for the von Bertalanffy growth function (length-age), maximum lifespan, and length-at-maturity were obtained from Andrews et al.(2012) and Luers, DeMartini, and Humphreys (in review). Opakapaka catch was derived from commercial catch reported to the Hawaii Department of Aquatic Resources (DAR) and an expansion factor to account for unreported catch and recreational catch (Zeller et al., 2008) as used in previous stock assessments.

Total instantaneous mortality rate (Z) in the exploited phase of the population was estimated using the length-based model of Ehrhardt and Ault (1992),

Equation 3

$$\left[\frac{L_\infty - L_\lambda}{L_\infty - L_c}\right]^{\frac{\hat{Z}(t)}{K}} = \frac{\hat{Z}(t)\left(L_c - \overline{L}(t)\right) + K\left(L_\infty - \overline{L}(t)\right)}{\hat{Z}(t)\left(L_\lambda - \overline{L}(t)\right) + K\left(L_\infty - \overline{L}(t)\right)},$$

where L_c is length at first capture, L_λ is average length at the oldest age a_λ, $\overline{L}(t)$ is the average length in the exploited phase (i.e., between L_c and L_λ) at time *t* (i.e., year), and K and L_∞ are parameters of the von Bertalanffy growth equation. Estimates of $\overline{L}$ from the survey and commercial catch were used to develop a feasible range of Z estimates. A stratified random design ratio-of-means procedure (Lohr, 2010) was used to estimate $\overline{L}$ for opakapaka from survey observations of numbers-at-length, (Table 2, eqs. T-11 and T-12). For fishery data, estimates of mean fish weight from reported commercial data over the 2016 state fiscal year (July 1, 2015 – June 30, 2016) were converted to a distribution of mean lengths using the allometric function for opakapaka, and $\overline{L}$ was subsequently estimated as the average of this distribution. Natural mortality rate M was estimated from lifespan applying the procedure of Alagaraga (1984) and Hoenig (1983), which assumes that 5% of a cohort survives to the maximum age/length, and fishing mortality rate F was estimated by subtracting M from Z (Ault et al., 1998).

The estimated total annual catch from the parameterized stochastic length-based cohort-structured model of Ault et al. (1998) was matched to the total fishery catch (commercial and recreational combined) for opakapaka by adjusting annual recruitment to the population. A calibration check for the numerical estimation-simulation model compared model-predicted length frequencies in the exploited phase with observed length frequencies from the survey. The final calibrated model was then used to produce a feasible range of estimates of average population biomass, then to derive a feasible range of estimates of SSU effective area sampled and next applied to estimate total abundance from the survey data.

Results

A total of 540 PSUs were sampled in the 2016 BFISH survey (n=455 fishing gear, n=85 camera gear). For the principal design metric, mean number per unit $\overline{U}_N$, CVs ranged from 14.8% to 23.8% for more abundant species (ehu, opakapaka, kalekale) and from 24.1% to 44.2% for less abundant species (lehi, onaga, hapu’upu’u, gindai) (Table 3).

Table 3. Estimates of MHI-wide mean number per unit , standard error, and CV (%) for Deep 7 bottomfishes (all sampled life stages) for the 2016 survey (n=540).

Species	$\overline{U}_N$	$SE(\overline{U}_N)$	$CV(\overline{U}_N)$
Opakapaka	1.0365	0.2120	20.5
Ehu	0.4369	0.0648	14.8
Kalekale	0.3947	0.0941	23.8
Onaga	0.0712	0.0229	32.2
Lehi	0.0521	0.0231	44.2
Gindai	0.0364	0.0088	24.1
Hapu’upu’u	0.0155	0.0050	32.5

Estimated allometric weight-length functions (Table , Figure) were used to compute survey mean biomass per unit $\overline{U}_B$, the relative index of abundance needed for total population biomass estimates. The procedure for estimating $\overline{U}_B$ and its associated standard error for the survey frame from stratum-level estimates is illustrated for opakapaka over the exploited phase (length > 37 cm) in Table 5. The slight difference in sample size between the exploited phase estimates (n=531, 9 Table) and the full life-stage estimates (n=540, Table 3) is due to the exclusion of observations with missing length values.

