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A MORPHOLOGICAL, MERISTIC AND ELECTROPHORETIC
INVESTIGATION OF SIX ALLOPATRIC LAKE CHARR
(SALVELINUS NAMAYCUSH) POPULATIONS FROM
ALGONQUIN PARK, ONTARIO.

by

Lawrence Irwin Speers, B.Sc.

A thesis submitted to the Faculty of Graduate
Studies and Research in partial fulfilment
of the requirements for the degree of
Master of Science

Department of Biology

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LIST OF TABLES

1. Location of the six study lakes	63
2. List of the external linear measurements examined in the morphological investigation	64
3. List of meristic characters examined in the meristic investigation	66
4. Summary of the size and age distribution of the samples	67
5. Regression coefficients from the analysis of allometric growth	68
6. Univariate summary statistics of the size adjusted morphological variables	70
7. Analysis of variance of the size adjusted morphological variables	76
8. F-matrix from the canonical variate analysis of the size adjusted morphological variables	78
9. Classification matrix from the canonical variate analysis of the size adjusted morphological measurements	79
10. The amount of overlap between populations based on the morphometric analysis	80
11. Mahalanobis generalized distance matrix from the morphometric analysis	81
12. Coefficients of the classification functions based on the morphometric variables expressed as a ratio of fork length	82

ABSTRACT

The amount and distribution of morphological, meristic and electrophoretic variation was investigated in six allopatric lake charr (Salvelinus namaycush) populations from Algonquin Park, Ontario. Morphological variation was estimated from differences in body shape as approximated by the analysis of 40 linear measurements. Meristic variation was estimated from counts of 9 serially repeating anatomical structures. The electrophoretic variation was measured on the basis of 40 protein loci.

Canonical variate analysis of the morphometric and meristic data demonstrated significant phenotypic differences between populations. The electrophoretic analysis revealed low levels ($H=0.7\%$) of electrophoretically detectable variation but significant amounts of population differentiation. The morphological and meristic variation appear to be the result of environmental and ecological differences between lakes but the possibility that some of the observed phenotypic differences were the result of genetic differentiation between these populations could not be discounted. The management implications of these findings are discussed.

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TABLE OF CONTENTS

Abstract	iii
Acknowledgements	iv
Table of Contents	v
List of Tables	vi
List of Figures	vii
Introduction	1
Methods	8
Study Sites	8
Collections	10
Morphological Investigation	11
Meristic Investigation	14
Electrophoretic Investigation	15
Statistical Analysis	17
Results	18
Morphological Investigation	19
Meristic Investigation	26
Electrophoretic Investigation	30
Synopsis of Results	33
Discussion	35
Morphological Investigation	35
Meristic Investigation	39
Electrophoretic Investigation	42
Conclusions	52
References	54
Tables	63
Figures	105

LIST OF TABLES

1. Location of the six study lakes	63
2. List of the external linear measurements examined in the morphological investigation	64
3. List of meristic characters examined in the meristic investigation	66
4. Summary of the size and age distribution of the samples	67
5. Regression coefficients from the analysis of allometric growth	68
6. Univariate summary statistics of the size adjusted morphological variables	70
7. Analysis of variance of the size adjusted morphological variables	76
8. F-matrix from the canonical variate analysis of the size adjusted morphological variables	78
9. Classification matrix from the canonical variate analysis of the size adjusted morphological measurements	79
10. The amount of overlap between populations based on the morphometric analysis	80
11. Mahalanobis generalized distance matrix from the morphometric analysis	81
12. Coefficients of the classification functions based on the morphometric variables expressed as a ratio of fork length	82

13. Coefficients of the classification functions based on the five morphometric variables expressed as a ratio of fork length that gave the best separation between groups	83
14. Univariate summary statistics of the meristic variables	84
15. Analysis of variance of the meristic variables . .	88
16. Scheffe multiple range test of meristic variables	91
17. Summary of the Scheffe multiple range test	96
18. F-matrix from canonical variate analysis of meristic variables	97
19. Classification matrix from the canonical variate analysis of the meristic variables	98
20. The amount of overlap between populations based on the classification matrix from the meristic analysis	99
21. Mahalanobis generalized distance matrix from the meristic analysis	100
22. Proteins and electrophoretic conditions employed in the electrophoretic investigation	101
23. Genotype frequencies for 4-methylumbelliferyl phosphate and malate dehydrogenase	102
24. Summary of the allelic frequencies from the electrophoretic investigation	103
25. Genetic distances between the study populations	104

LIST OF FIGURES /

1. Algonquin Park region showing locations
of study lakes 105
2. Plot derived from canonical variate analysis of
morphometric variables 106
3. Dendrogram produced by UPGMA cluster analysis of
the morphometric variables 107
4. Plot derived from canonical variate analysis of
meristic variables 108
5. Dendrogram produced by UPGMA cluster analysis of
the meristic variables 109
6. Distribution of malate dehydrogenase allelic
frequencies 110
7. Distribution of 4-methylumbelliferyl phosphate
allelic frequencies 111
8. Dendrogram produced by UPGMA cluster analysis of
Nei's genetic distance 112

INTRODUCTION

Evolution can be defined as a change over time in the genetic composition of a population (Chambers 1983). Evolution in subdivided populations usually results in genetic differences between populations. The amount and pattern of these genetic differences can be used to characterize the population genetic structure of a species. The genetic structure of populations plays an important role in the genetic theory of evolutionary change (Wright 1969, Selander and Whittam 1983).

In freshwater fish species, the restriction of gene flow between allopatric populations often creates a genetically based subpopulation structure (Allendorf and Phelps 1981). In many cases subpopulations are adapted to local environmental conditions (MacLean and Evans 1981). Since these adaptations can affect productivity, an understanding of the population genetic structure of economically important species is necessary for their efficient management (Smith and Chesser 1981).

Differences between populations in ecological and phenotypic characteristics are often the first indication of important genetic differences. Although little quantitative data are available, the lake charr, Salvelinus namaycush, is phenotypically and ecologically a highly variable species. An indication of the amount of phenotypic variation that is found in this species is

given by its extensive nomenclature. It has been described, based on variation in such characteristics as skin colouration, body shape and the fat content of the flesh, under at least 35 common and 15 scientific names (Martin and Olver 1980). Many of the morphological variants were described from the Great Lakes and, although some of them occurred sympatrically, they were associated with ecological differences in diet, depth distribution, and time and depth of spawning (Goodier 1981, Brown et al. 1981).

