North Pacific Fisheries Commission

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Identifying potential VMEs on the Cobb-Eickelberg seamount chain based on predictive modelling

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ABSTRACT

Areas likely to be vulnerable marine ecosystems (VMEs) (i.e. potential VMEs) can be identified using model predictions when no data from visual surveys exist, as outlined in the North Pacific Fisheries Commission's (NPFC's) framework for identifying data to identify VMEs (See Annex 2.3 in NPFC 2023a and NPFC 2023b). We identify potential VMEs in the Cobb-Eickelberg seamount chain using predictive models of VME indictor taxa density by applying the regional VME indicator taxa density threshold (0.6 VME indicator taxa colonies m^{-2}, see Warawa et al. 2023). Our methods predict that potential VMEs are present on all seamounts in the Cobb-Eickelberg seamount chain. We invite feedback on our proposed method for identifying potential VMEs.

BACKGROUND

This working paper focuses on identifying areas where vulnerable marine ecosystems (VMEs) are likely to occur (henceforth *potential VMEs*) on seamounts along the Cobb-Eickelberg seamount chain in areas where visual data are not currently available. Previous iterations of these methods are described in NPFC-2021-SSC BFME02-WP05 (Warawa et al. 2021) and NPFC-2022-SSC BFME03-WP03 (Warawa et al. 2022). The key steps in our revised methodology are the same. In our revised predictive modelling method, however, we predict maps of VME indicator taxa density and apply our VME density threshold (0.6 VME indicator taxa colonies m^{-2}, Warawa et al. 2023) to our model predictions. One benefit of this updated approach is that the predictive model can use more information by providing the range of VME density from the visual data, rather than just the VME presence/absence.

We apply our model predictions and VME density threshold to the Cobb-Eickelberg seamount chain, where Canada fishes for sablefish (*Anopoploma fimbria*).

METHODS AND RESULTS

Study Area

Our study area, the Cobb-Eickelberg seamount chain, is located in the eastern part of the North Pacific Fisheries Commission's (NPFC's) Convention Area (CA), just outside of Canada's exclusive economic zone

(EEZ), approximately 450 km offshore Vancouver Island (Figure 1). This seamount chain is composed of 11 named seamounts and one ridge (Eickelberg Ridge) with Cobb Seamount having the shallowest pinnacle depth of 24 m (Parker & Tunnicliffe 1994). The Canadian commercial sablefish fishery has been active in the study area since the 1980s using mainly longline trap and some longline hook and line gear. Canada's sablefish fishery is currently the only fishery managed under the purview of the NPFC in the eastern part of its CA.

