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Parasites of Culled Resident and Migratory Double-Crested Cormorants

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ABSTRACT: The Double-crested Cormorant (*Phalacrocorax auritus*: DCCO) is lethally managed in many states because of damage to farmed and recreational fisheries. Because a majority of birds culled in the U.S. are migratory cormorants, parasite assemblages may differ from resident birds, due to the diversity of feeding habitats and prey community assemblages encountered over their geographic range. We used multivariate techniques to identify if distinct assemblages and/or proportions of parasites could be identified at the genus level, among geographically different colonies of DCCO. Additionally, we assess the efficacy of models to predict the foraging location of a cormorant based on parasite assemblage.

We assessed the intestinal parasites of 218 DCCO culled from 11 sites in Alabama, Minnesota, Mississippi, and Vermont. Intestines were frozen prior to analysis. Following thawing and defatting, contents including the endothelial layer, were collected from the entire length of the intestine. Parasites were identified to the lowest possible taxonomic level based on previously reported parasites of the *Phalacrocorax* genus in North America.

The majority of parasites (87%) recovered were digenetic trematodes. Four species of trematode were found to change significantly in abundance (prevalence and/or intensity) with latitude and/or longitude. Similar diversity was noted for cestodes, nematodes, and acanthocephalans recovered from the samples.

Using a 1,000-permutation iterated multivariate analysis of variance (Adonis), we identified five distinct assemblages among the 11 sites sampled: two sites in Alabama, one of the Minnesota sites, and three of the Mississippi sites. The Vermont site was indistinguishable from all other sampling with the exception of the two Alabama sites.

Correspondence analysis and discriminant analysis were used to develop predictive models for identifying parameters (sample site, region, migratory status) of cormorants based on individual parasite assemblages. Although the models had limited utility in predicting sample sites, accuracy in determination of migratory or resident status of an individual was >80%.

Based on these findings, while assemblages of cormorant parasites vary among locations predicting where a host cormorant has been feeding based on its intestinal parasite community does not appear to be an efficient means to determine origin of a cormorant. In states where conservation of resident cormorants is desired, distinguishing between the two groups may be an important component for management decisions.

Key Words: cormorants, migratory cormorants, parasite assemblage, resident cormorants

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