In contrast to the extensive literature on lake charr ecology and population dynamics (for a review see Martin and Olver 1980), few studies have tried to quantify the observed phenotypic differences between populations or to measure the relative influence that the genotype and the environment have on these differences. Differences in shape as measured by a series of linear measurements and differences in the number of serially repeating anatomical structures such as gill rakers and fin rays are the two most commonly quantified phenotypic differences between fish populations. The use of these morphological and meristic characteristics to differentiate between fish populations is reviewed by Ihssen et al. (1981).

Qadri (1967) and Khan and Qadri (1971) analysed the morphological and meristic variation in a number of allopatric lake charr populations, while Khan and Qadri

(1970) studied the variation in four sympatric forms from Lake Superior. These studies document significant differences in shape, number of anal fin rays, number of gill rakers and number of branchiostegal rays between different populations.

Characters like morphological and meristic variables, that do not show natural discontinuities are termed metric or quantitative characters. Reymont et al. (1984) review the use of morphological measurements to analyse variation in biological form. Ihssen et al. (1981) review the use of these techniques to differentiate between fish populations. Metric characters are under the influence of a few to many genetic loci and their phenotypic expression is usually the result of an interaction of genetic and environmental influences (Falconer 1981). In fishes, environmental factors such as differences in temperature (Taning 1952, Weisel 1955) and photoperiod (Lindsey 1958) during development influence meristic counts, while differences in growth rate which is environmentally influenced can result in differences in body proportions (Martin 1949, Barlow 1966).

Heritability is a measure of the relative contribution that genetic and environmental influences have on the expression of a phenotypic character (Chambers 1983). Heritability is commonly estimated by analysis of variance of the degree of resemblance between relatives

(Falconer 1981). This is most efficiently done through breeding studies under controlled environmental conditions but may also be accomplished by estimating the influence of environmental factors through the introduction of related individuals into different environments (Hartl 1980).

Martin (1966) through transplant studies showed that growth rate in lake charr from Lake Louisa, Ont. was to a large extent environmentally controlled. Berst et al. (1980) demonstrated environmental influences on the number of gill rakers, anal fin rays and dorsal fin rays by comparing these counts between hatchery reared and wild lake charr of the same genetic origin. In contrast, Plosila (1977) and MacLean et al. (1981) were able to demonstrate a correlation between the geographic origin of hatchery strains and the survival ability of planted lake charr.

In lake charr, few phenotypic characters, if any, have been genetically analysed through breeding studies. However, genetic differences between populations have been demonstrated for other traits. Ihssen and Tait (1974) were able to demonstrate genetic differences between two populations of lake charr in their ability to retain swim bladder gas, a character correlated with the ability to live in deep water. This genetically based physiological difference between the two populations was correlated with

differences in the environmental characteristics of the lake of origin of the populations.

The demonstration of genetic differences between populations on the basis of morphological or physiological differences is difficult and tedious (Ryman 1983; Todd et al. 1981). In the last decade the use of biochemical markers identified through the use of electrophoretic techniques has become increasingly important in the identification and assessment of genetic diversity in natural populations (Allendorf and Utter 1979, Ryman 1983, Ihssen et al. 1981).

Dehring et al. (1981) used this technique to study the amount and distribution of genetic variation in lake charr from eastern Lake Superior. Although they found low levels of electrophoretically detectable variation, they observed a high degree of heterogeneity among their sample groups and were able to demonstrate that genetically distinct groups of lake charr exist in eastern Lake Superior.

Some of the most extensively studied populations of lake charr (Fry 1949; Fry and Chapman 1948; Martin 1952, 1954, 1957, 1966), occur in the relatively small precambrian lakes inside the present boundary of Algonquin Provincial Park, Ont. Martin (1966) documented differences between populations in growth rate, age at first maturity, longevity, maximum size, and size at first

maturity and pointed out the management implications of these differences. He was able to correlate these differences with differences in diet during the summer months. Those populations that fed mainly on plankton had a slower growth rate and a shorter life span than those that fed mainly on fish. Martin and Sandercock (1966) observed a correlation between the amount of plankton in the diet during the summer months and the mean number of gill rakers, a character assumed to be important in feeding. It is not known to what extent if any these observed differences are genetically based or environmentally induced.

Many lake charr populations in the Great Lakes region are already extinct due to overexploitation, loss of habitat through eutrophication and the effects of the invasion into the upper Great Lakes of the sea lamprey Petromyzon marinus. Many other populations are in danger of extinction due to continued overexploitation and habitat degradation due to eutrophication and the effects of acid rain. If, as it appears, different lake charr populations have developed genetically based biologically important differences, then information on the distribution of genetic variability in this species is urgently needed if these genetic resources are to be protected. McLean and Evans (1981) discuss the fisheries management implications of the concept that a fish species

can be subdivided into more or less genetically distinct subunits or "stocks". Determining the amount of genetic differentiation between a few allopatric lake charr populations from a restricted geographic area is one of the first steps in the analysis of the genetic diversity of this species.

This study is a morphological, meristic and genetic investigation of the amount of variation within and between six allopatric lake charr populations from Algonquin Provincial Park, Ont. The morphological and meristic variation was assessed using multivariate morphometric techniques while the technique of protein electrophoresis was used to assess genetic variation. The observed variation will be discussed in relation to the ability of these techniques to differentiate between these populations.

METHODS

STUDY SITES

The lakes chosen for this study were all located within Algonquin Provincial Park, Ontario (Table 1). The geomorphological and biogeographical history of this area has been described by Martin and Chapman (1965); Dadswell (1974) and Ihssen et al. (1981). All the study lakes lie on the Madawaska Highlands of the Canadian Shield. They are relatively small and range from 1469 to 230 hectares for Big Trout Lake and Wilkins Lake respectively. They occur in an area of moderately broken relief and although they are in a relatively small geographic area, less than 2000 sq. kms., they form the headwaters of five river systems. This results in lakes that are in close geographic proximity being separated by long distances through riverine connections. Merchants Lake and Happy Isle Lake, for example, are only 340m apart but Merchants Lake drains to the north through the Petawawa River system while Happy Isle Lake drains to the south through the Opeongo River system. The study lakes are relatively nutrient poor (oligotrophic) and have little buffering capacity to counteract acidification. Due to this low buffering capacity, these lakes are very sensitive to the effects of acid rain and it is likely that under the present conditions the lake charr populations in these lakes will in the near future begin to show the effects of

acid stress.