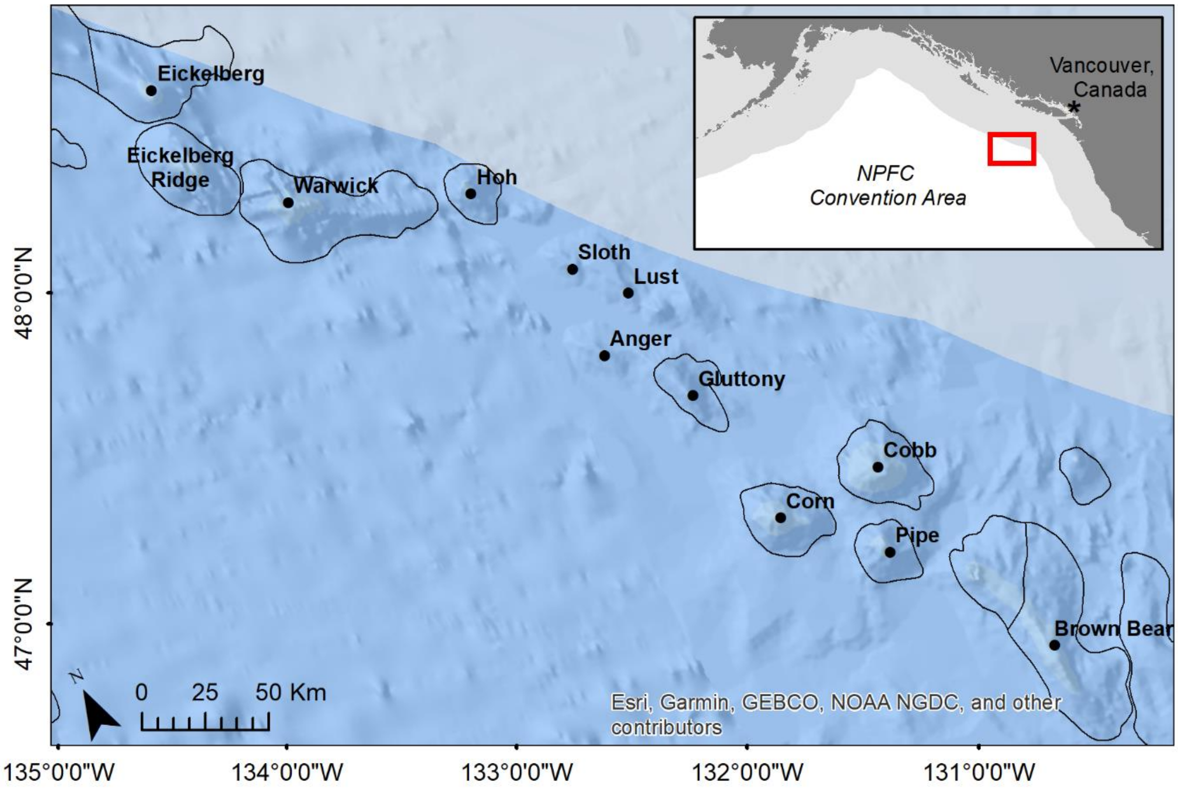

Figure 1. The Cobb-Eickelberg seamount chain study area in the eastern NPFC Convention Area, next to the Canadian EEZ (light grey). Black dots represent named seamounts and black outlines represent seamounts identified from geomorphic features in Harris et al. (2014).

Predictive models of VME indictor density

Due to the lack of retention of corals and sponges in longline fishing gear for Sablefish and limited visual data (but see preliminary results from Rooper et al. 2023) there is a lack of data on the distribution and density of the NPFC's VME indicator taxa on the Cobb-Eickelberg seamount chain. Therefore, to identify potential VMEs, we applied our calculated indicator taxa density threshold for VME identification (0.6 VME indicator taxa colonies m^{-2}, see Warawa et al. 2023) to model predictions of VME indicator taxa densities.

Dependent data

We use the combined VME indicator taxa densities from 50-m^2 transect segments (n=221, Warawa et al. 2023) of the 2012 Cobb Seamount Survey AUV data (Curtis et al. 2015) as the dependent data in models of VME density in the Cobb-Eickelberg seamount chain. Abundances of all structure forming corals, glass sponges, and demosponges were summed to calculate NPFC VME indicator taxa densities.

Environmental data

We considered the following environmental raster layers from Chu et al. (2019) for modelling VME indicator density based on prior knowledge of environmental conditions that strongly influence the density and distribution of corals and sponges: depth, calcite, dissolved oxygen, percent organic carbon, northness, silicate, slope, bottom temperature, topographic position index (TPI) at spatial scales of 1000, 500, and 100 meters, eastness, and sea surface temperature. We considered eastness and northness as proxies for other variables that were not available or were not well resolved over the seamounts along the Cobb-Eickelberg seamount chain, such as current velocity and shear stress. Environmental raster layers were downscaled to 100 m x 100m. We extracted model covariates from the environmental raster layers at the centroid locations of the AUV segments, using the *terra* R package (Hijmans 2022). We checked for high collinearity among the model covariates using Pearson's correlations and Variance Inflation Factor (VIF) using the *usdm* R package (Naimi et al.2014). We removed silicate, bottom temperature, calcite, sea surface temperature, TPI 100, and TPI 1000 covariates to limit VIF values to less than 10.

Model fitting and selection

We fit a generalized additive model (GAM) using the *mgcv* R package (Wood 2011). We modelled VME indicator taxa density using the Tweedie distribution with a log link, setting the power parameter p to 1.5. Predictions were limited to areas between 400 m and 1200 m depth to avoid extrapolating beyond the depth range of the observations of VME density (dependent data). We limited complexity by modelling all covariates using a low basis dimension (k=3) in order to avoid biologically unrealistic response curves. We completed backwards model selection, starting with the full model and removing covariates based on model out-of-sample predictive performance and marginal response curves. We favoured models with higher R^2 calculated by comparing test observations and predictions, and models with more realistic response curves that showed no large deviations in VME density predictions within extrapolated covariate space. We calculated marginal response curves following the evaluation strip method (Elith et al. 2005). During model selection, we removed the covariates dissolved oxygen, percent organic carbon, eastness, and TPI 500. The final model structure included only the covariates depth, northness and slope. Model validation was completed using the *gam.check* function from the *mgcv* R package to examine residuals. Figure 2 shows the predictive map produced by the final model.