Table 4. Bottomfish allometric relationships for Hawaiian Deep 7 bottomfish species. The units are cm for length (L) and pounds for weight (W). Letters for each species correspond to Figure 1.

Species		β	α	**df**
Opakapaka	(D)	2.311E-05	2.928	1,442
Onaga	(A)	6.005E-05	2.673	1,436
Hapu’upu’u	(F)	3.065E-05	2.884	857
Ehu	(B)	1.551E-05	3.026	1,164
Kalekale	(C)	2.243E-05	2.932	556
Lehi	(G)	1.298E-04	2.458	128
Gindai	(E)	3.526E-05	2.859	144

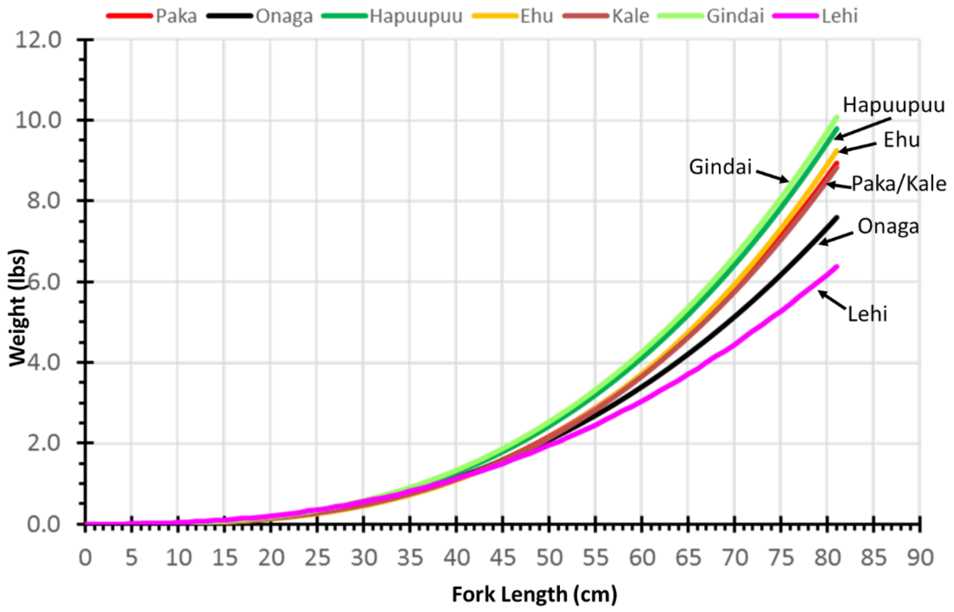

Figure 3. Comparison of allometric curves for Hawaiian Deep 7 bottomfish species.

Table 5. Illustration of estimation of survey frame mean biomass per unit and standard error (lb) from stratum-level estimates for opakapaka. Stratum codes are defined in Table 1.

Stratum Code	n_h	w_h	$\overline{U}_{Bh}$	$\mathrm{var}\left(\overline{U}_{Bh}\right)$
HB_H_S	141	0.1845	4.9466	2.2245
SB_A_M	14	0.0720	4.0690	8.0369
HB_L_M	47	0.1038	0.5559	0.1485
HB_H_M	112	0.0932	0.3689	0.0299
HB_L_S	65	0.1762	0.3680	0.1335
SB_A_M	16	0.0560	0.0000	0.0000
SB_A_D	21	0.0614	0.0000	0.0000
HB_L_D	54	0.1468	0.0000	0.0000
HB_H_D	61	0.1062	0.0000	0.0000

$n =$ 531

$\overline{U}_B = \sum_h w_h \bar{\iota}$

1.3623

$\mathrm{var}\left(\overline{U}_B\right) = \sum_h w_h^2 \,\mathrm{var}\left(\overline{U}_{Bh}\right) =$ 0.1233

$SE\left(\overline{U}_B\right) = \sqrt{\mathrm{var}\left(\overline{U}_B\right)} =$ 0.3512