On the basis of geomorphological and biogeographical evidence, it is believed that the present fish fauna invaded this area shortly after the retreat of the last glaciation, between 8,000 and 10,000 years B.P.. The differences between the study lakes in elevation and the fact that the study lakes form the headwaters of five river systems (Fig. 1) makes the possibility of gene flow between these lake charr populations unlikely. Because of this, it is likely that these populations have been genetically isolated for 8,000 to 10,000 years. In addition, these lakes have never been stocked with hatchery reared lake charr (staff Ministry of Natural Resources personal communication) and as a result I could be sure that I was sampling only from indigenous lake charr gene pools.

Collections

During the summers of 1980 and 1981 graded mesh gill nets were used to obtain samples of different size classes from each study lake. All samples were collected between early June and mid September. The study was designed based on sample sizes of 25 for 4 lakes and 50 for the other 2 lakes. These sample sizes were usually obtained within a 2 day sampling period. Upon removal from the nets, the sex, standard length, total length, body depth at the origin of the dorsal fin, and the fresh weight of each individual were recorded. Tissue samples of liver (L), heart (H), epaxial muscle (M) and eye (vitreous fluid) (E) were taken and frozen on dry ice until they could be transported to the laboratory where they were stored at -60 C until required for electrophoresis. The remaining carcass was frozen and stored at -20C until required for morphometric and meristic analysis.

The ages of the specimens were estimated by analysis of fin ray sections by staff of the Stock Assessment Unit MNR Maple Ontario.

Morphological Investigation

To analyse morphological variation in terms of body proportions, a total of 41 external linear measurements were taken on each individual (Table 2). The measurements followed those outlined by Oulette and Qadri (1968). Total length, standard length and fork length were measured using a standard fisheries measuring board. The remaining measurements were taken with manual dial calipers and manually recorded, or with automatic calipers (McAllister and Planck 1981), and the data electronically stored. Preliminary tests showed no significant differences between the two methods.

The linear measurements were tested for allometry using standard allometric growth equations (Gould 1966).

$$M = a(Fklg)^b$$

$$\log M = \log a + b \log (Fklg)$$

where, M = linear measurement

b = the regression coefficient obtained from an analysis of covariance of $\log (M)$ on $\log (Fklg)$

a = proportionality constant required by allometric relationship

Since I was interested in differences in shape rather than absolute size, the external measurements were

transformed to eliminate, or at least minimize, the effect of mean size differences among populations (Todd and Smith 1980; Ihssen et al. 1981) by the formula

$$M_c = M (\overline{Fklg}/Fklg)^b$$

where, M_c = transformed measurement

M = original measurement

$\overline{Fklg}$ = overall mean fork length

$Fklg$ = fork length of specimen

b = regression coefficient of $\log M$ on $\log Fklg$ within populations obtained from an analysis of covariance.

This transformation has the effect of adjusting all the morphological measurements "to values they would assume if the specimen were of mean body size" (Thorpe 1976). In this study the grand mean of the fork length for all specimens in the analysis was used as a measure of mean body size.

To test for significant differences between groups and to identify those variables, that when combined, best summarize these differences, the resulting 40 transformed variables were subjected to a canonical variate analysis (Albrecht 1980, Klecka 1975). Canonical variate analysis is the term for a classical discriminant function analysis where the objective of the study is to display the information content of a multivariate data set in "a space of reduced dimensions that maximizes the amount of variation among groups relative to that within groups"

(Neff and Marcus 1980). Linear discriminant functions that can be used to classify unknown individuals to the groups being studied can be derived from the scores produced from this analysis.

The Mahalanobis generalized distance (i.e. the square of the euclidian distance in canonical variate space between population centroids) obtained from the canonical variate analysis was used in an unweighted pair-group arithmetic average (UPGMA) cluster analysis (Sneath and Sokal 1973) to diagram the relationships between populations.

MERISTIC INVESTIGATION

To analyse variation in terms of meristic characters a total of 9 serially repeating anatomical structures were counted on each specimen (Table 3). The number of vertebrae was counted following dissection and included all visible segments. All fin ray counts included all visible rays. The number of gill rakers was counted by removing the first gill arch and counting all visible rakers.

A regression analysis of the meristic data on fork length was performed to study the influence of overall size differences on the counts. Analysis of variance was used to compare the variation among populations for each count separately. Since all comparisons were significant, a Scheffe multiple range test (Kim and Kahout 1975) was used to compare populations. A canonical variate analysis was performed on these data. The Mahalanobis generalized distance between population centroids derived from this analysis was used in a UPGMA cluster analysis to construct a diagram of the relationships between the populations.

ELECTROPHORETIC INVESTIGATION

Starch gel electrophoresis was conducted using the technique of May et al. (1979). Gels of 9.5mm thickness were prepared using 52g of a 1:1 mixture of Electrostarch lot 392 and Connaught starch lot 373-1 in 370 ml of the appropriate buffer (Table 22). Cooling was achieved by circulating an ethylene glycol solution at -6 C through plexiglass plates placed on top of the gel.

The tissue samples were prepared for electrophoresis by manually grinding them with an equal volume of deionized water and centrifuging at 15,600 g for three minutes. The supernatant absorbed into filter paper wicks was then inserted into the starch gel. The appropriate buffer systems and tissues used for each enzyme system are given in Table 22. Four different buffer systems were used:

R Described by Ridgway et al. (1970).

Gel buffer: 0.03M Tris - 0.005M citric acid, pH 8.5.

Electrode buffer: 0.06M lithium hydroxide - 0.3M boric acid, .
pH 8.1

Gels were made using 99% gel buffer and 1% electrode buffer.

CT Described by Clayton and Tretiak (1972).

Electrode buffer: 0.04M citric acid adjusted to pH 6.1 with N-(3-Aminopropyl)-morpholine.

Gel buffer 1:20 dilution of electrode buffer

MF Described by Markert and Faulhaber (1965).

Electrode buffer: 0.018M Tris - 0.1M boric acid -
0.004M Edta

Gel buffer 1:4 dilution of electrode buffer

TC Described by Clayton and Tretiak (1972).