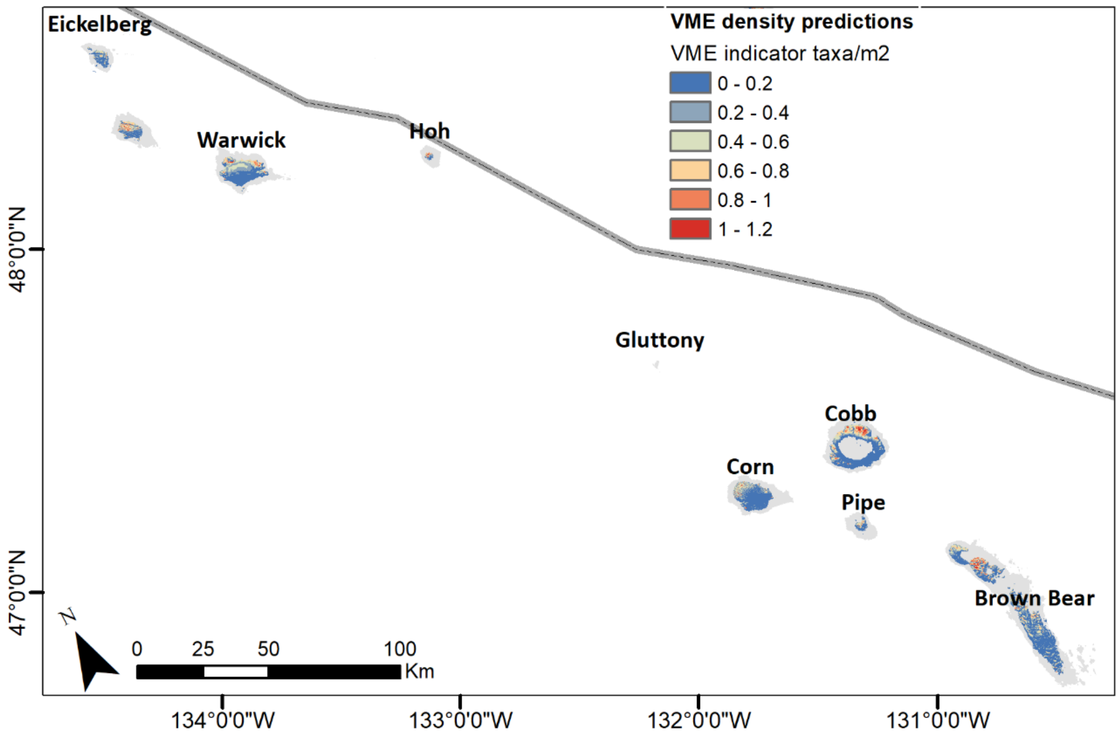

Figure 2. GAM-based VME density prediction map for the Cobb-Eickelberg seamount chain where red represents predicted high density and blue represents predicted low density. Grey line delineates the boundary of the Canadian exclusive economic zone. Grey shaded area represents depths outside of the prediction area, which was limited to 400-1200m in depth.

Model evaluation

AUV segments were grouped into five roughly equal folds for cross-validation (CV; 44 or 45 AUV transect segments in each fold). The folds were spatially aggregated along each transect to reduce the amount of spatial autocorrelation between training and testing data. For each CV model, we made predictions at the test (hold-out) data locations. We pooled the test predictions from the CV models to calculate R^2 as the squared Pearson's correlation between all test observation and test predictions. We opted to pool test predictions to calculate a single R^2 because of our small sample size and a high proportion of zero observations in one fold. Training data R^2 was 0.51 and testing data R^2 was 0.43.

Identifying Potential VMEs

We converted the VME indicator taxa density predictions to binary predictions of potential VME presence areas using the 0.6 VME indicator taxa colonies m^{-2} threshold described in our methods for identifying VMEs (Warawa et al. 2023). We applied the mean threshold (0.6 indicator taxa colonies m^{-2}) as well as the lower (0.5 indicator taxa colonies m^{-2}) and upper (0.7 indicator taxa colonies m^{-2}) 95% confidence interval threshold values to obtain the possible lower and upper bounds of potential VME area predictions in the region (Figure 3).