Demographic parameters for opakapaka synthesized from empirical studies and used as inputs for the numerical cohort-structured population model are provided in Table 6. The estimated total catch for opakapaka is given in Table. Mortality rates Z were estimated from two different length frequency distributions for opakapaka: (1) BFISH survey and (2) commercial fishery catches, derived from a distribution of mean weight per fish per record (Figure). The different mortality rates were used in separate runs of the population model to estimate the expected population biomass (Table) that produced the total catch for opakapaka (Table). The resulting estimated radius distance for camera sampled area ranged from 20.2 m to 41.6 m (Table) compared to the radius range of 10.6 m to 30 m from known diver effective sampling areas.

For verification, the model-simulated population length structure in the exploited phase was compared with the observed length structure from the survey. Model 2 provided the best match between model-predicted and observed length frequencies (Figure). While there is disparity between the predicted and observed frequencies for length classes < 44 cm in both models, Model 2 provided a better match for larger length classes > 50 cm. Model 1 underestimated the frequency of larger length classes which was unrealistic given that both survey and commercial catch data show larger fish exist. Based on this comparison and the fact that a radius of 20.2 m lies within the feasible radius range based on known diver effective sampling areas, the estimated radius of 20.2 m for effective sampled area was used to estimate absolute population biomass $\overline{B}$ for Deep 7 species from the survey (Table) following equation T-10 (Table 2).

Table 6. Values for demographic parameters of Hawaiian opakapaka (Pristipomoides filamentosus) used in the numerical cohort-structured model.

Parameter	Definition	Units	Value	Source
a_λ	Maximum observed age	yrs	43	Andrews et al. (2012)
$\boldsymbol{M}$	Natural mortality rate	yr^{-1}	0.0695	Ault and Smith (2017)
L_∞	Ultimate length	cm	67.5	Andrews et al. (2012)
$\boldsymbol{K}$	Brody growth coefficient	yr-1	0.242	Andrews et al. (2012)
$\boldsymbol{a_0}$	Age at which length equals zero	yrs	- 0.29	Andrews et al. (2012)
α	Weight-length scalar		2.31E-05	Humphreys et al. (2017)
β	Weight-length power coefficient		2.928	Humphreys et al. (2017)
L_c	Minimum length at first capture	cm	37.05	Langseth and Yau (2017)
L_m	Minimum length of first maturity	cm	39.1	Luers et al. (2016)

Table 7. Estimated catch of Deep 7 species for Hawaii state fiscal year 2016 (July 1, 2015 – June 30, 2016). Estimates were calculated from Hawaii DAR Fisherman Reporting System data for commercial catch. Expansion factors from Zeller et al. (2008).

Species	Commercial catch (lb)	Expansion Factor	Total (lb)
Opakapaka	140,722	2.97	**417,945**
Hapu'upu'u	10,537	1.59	16,754
Kalekale	13,576	1.28	17,377
Ehu	32,747	1.25	40,933
Onaga	73,706	1.05	77,392
Lehi	7,802	1.10	8,582
Gindai	1,989	1.61	3,202
TOTAL	**281,079**		**582,185**