Electrode buffer 0.04M citric acid adjusted to pH 8.0
with Tris.

Gel buffer 1:20 dilution of electrode buffer.

The system of nomenclature used for the enzymes is that described by Allendorf and Utter (1979). The following enzyme systems were examined (abbreviations in parenthesis) : aspartate aminotransferase (AAT), alcohol dehydrogenase (ADH), creatine phosphokinase (CPK), glucosephosphate isomerase (GPI), glycerol-3-phosphate dehydrogenase (G3PDH), isocitrate dehydrogenase (IDH), lactate dehydrogenase (LDH), malate dehydrogenase (MDH), malic enzyme (ME), mannosephosphate isomerase (MPI), 4-methylumbelliferylphosphate (MUP), phosphoglucomutase (PGM), 6-phosphogluconate dehydrogenase (6-PGD), sorbitol dehydrogenase (SDH) and superoxide dismutase (SOD). The stain recipes used to visualize the proteins are given in May (1980).

STATISTICAL ANALYSIS

The canonical variate analysis, analysis of variance and covariance and the regression analysis were computed using the June, 1981 version of BMDP Statistical Software (Department of Biomathematics University of California, Los Angeles). The Scheffe multiple range test was performed using the Statistical Package for the Social Sciences (SPSS) release 9.1.

RESULTS

A total of 228 individuals was sampled. Sample sizes, estimates of mean age, mean fresh weight, and the sex ratio of the samples are given in Table 4. Martin (1966), on the basis of extensive samples from these lakes showed that these populations varied in age distribution and growth rate. These results are in agreement with his observations. These differences accounted for the observed mean size differences between lakes (Table 4).

An initial canonical variate analysis was performed on the linear measurements to detect differences in shape between males and females. Using this technique only 61% of the individuals in the classification matrix were correctly identified compared with an expected 50% through random assignment of individuals. Although there was a statistically significant difference between the group centroids of males and females ($F = 15.75$, on 1 and 199 d.f., $P > .001$), it was felt that the large amount of overlap (39%) indicated little biologically important difference in shape between the sexes. As a result, the sexes were not differentiated in any of the subsequent analyses.

Tables 12 and 13 respectively. The scores for an unknown specimen on these functions is an estimate of the distance in canonical variate space from the specimen to the group centroid. Group membership is based on the smallest distance from a group centroid. A correct assignment of better than 90% accuracy should be obtained by using 20 linear measurements expressed as a ratio of fork length and then scaled by a mean fork length of 380.4mm while a better than 80% correct assignment will be obtained by using the classification functions based on only 5 measurements that have been similarly adjusted.

The results from these analyses demonstrate that there are significant differences in body proportions between these populations and that individuals from these lakes can, on the basis of a few linear measurements, be correctly assigned to their lake of origin with a high rate of success.

regression coefficient derived by pooling all samples or by simply expressing each measurement as a ratio of fork length but these methods would have resulted in a greater loss of information concerning group differences.

The use of the within-lake regression coefficient in the allometric transformation makes it necessary to know the lake of origin of a specimen before its measurements can be adjusted for size differences. This precludes the use of the discriminant functions derived from the canonical variate analysis of this data set from being used to classify unknown specimens. Since it was felt that it would be useful, as a test of the classification functions, to be able to classify unknown specimens from these lakes back to their lake of origin, a second analysis was performed using a transformation that did not require the within-lake regression coefficient.

The simplest method of correcting for size differences is to express each linear measurement as a ratio of fork length. If this ratio is then scaled by a constant, in this case the overall mean fork length, this transformation is equivalent to applying the allometric transformation using a regression coefficient of 1 for all measurements. Unless the measurements demonstrate very positive or very negative allometry the pattern of variation in the data set obtained using this method will be very similar to the pattern in the data set obtained by

using the within-lake regression coefficient in the allometric transformation. This method may result in a loss of information concerning group differences but since it is not necessary to analyse for differences in allometric growth, it is the most practical method to use if one is only interested in being able to classify unknown samples in routine field studies.

After being corrected for size differences using the within-lake regression coefficient for each population separately, 39 of the 40 morphological measurements were significantly different at the 5% level among the six populations (Table 6). The univariate statistics for the linear measurements adjusted using the within-lake regression coefficients are given in Table 7.

The canonical variate analysis based on the morphological measurements adjusted for size differences using the within-lake regression coefficients gave highly significant differences among group centroids (approximate F-statistic = 23.01, on 85 and 923 d.f., $P < .001$). All 15 pairwise comparisons (Table 8) were significant. The variables giving maximum separation among groups are in order INOW, PMXO, DFIH, VFOH, ADFH, LADF and MAXH. All of the statistically significant variation in the original data set was accounted for in the five canonical variates. All of the statistically significant variation in the original data set was accounted for by using only 17 of

the 40 original variables. This is an indication of the amount of redundancy of information in the original data set. The first five canonical variates accounted for 48, 23, 16, 9 and 4% of the variability respectively.

The values of the group centroids on the first two canonical variates which account for 71% of the total variability were plotted and the limits of each population on these two axes were outlined (Fig. 2). From the standardized coefficients for the canonical variables, the first canonical variate is based mainly on the positive contributions of INOW, LADF and VFOH; and the negative contributions of MAXH, UJWL, ADFH and PMXO. Separation, on this axis, is based on head shape, the size of the adipose fin and the length of the ventral fin. The second canonical variate is based mainly on the positive contributions of MAXH and LADF, and the negative contributions of INOW, PMXY, DFIH and ADFH. Separation on the second canonical axis is also based on head shape and the size of the adipose fin. The success of the canonical variate analysis in separating the groups is shown in the classification matrix (Table 9). 204 individuals of a total of 211 or 96.7% were correctly classified to their lakes of origin. A "jackknifed" classification procedure was also used. In this procedure, the analysis is repeated N times, where N is the total sample size, leaving out a different specimen each time. The resulting

function is the weighted average of the N analyses (Neff and Marcus 1980). This procedure gives a better estimate of the overall separation of the groups in canonical variate space. The "jackknifed" classification correctly assigned 194 of 211 or 91.9% of the specimens to their lake of origin. The percentage of overlap between populations from this classification is shown in Table 10.

