Estimating the distribution of harvested estuarine bivalves with natural-history-based habitat suitability models

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Habitat suitability models are useful to forecast how environmental change may affect the abundance or distribution of species of concern. In the case of harvested bivalves, those models may be used to estimate the vulnerability of this valued ecosystem good to natural or humancaused stressors. Using natural history information, rule-based habitat suitability models were constructed in a GIS for five recreationally and commercially harvested bivalve species common to NE Pacific estuaries (N. California to British Columbia). Tolerance limits of each species to salinity, depth, sediment grain size, and the presence of estuarine ecosystem engineering species (i.e., eelgrass and two species of thalassinid shrimps) were determined through literature review. Spatially-explicit habitat maps were then produced for Yaquina estuary (Oregon) using environmental data from multiple studies of the estuary (1960-2008). Suitability of a given location was ranked on a scale of 1-4 (lowest to highest) depending on the number of variables that fell within a bivalve's tolerance limits. The models were tested by comparison of the distribution of each suitability class to observed distributions of juvenile bivalves reported in benthic community studies (1996-2006). Results showed that the areas of highest habitat suitability (value=4) within our model contained the greatest proportion of bivalve observations for four of five target species, while the greatest proportion of the fifth species was still found within areas of moderately high suitability (value=3). Our next step is to test the model for juvenile and adult size-classes of these bivalves in other Pacific NW estuaries, and then to forecast changes in habitat suitability under scenarios of climate change. Natural-history-based habitat suitability models should be highly transferable across locations since they are based on empirically-derived, species-specific tolerance limits to relevant biophysical variables.