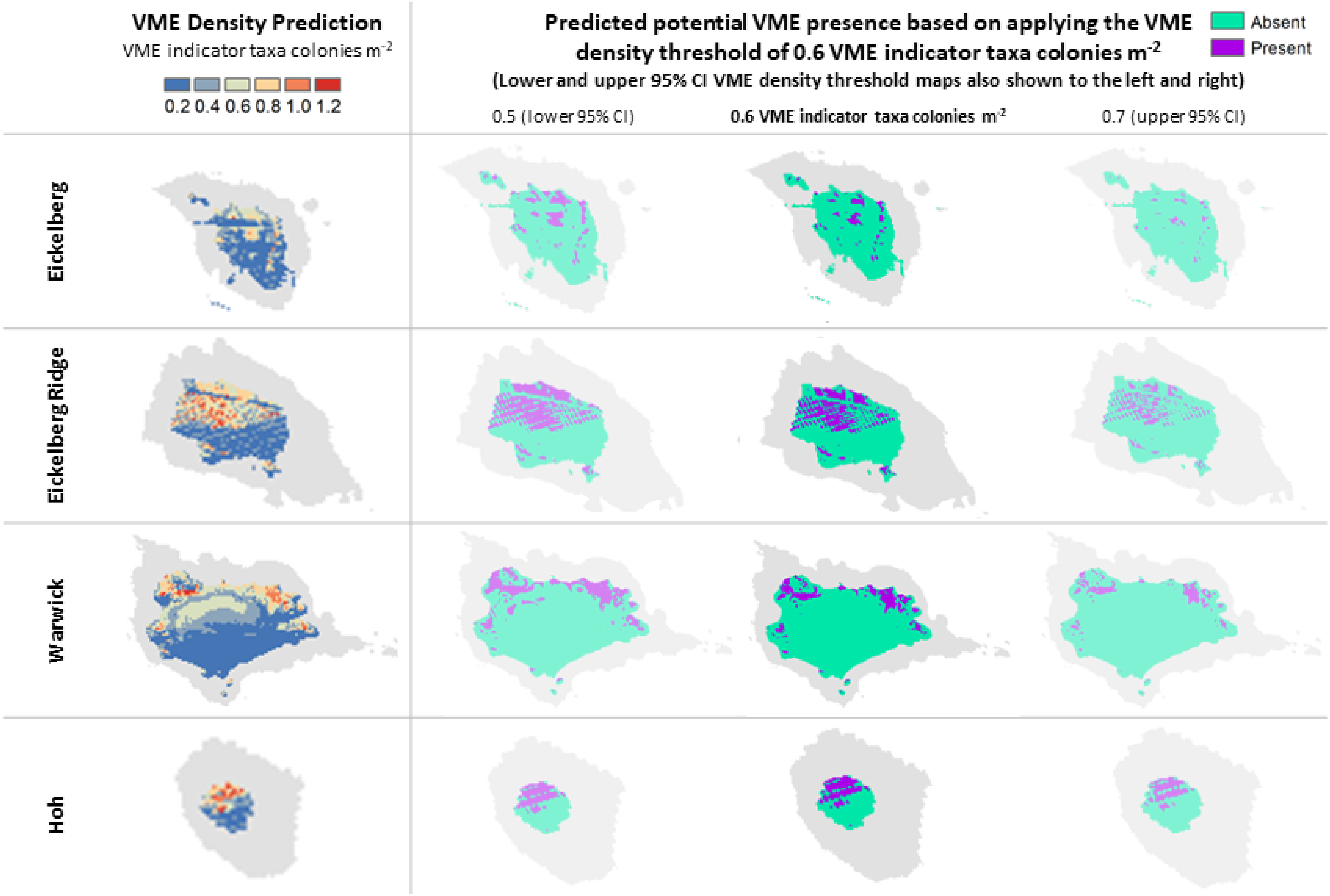

Figure 3. VME indicator taxa density model prediction maps and potential VME presence by seamount (not to scale). Potential VME presence (purple) is determined by applying the VME density threshold (see Warawa et al. 2023) to the VME density prediction model output. Potential VME presence maps using the lower and upper 95% confidence interval of the VME density threshold (0.5 and 0.7, respectfully) is shown for comparison. Grey shaded area represents depths outside of the prediction area, which was limited to 400-1200 m in depth.