The dendrogram derived by UPGMA cluster analysis of the Mahalanobis distance matrix from this analysis (Table 11) is shown in Fig. 3. The pattern of branching in this dendrogram does not appear to be correlated with the geographic proximity of the samples or with the watershed pattern of the study area. The samples from Lake Louisa and Merchant Lake have the highest branching point in the dendrogram (i.e. are the most similar morphologically). These lakes are in different drainage systems and except for Wilkins Lake are the most geographically distant of the six study lakes. Wilkins Lake and Happy Isle Lake whose samples are connected by the second highest branching point are also found in different drainage systems and are geographically isolated. This is in agreement with the observation that lake charr are very limited in their ability to disperse through riverine connections.

The results of the canonical variate analysis of the data set adjusted for size differences by expressing each

measurement as a ratio of fork length and then scaling by overall mean fork length, are almost identical to the results from the previous analysis. The variables giving the most separation between groups are, in order, PMXO, INOW, DFIH, VFOH, ADFH, LADF, PMXY and MAXH. The classification functions derived from this analysis are based on only 20 of the original 40 variables. These functions correctly assigned to their lake of origin 97.2% of the sample while the "jackknifed" classification correctly assigned 92.5%.

To estimate the ability of these classification functions to correctly assign unknown specimens to their lake of origin using a reduced number of measurements, the analysis was repeated using only the variables giving the best separation between groups. The classification functions derived from the 10 linear measurements that gave the most separation among groups, correctly assigned 89.9% of the sample to their lake of origin, while the classification functions derived from the 5 measurements that gave the best separation correctly identified 82.9% of the sample. This demonstrates the power of these techniques to differentiate between these groups.

The coefficients of the classification functions giving the maximum separation and the coefficients of the classification functions derived from the 5 measurements giving the best separation between groups are given in

SYNOPSIS OF RESULTS

1. Growth rates and age distributions varied between populations.
2. Body proportions did not allow discrimination between the sexes.
3. The differences in body proportions allowed for a high level of discrimination between lakes. Individuals were correctly identified with their lake of origin in greater than 90% of the sample. The discriminant functions were based mainly on differences in head shape and fin size.
4. There were significant differences among lakes for all meristic variables. The canonical variates based on meristic variables allowed 50% of the sample to be correctly identified to their lake of origin. The canonical variates were based mainly on differences in number of gill rakers, number of anal fin rays and number of branchiostegal rays.
5. The level of genetic variability as measured by protein electrophoresis was low with an overall average heterozygosity of only .7%. The average gene diversity between populations accounted for approximately 17% of the total gene diversity.
6. The dendrograms from the meristic and morphometric

MERISTIC INVESTIGATION

The summary univariate statistics for the 9 meristic variables are shown in Table 14. The values of NLBR, NRBR and NDFR all fell within the values reported in the literature (Martin and Olver, 1980). Each of the other variables; NGR, NAFR, NPVFR, NPCFR, NMP and NVERT, showed a slight increase in range over the literature values. This increase may reflect real differences or may be due to differences between studies in the way the meristic characters were defined. In this study, for example, all visible fin rays and gill rakers were counted while in many of the studies in the literature only the major rays were counted.

Six of the nine meristic variables (NRBR, NDFR, NPVFR, NPCFR, NMP, NVERT) were independent of FKLG, while NLBR and NAFR were positively correlated and NGR was negatively correlated with FKLG at the 1% level. Further analysis of NLBR, NAFR and NGR, treating each population as an independent sample showed that within individual lakes 17 of 18 possible comparisons were independent of FKLG at the 1% level. This means that within each lake these characters were not correlated with an increase in size as measured by fork length. It seems likely that the observed overall correlations were the result of the interaction of mean size differences among lakes (Table 4) with differences among lakes in the means of NLBR, NAFR

and NGR rather than a correlation between these meristic variables and a size related growth factor as measured by fork length.

The means of all 9 meristic variables were significantly different ($P < 0.01$) (Table 15) among the 6 samples. A multiple range test (Scheffe) was used to test for significant pairwise differences between the means (Table 16). Table 17 shows a summary of the pairwise comparisons between populations for the 9 variables. The sample from Lake la Muir was significantly different at the 5% level for 15 of the 45 possible pairwise comparisons while none of the comparisons between Merchant Lake, Happy Isle Lake and Big Trout Lake was significant. From this table it can be seen that, on the basis of the meristic variables, the samples from Lake la Muir, Wilkins Lake, and Lake Louisa are the most distinct.

The canonical variate analysis showed highly significant differences among group centroids (approximate F-statistic = 9.5, on 40 and 914 d.f., $P < .001$). All 15 pairwise comparisons (Table 18) were significant. The variables giving the best separation among groups are, in order, NGR, NLBR and NAFR. The first four canonical variates, accounting for 55, 24, 13 and 5% of the variability respectively, were highly significant.

The values of the group centroids on the first two canonical variates which account for 79% of the total

variability were plotted and the limits of each population on these two axes were outlined (Fig. 4). The first canonical variate based, mainly on the positive contribution of NLBR and the negative contribution of NGR, partially separates the Lake la Muir sample from the Lake Louisa sample. The second canonical variate based, mainly on the positive contribution of NAFR and the negative contribution of NDFR and NPCFR, partially separates the Merchant Lake sample from the Big Trout Lake, Wilkins Lake and Happy Isle Lake samples.

The success of the canonical variate analysis in separating the groups is shown in the classification matrix (Table 19). A total of 53% of the individuals were correctly assigned compared with approximately 17% expected from a random assignment of individuals. The jackknifed classification also correctly assigned 53% of the individuals. Fish from Lake la Muir had a correct identification of 84%. This is in agreement with the results from the Scheffe multiple range test that showed Lake la Muir to be significantly different from at least one other population for 6 of 9 counts. The second most distinct population Lake Louisa had a correct identification of 59%. It was significantly different from at least one other population on 7 of 9 counts. The percentage of overlap between populations from this classification is shown in Table 20.

The level of separation among samples based on the meristic data as compared to the morphological data is illustrated by comparing the respective plots of the first two canonical variates (Fig. 2 and Fig. 4) and the classification matrices (Table 9 and Table 19). The lower level of successful separation using the meristic variables may in part be due to the smaller number of variables (i.e. 9 meristic variables compared to 40 morphometric variables) and the inherent differences in the two types of data (i.e. discrete meristic data compared with continuous morphometric data).

