

A MORPHOLOGICAL EXAMINATION OF SYMPATRIC CISCO
FORMS IN FOUR LAKES WITH SPECIFIC REFERENCE TO THE
OCCURRENCE OF SHORTJAW CISCO (*COREGONUS ZENITHICUS*)
IN MANITOBA

BY

LEE MURRAY

A Thesis submitted to
the Faculty of Graduate Studies
In Partial Fulfillment of the Requirements for the Degree of

MASTER OF SCIENCE

Department of Zoology
University of Manitoba
Winnipeg, Manitoba

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FACULTY OF GRADUATE STUDIES

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ABSTRACT

The shortjaw cisco (*Coregonus zenithicus*) is a widespread species ranging from the Great Lakes region, northwest to Great Slave Lake. Beyond the Great Lakes region, the validity of this species has been questioned due to genetic and morphological variability. Ciscoes were collected from four lakes reported to contain putative *C. zenithicus* (Lake Athapapuskow, George Lake, and Clearwater Lake, MB; and Reindeer Lake, SK). An examination of gillraker count and arrangement, jaw position, body size, and dorsal colouration was used to initially identify cisco forms within each lake. Multivariate analyses including Principal Component Analysis and Discriminant Analysis incorporating additional meristic and morphometric characters were used to examine within-lake and between-lake variation. Sympatric low and high gillraker forms were found within each lake. The low forms were found to conform to populations of *C. zenithicus* reported in the literature and the high forms were found to be consistent with descriptions of *C. artedi*.

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1. INTRODUCTION

The Question

The occurrence of multiple sympatric forms of ciscoes in Manitoba lakes has been examined several times in the past (Dymond 1943, Keleher 1950, Clarke 1969, Clarke 1973). The outcome of these studies is that two species of ciscoes are currently considered present in Manitoba, *Coregonus artedi* LeSueur 1818, cisco, and *C. zenithicus* (Jordan and Evermann 1909), shortjaw cisco. Recent genetic studies have suggested that sympatric populations of *C. artedi* and *C. zenithicus* found outside of the Great Lakes region may be more closely related to each other than to conspecific populations in other lakes suggesting a sympatric origin of these forms (Turgeon and Bernatchez 2003). Morphological variability between the Great Lakes *C. zenithicus* populations and those found within inland lakes suggests they may represent two distinct taxa, divergent genetic lineages, or phenotypes of a common morphotype (i.e., allopatric origin of forms) (Todd and Steinhilber 2002, Todd 2003). The main objective of this study was to examine morphological variation within and between various cisco populations for evidence supporting the presence of these taxa. This group provides the basis for exciting research with respect to taxonomic differentiation, definition of species limits, and resolution of identification problems in northern fishes.

Due to the geological history of the area, the fish fauna of northern North American freshwater lakes represents recently evolved clades and colonizing populations. Salmonids tend to display the greatest amount of taxonomically unrecognized diversity of all northern freshwater fishes. These fish provide many examples of different

morphological forms repeatedly occurring within and among lakes (Koelz 1929, Dymond 1943, Lindsey et al. 1970, Clarke 1973, Smith and Todd 1984, Bodaly et al. 1992, Bernatchez et al. 1996, Pigeon et al. 1997, Steinhilber et al. 2002, Turgeon and Bernatchez 2003). The origin of these sympatric morphs is of utmost importance to how we view adaptive radiation and speciation in northern freshwater fishes and provides an opportunity for studying evolutionary mechanisms and the role of ecological factors (Smith and Skúlason 1996, Gislason et al. 1999). The evolutionary processes responsible for the taxonomic landscape we see today are difficult to determine; however, the products of these processes are available for us to study. Products of evolutionary processes exist in the differing forms of taxa at varying levels of differentiation. The sympatrically occurring cisco forms found in many northern lakes, often of uncertain taxonomic status, are an example.

Several questions exist regarding these cisco forms. Most notably did these forms have a sympatric or allopatric origin?, if and how did they arise multiple times?, and what taxonomic level do these forms represent? The first two questions are inherently linked by the evolutionary processes that created them, either through allopatry, sympatry, or a combination of the two. The third question is a human perception problem in how we recognize taxa and define species limits. Applying species boundaries to this group of fishes has been problematic to researchers for decades due to the phenotypic variability displayed across North America.

The extreme morphological and ecological variation displayed by North American ciscoes has plagued attempts by α -taxonomists to consistently identify diagnostic characters. Only a few identification keys exist for this group and they often fail to separate forms when several locations are considered. These keys have relied heavily on gillraker counts, which usually separate forms within a single lake, however, when applied to multiple lakes their effectiveness for distinguishing between forms is reduced due to overlapping values. Some phenetic studies based on morphology have resulted in polytomies that phylogenetic studies using molecular markers have failed to corroborate (Bodaly et al. 1991, Bernatchez et al. 1991, Lockwood 1993, Sajdak and Phillips 1997, Reed et al. 1998). This lack of agreement between morphology and genetics has made it difficult to identify the appropriate conservation units for the cisco group (Turgeon and Bernatchez 2003).

A reasonable approach to examining species boundaries in a plastic group like the ciscoes (where cross fertilization studies are not practical for examining reproductive isolation) is to use multivariate phenetic analyses. These methods incorporate a large number of morphological variables simultaneously, reducing them into phenetic space so the patterns of variation can be more easily examined. Similarities and differences displayed by the analysis of the morphological data can then be used to make inferences about underlying genetic relationships.