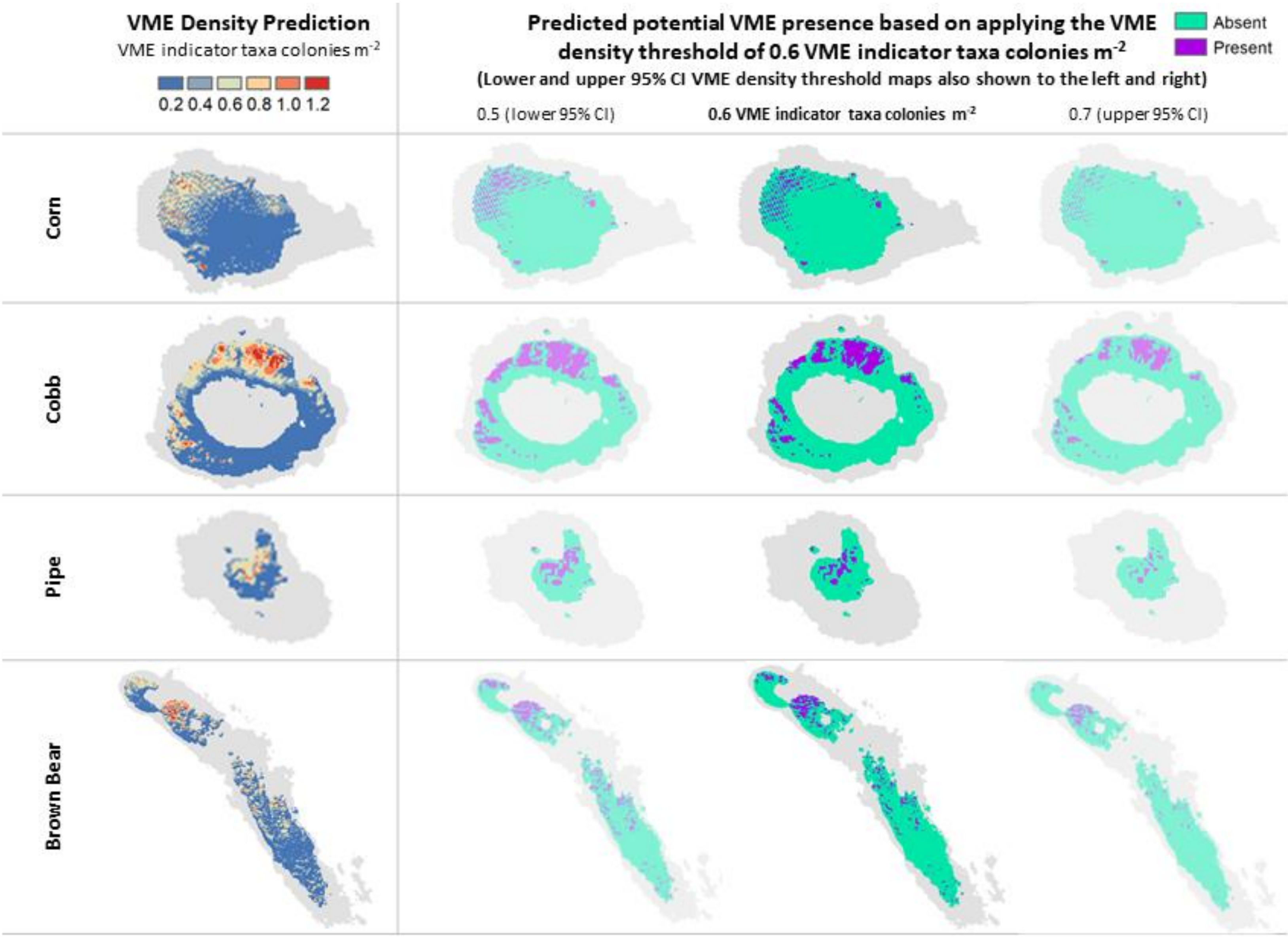

Figure 3. continued…

DISCUSSION

Based on our predictive models of VME indicator taxa density, we hypothesize that there are high VME indicator taxa densities on all seamounts in the Cobb-Eickelberg seamount chain. Potential VMEs were predicted on all seamounts in the study area based on application of our VME indicator taxa density threshold of 0.6 VME indicator colonies m^{-2} to our model predictions (Figure 3). According to the flow chart for identifying data to identify VMEs (NPFC 2022), areas identified as potential VMEs are high priority areas to undertake visual surveys to groundtruth predictions and confirm whether or not potential VMEs are indeed VMEs.

Next steps:

- Invite feedback on proposed methodology to identify areas where vulnerable marine ecosystems (VMEs) are likely to occur (i.e., *potential VMEs*).
- Revise method, apply it along the Cobb-Eickelberg seamount chain, and provide advice to the NPFC on the locations of these potential VMEs.

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