The dendrogram derived by UPGMA cluster analysis of the Mahalanobis distance matrix (Table 21) is shown in Fig. 5. The pattern of branching is similar to that obtained from the morphometric analysis (Fig. 3). The branching pattern for Wilkins Lake, Happy Isle Lake, Lake Louisa and Merchants Lake is the same in both analyses. In the meristic analysis the Big Trout Lake sample is joined to the Wilkins Lake, Happy Isle Lake branch rather than the Lake la Muir branch. These results, like the morphometric analysis, do not appear to be correlated with either the geographic proximity of the populations or with the drainage pattern of the area.

ELECTROPHORETIC INVESTIGATION

The number of loci, tissues of expression and appropriate buffer systems are given in Table 22. These 15 enzyme systems represent an estimated 40 genetic loci. Fourteen of these enzyme systems showed no variation (i.e. all populations were monomorphic for the same electrophoretic allele). Three systems AAT(1,2), MDH(3,4) and MUP were variable. The AAT(1,2) polymorphism, although it was found in a number of populations, was not used in the subsequent analysis because electrophoretic patterns obtained from frozen samples did not give consistent results. Through breeding studies, Clayton and Ihssen (1980) and, May (1980) demonstrated the genetic basis of the MDH polymorphism. The genetic basis of the variation at the MUP locus has similarly been demonstrated by staff of the Stock Assessment Unit, Ministry of Natural Resources, Maple Ont. (B. Martin MNR, personal communication).

The observed phenotypic distributions for the variable loci are given in Table 23. The phenotypic distributions were tested for goodness of fit to the expected Hardy-Weinberg equilibrium by using a likelihood-ratio test (Sokal and Rohlf, 1981). The expected phenotypic proportions for MDH(3,4) were calculated assuming equal allele frequencies at the two

loci (see Casselman et al. 1981). There was no significant deviation from Hardy-Weinberg expectations (largest $G = 1.79$ $P > .5$).

The distribution of alleles at the polymorphic loci are shown in Figs (6-7). The variant allele (170) at the Mdh 3-4 loci was observed only in the Petawawa and Little Madawaska drainage systems (Fig. 1) in the northern part of the study area. The variant allele (-170) at the MUP locus appears to have a more random distribution. A contingency chi-square for overall homogeneity at each of the polymorphic loci showed highly significant allele frequency differences among populations (Table 24) ($P < .001$).

The percentage of polymorphic loci varied from 0 to 5% with an average of 2.6%. The average heterozygosity ranged from 0 to 1.2% with a mean of .7%.

The distribution of gene diversity within and between populations, as estimated from all 38 loci, was analysed according to the methods of Nei (1973). The total amount of gene diversity ($H_t = 0.006$) was divided into two components; the amount of diversity within subpopulations ($H_s = 0.005$) and the amount of genetic diversity between populations ($D_{st} = 0.001$). The average gene diversity between populations ($G_{st} = D_{st}/H_t = 0.172$) accounted for approximately 17% of the total amount of gene diversity.

The genetic distances between populations as

estimated by Nei's (1972) standard distance (D) using only the variable loci are given in Table 25. A dendrogram showing the relationships between populations (Fig 8) was constructed from these data using a UPGMA cluster analysis. The branching pattern from this analysis like those obtained from the morphometric and meristic analyses shows no apparent correlation with geographic proximity or drainage pattern. There is also a lack of similarity between this dendrogram and those obtained from the morphometric and meristic analyses. These results demonstrate the lack of taxonomic congruence (Mikevich 1978) between the electrophoretic data, of known genetic basis, and the morphological and meristic data. The observed genetic differences between populations are probably due to the interaction of differential selection based on differences in environmental and ecological parameters and stochastic events such as random genetic drift or founder effect. The observed morphological and meristic differences may be the result of environmental influences or the result of an interaction of environmental differences between lakes and genetic differences between these populations.

SYNOPSIS OF RESULTS

1. Growth rates and age distributions varied between populations.
2. Body proportions did not allow discrimination between the sexes.
3. The differences in body proportions allowed for a high level of discrimination between lakes. Individuals were correctly identified with their lake of origin in greater than 90% of the sample. The discriminant functions were based mainly on differences in head shape and fin size.
4. There were significant differences among lakes for all meristic variables. The canonical variates based on meristic variables allowed 50% of the sample to be correctly identified to their lake of origin. The canonical variates were based mainly on differences in number of gill rakers, number of anal fin rays and number of branchiostegal rays.
5. The level of genetic variability as measured by protein electrophoresis was low with an overall average heterozygosity of only .7%. The average gene diversity between populations accounted for approximately 17% of the total gene diversity.
6. The dendrograms from the meristic and morphometric

analysis show similar branching patterns in contrast to the branching pattern of the dendrogram obtained from the electrophoretic analysis.

7. None of the three dendrograms shows a correlation with geographic or riverine proximity of the lakes.

DISCUSSION

MORPHOMETRIC INVESTIGATION

Body form in biological organisms is the end product of the interaction between a measure of absolute magnitude (i.e. a size component) and differences in proportion between body parts (i.e. a shape component) (Sprent 1972). Allometry is the study of the relationship between these two components (Gould 1966). The observed differences among lakes in the regression slopes of the log transformed linear measurements on log fork length demonstrate that there are differences in allometric growth between these populations. These differences in the developmental pattern of body form indicate significant biological differences between these populations but it is difficult to determine to what extent these differences are the result of genetic or environmental factors. Thorpe (1976) points out that these differences, as measured by the angle of the regression slopes, could be used as a taxonomic character to differentiate between the populations. If it were possible to estimate growth rates for individuals from these populations by measuring the size of annual increments of annular rings on scales or otoliths, then it should be possible on the basis of differences in growth rate to identify, with a fair degree of accuracy, the lake

of origin of an unknown specimen.

Martin (1949) characterizes the relative growth of any body part in fishes by a series of "relative growth stanzas" that are delimited by different life stages. One of the life stages that delimits a relative growth stanza is the attainment of sexual maturity. It is probable that the interaction of differences in growth rate and differences in age of maturity as demonstrated for these populations by Martin (1966) accounts to a large extent for these differences in developmental pattern.