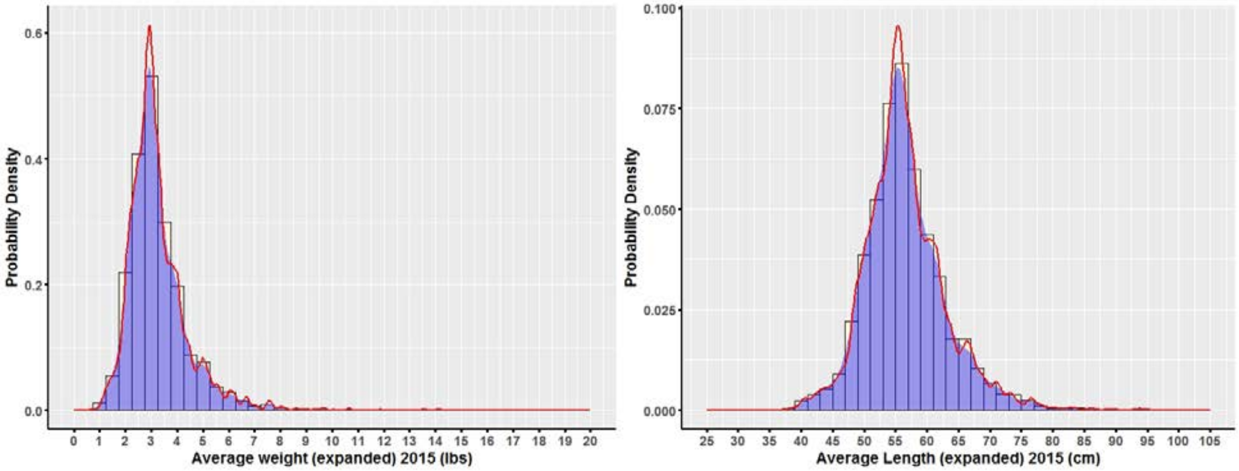

Figure 4. Frequency distribution of opakapaka mean weight per fish for reported commercial records (left panel) and the resulting distribution of mean length per fish after conversion using the allometric weight-length function (right panel).

Table 8. Estimates of opakapaka total mortality rate (Z), abundance ( ), biomass ( ) and recruitment (R) using two different length frequency distributions: Model 1, fishery-independent survey; Model 2, fishery catches (Figure 4, right panel).

	$\overline{L}$	Z	$\overline{N}$	$\overline{B}$	R	**radius (m)**
Model 1	50.00	0.3270	703,031	1,623,999	281,713	41.6
Model 2	56.60	0.1340	1,951,837	6,874,297	321,886	20.2

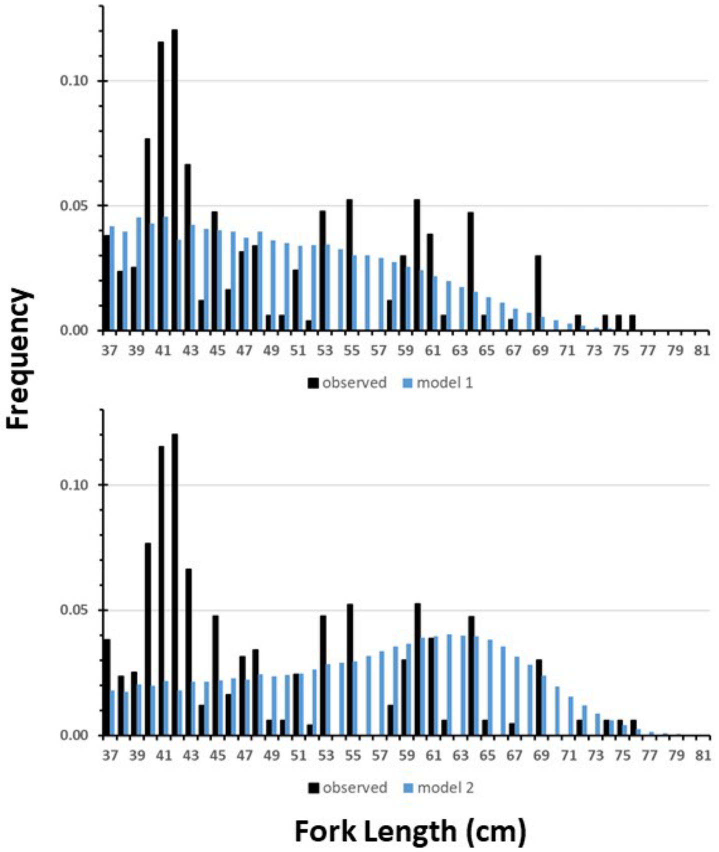

Figure 5. Comparison of survey-observed (black bars) and numerical population model-predicted (Model 1 and 2, Table 8) length frequency distributions for opakapaka.

Table 9. MHI 2016 survey estimates of Deep 7 species exploited phase mean biomass per unit and total population biomass for camera sampled area radius=20.2 m.