The results of the canonical variate analysis of the size corrected variables demonstrate that after the size component has been removed or at least minimized, significant shape differences still remain between these populations. Although factors affecting morphological variation in fishes are poorly understood, body form is known to be influenced by growth rate, with slower growing populations generally having smaller heads, narrower maxilla and smaller fins than faster growing populations (Martin 1949, Barlow 1961).

Martin (1966) on the basis of extensive samples from these lakes, showed significant differences in growth rate between these populations. On the basis of these differences in growth rate, one would predict that the populations from Big Trout Lake and Lake la Muir would have larger heads, wider maxilla and larger fins than the

populations from Lake Louisa, Wilkins Lake and Happy Isle Lake. It appears from the results of the canonical variate analysis that this is in fact the case.

Separation on the first canonical variate is based to a large extent on head length, height of the maxilla and interorbital width. It appears that the observed morphological differences accounted for by the first canonical variate can be correlated with differences between populations in growth rate. Populations with high growth rates such as Big Trout and la Muir have longer, narrower heads and wider maxilla than populations with lower growth rates such as Wilkins Lake and Happy Isle Lake. This is reflected in their scores on the first canonical variate.

Although he did not analyse body shape, Martin (1966) by transplanting fish from Lake Louisa into Lake Opeongo and observing an increase in growth rate in the new environment demonstrated that the slow growth rate of Lake Louisa lake charr was not genetically fixed. It is likely that the observed differences in growth rate and the resulting differences in body form are to a large extent dependent on environmental and ecological differences between lakes. These observations do not eliminate the possibility of some genetic basis for the observed differences, but without breeding studies in controlled environments it is not possible to demonstrate this basis.

Lewontin (1984) on a theoretical basis, showed that it is more difficult, because of the polygenic nature of most quantitative characters, to demonstrate significant genetically based differences in metric variables compared with discrete variables.

One of the characteristics that is important in separating these populations on both the first and second canonical variates is the shape of the adipose fin. This character has not been previously used in attempts to differentiate between populations of lake charr and should be considered in any future investigations. It may be that the shape of this character could be used as an indicator of growth rate.

It appears that the dendrogram derived from the cluster analysis of the Mahalanobis distance matrix of the morphological data reflects similarities more in the ecological and environmental background of these populations than genetic differences.

MERISTIC INVESTIGATION

Meristic variables in fish are affected by developmental rates (Barlow 1961), slower development usually results in a higher number of serially repeating elements. These differences can be correlated with environmental factors such as temperature, oxygen levels and salinity that affect the rate of development. In contrast to morphological variables which can change, due to the indeterminate growth of fishes, throughout the life of an individual, it is felt that meristic variables are fixed at a very early stage in development. It has been shown for salmonids (Taning 1952) that the number of vertebrae and the number of fin rays are determined before hatching. This suggests that the observed meristic differences between these populations are the result of genetic differences or differences in the environmental conditions between their natal spawning shoals, rather than posthatching environmental or ecological influences.

In a meristic comparison of a wild strain of lake charr with a hatchery population of the same strain, Berst et al. (1980) demonstrated differential effects of environmental influences on different characters. They observed significant differences in the number of gill rakers, dorsal fin rays and anal fin rays but found little difference in the number of vertebrae between the two populations. They interpreted this to mean that the

number of vertebrae was more strongly influenced by genetic factors than were the other three characters. They suggest that the observed increase in counts was not due to an actual increase in the number of elements displayed by these characters but was the result of gill raker buds and very small fin rays that would not usually be counted increasing because of environmental influences to a size where they are included in the counts. This suggests that although the actual number of these serially repeating elements is fixed by the time of hatching, the effect of the environment on the posthatch development of these elements can affect the results of a meristic analysis.

Martin and Sandercock (1966) observed a positive correlation between the mean number of gill rakers and the % plankton in the diet of three populations of lake charr from the area of this study. This relationship also holds for these six study populations ($r=0.828$). It is possible that this correlation is the result of gill raker buds increasing to a size where they are counted due to the influence of differences in diet rather than an increase in the number of gill raker buds. Martin (1966) suggests that these differences in diet were due to ecological differences between lakes. He suggests that because of environmental differences between lakes bait fish were not available to the planktonivorous populations during the

summer months because of temperature restrictions due to the level of the thermocline.

The meristic variables giving the best separation between populations are number of gill rakers, number of left branchiostegal rays and number of anal fin rays. Berst et al. demonstrated that the number of gill rakers and number of anal fin rays can be environmentally influenced. This suggests that the results of both the morphological and meristic analysis probably are to a large extent dependent on environmental factors.

The mean number of gill rakers and the growth rate of these populations appear to be dependent on the amount of plankton in their diet during the summer months. It is likely that the observed pattern of differentiation of these populations on both meristic and morphometric analysis is based to a large extent on differences in diet. This explains the similarity between the dendrograms from the cluster analysis of the Mahalanobis distance matrices of the meristic and morphological analysis.

ELECTROPHORETIC INVESTIGATION

Over the last decade hundreds of studies have used electrophoretic techniques, coupled with histochemical staining of proteins, to analyse genetic variation in natural populations. Almost all of our understanding of the amount and distribution of genetic variability in natural populations, is based on information obtained from these techniques.

Average heterozygosity (i.e. the average proportion of heterozygotes per locus) is the measure most commonly used to compare the amount of genetic variation between populations and species. The overall average heterozygosity from studies of 77 species of fishes (Avice and Aquadro 1982) was 5.4%. Allendorf and Utter (1979) in studies of 9 species of salmonids, where at least 30 loci were analysed, found an overall average heterozygosity of 3.1%. From these results, it appears that salmonids contain less of genetic variation than other groups of fishes, but it should be recognized that this type of comparison, based on a relatively small number of loci, may not be biologically meaningful.

Lewontin (1974) pointed out that these estimates are very dependent on the number and range of isozyme loci that are examined and warned against placing much reliability in estimates based on fewer than approximately 100 loci. Only electrophoretic studies of allozyme

variation in man have approached this number of loci.