Species	**n**	$\overline{U}_B$	$SE(\overline{U}_B)$	$\overline{B}$ **(lbs)**	$SE(\overline{B})$
Opakapaka	531	1.3623	0.3512	6,874,297	1,772,091
Ehu	533	0.2506	0.0433	1,272,166	363,735
Onaga	538	0.1234	0.0600	626,154	503,702
Hapu’upu’u	538	0.0987	0.0378	500,963	317,799
Lehi	536	0.0848	0.0495	430,685	415,602
Kalekale	531	0.0768	0.0286	389,578	240,193
Gindai	537	0.0113	0.0051	57,546	42,842
Total				**10,151,389**	**1,964,580**

Discussion

This study presents a new method for estimating biomass for the Deep 7 complex. The first MHI-wide fishery-independent survey for Deep 7 bottomfish was conducted to generate estimates of abundance and biomass at length, fulfilling a Priority 1 recommendation by Yau and Oram (2016). Absolute abundance and biomass estimates were derived by starting with a feasible range of effective sampling area for the reference survey gear. This area was validated using a length-based modeling approach that incorporated life history demography to match observed length-structure and catch. The long-term focus of this effort is to provide a new robust source of stock biomass estimates to improve stock assessments to ensure sustainability of the resources.

Recent Deep 7 stock assessments have used biomass-dynamic models to infer stock dynamics that rely on CPUE data that are assumed to be proportional to stock abundance. However, fishery-dependent data have been shown in other systems to produce biased estimates of stock abundance (Hilborn and Walters, 1992; Walters and Martell, 2004). For example, (1) fish can be heterogeneously distributed, (2) fishing is not generally distributed proportionally to the resource, and (3) fish may aggregate as resources are depleted, giving a false sense of density. In addition, uncertainty exists regarding the magnitude of unreported catch. Fishery-independent survey methods have several advantages which may ameliorate some of the above issues. Fishery-independent surveys, if properly designed, explicitly compensate for heterogeneous distributions by allocating effort proportional to resource density and variance (Smith et al., 2011; Richards et al., 2016).

The BFISH survey produced robust estimates of relative abundance and biomass, especially for the most abundant Deep 7 species (Table 3). However, obtaining estimates of total species-specific biomass necessitated a method to translate survey density to total stock biomass. In this regard, the principal uncertainty was the effective area sampled by the reference gear (cameras). A feasible range of effective sampling area for the reference camera gear is presented, based on known comparable diver survey effective sampling areas. The sampling area is validated using length-based modeling, resulting in an effective radius of 20 to 40 meters. Modeling results based on matching length distributions suggested 20 m was the most feasible radius in our survey.

These modeling results were highly dependent upon the availability of high-resolution habitat data (Richards et al, in review) and quality of life history demographic data, which were only available for one (opakapaka) of the Deep 7 species. As a result, the radius estimation was determined for opakapaka, which was extrapolated to the other Deep 7 species. The length-based biomass estimation method was also sensitive to observed length-frequency distributions and reported total catches. Additional uncertainty arises from the MaxN method used to estimate density from video footage (Cappo et al., 2006). MaxN can bias density estimates as it is nonlinearly related to true length-structured abundance (Schobernd et al., 2014).

The identified uncertainties should serve to prioritize future work. The uncertainty around the effective area sampled by the reference gear could be assuaged by technology that provides a clear 360 field of view. This could eliminate the need for bait but may increase required sampling effort. It was also assumed that the effective area sampled by the camera and hook-and-line gears does not differ among species or habitat types. However, this is likely not the case, and future research in this area could serve to improve these estimates. Hydroacoustics could provide a more synoptic method to estimate length-structured density of target fishes within a known area. However, present technologies are not sufficient to discriminate Deep 7 species or detect individuals in complex environments (Richards et al., 2016). To conform with the format of commercial fishery data, mean length in exploited phase was computed from the distribution of average fish weights per record, which may overestimate the frequency of the fish of intermediate sizes. Future estimates would benefit from records of individual length composition, possibly obtained by sampling of catch or changing reporting requirements. Finally, obtaining the full spectrum of life-history demographics for the entire Deep 7 complex would allow for more precise population and community modeling which can serve as a check for fishery-independent biomass estimates.

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