It is possible that this large a sample of loci may still not give an unbiased estimate of genetic variation. The use of electrophoretic data to compare the amount of genetic variation between species is dependent on the assumption that the protein loci that are analysed are a random sample of the total genome and that the amount of variation that is observed in this sample is representative of the variation in the total genome. Recent studies have demonstrated that this assumption is not valid (Mitten and Grant 1984). Ward (1977,1978) demonstrated that the level of allozyme variation is dependent on the quaternary structure and subunit size of the proteins studied. McConkey et al. (1979) showed that there were differences in the amount of observed genetic variation between different classes of proteins (i.e. structural, metabolic and regulatory).

It should also be pointed out that estimates of genetic variation obtained from electrophoretic data are minimum estimates. It is generally assumed that only about one-third of the changes in shape and charge of protein molecules, due to amino acid substitutions, are detectable by electrophoretic techniques (Lewontin 1974). Recent studies (Aquadro and Avise 1982, Coyne 1976, Coyne et al. 1979) using different electrophoretic conditions (i.e. varying pH, ion type, gel concentration) have

demonstrated an increase in the amount of detectable variation between groups. It is not known to what extent this type of "cryptic variation" is present in fishes.

Differences between studies, both in the number and kinds of proteins examined, and possible differences between species in the distribution of allozyme variation over different classes of proteins, make it very difficult, on the basis of electrophoretic data, to draw meaningful conclusions concerning differences between species in amounts of genetic variability. The way electrophoretically detectable variation is distributed between populations however, still reflects the population structure of the species under consideration. In general, comparisons between studies of different populations of the same species give more meaningful results than comparisons between different species. This is because loci that are highly polymorphic in one population of a species are usually polymorphic in most of the other populations of that same species. The inclusion of additional loci in a study will tend to have a similar effect on all the populations studied (Allendorf and Utter 1979).

Electrophoretic techniques have been used to analyse the amount and distribution of allozyme variation in a number of species of the genus Salvelinus. McGlade and MacCrimmon (1979) in a study of three populations of brook

charr (S. fontinalis) from northeastern Quebec found, in an analysis of 22 loci, an overall average heterozygosity of 8.5% with a range between populations of 8.5% to 9%. In a study of eight populations of brook charr from the eastern United States, Stoneking et al. (1981) found, in an analysis of 39 loci, an overall average heterozygosity of 8.1% with a range between populations of 2.8% to 11.4%. The differences between these two studies in the amount and distribution of observed genetic variation probably reflect differences in the number of loci analysed and the wider geographic area that was sampled in the latter study.

The amount of allozyme variation in the arctic charr (S. alpinus) has been analysed from a number of geographic locations. Kornfield et al. (1981) in an analysis of six geographically isolated populations from North America, found an overall average heterozygosity of 3% with a range in average heterozygosity between populations of 0.5% to 6.9%. Andersson et al. (1983) in a study of ten populations of arctic charr from Sweden based on 37 loci found an overall average heterozygosity of 2.7% with a range between populations of 0% to 5.4%. It is interesting to note the similar levels of variability in these populations from widely separated geographic areas.

Dehring et al. (1981) observed an overall average heterozygosity of 1.5% with a range of 1.4% to 1.6% in

their analysis of three "morphotypes" of lake charr from eastern Lake Superior. The overall average heterozygosity for the six populations of lake charr sampled in this study was 0.7%. The range of average heterozygosity between populations was from 0% to 1.2%. The differences in overall average heterozygosity between these two studies are probably accounted for by the highly polymorphic AAT-1,2 loci. These loci were not included in this study because of inconsistent results from frozen samples but they were analysed by Dehring et.al. (1981). Preliminary studies of my samples showed that these two loci were the most polymorphic of all the loci studied, with average heterozygosities approaching 50% in at least two populations. The inclusion of these two loci in this study would have resulted in observed average heterozygosities equal to or larger than those found by Dehring et al. (1981). This demonstrates the effect that the addition of a highly variable protein system can have on observed levels of heterozygosity. This effect is particularly evident when levels of variability are low.

Although the results of these studies suggest that the lake charr have the lowest amount of genetic variation, as measured by allozyme differences, it is not clear whether this observation is the result of real differences or is due to problems, as previously discussed, in using electrophoretic data to compare the

amount of genetic variation between species. Further studies of populations from a wider geographic area and based on a much larger sample of loci would give a better estimate of allozyme variation in this species.

The way genetic variation is distributed within and between populations on both a micro- and a macro-geographic scale allows us to estimate the amount of differentiation between populations. This measure of differentiation has important implications for the conservation and efficient management of genetic resources. Gene diversity analysis (Nei 1973, 1975) is one of the methods used to quantify the pattern of distribution of genetic variation within and between populations of a species. These methods decompose the total observed genetic diversity (H_t) into two components, the average gene diversity within populations (H_s) and the amount of gene diversity due to differences between populations (D_{st}). The relative importance of these components is expressed as a ratio (G_{st}) between the component and the total gene diversity.

In brown trout (Salmo trutta), 13.4% of the total gene diversity is distributed between populations (Ryman 1983), while in the rainbow trout (Salmo gairdneri) only 8% (Allendorf and Phelps 1981) of the total gene diversity was due to differences between populations. Andersson et al. (1983) found that, in Sweden, 24% of the genetic

diversity in arctic charr was due to differences between subpopulations. These differences between species in the distribution of genetic variation probably reflect differences in the degree and duration of isolation between populations.

Few of these studies were restricted to as small a geographic area as this study. The observation that 17% of the total gene diversity of these six lake charr populations is accounted for by differences between populations indicates a high degree of population differentiation. It is unlikely that this amount of differentiation would develop in this small a geographic area without a complete lack of gene flow between populations over a relatively long period of time. This suggests that these populations have indeed been isolated since shortly after they were founded 8,000 to 10,000 years ago.

The pattern of divergence as illustrated by the dendrogram obtained from the cluster analysis of Nei's genetic distance does not appear to reflect the geographic separation of these populations. It is more likely that this dendrogram reflects changes in the genetic structure of these populations due to selection or stochastic processes such as founder effect or random genetic drift. Mitten and Grant (1984) review the evidence for a correlation between individual heterozygosity at allozyme

loci and differences in growth rate and developmental stability. They argue that this evidence suggests that the degree of heterozygosity as measured by electrophoretic techniques can be correlated with individual fitness. This implies that electrophoretically detectable variation is biologically important and would be influenced by selective forces. Other authors (for a review see Kimura 1983) argue that this type of variation is selectively neutral and controlled only by stochastic influences. Regardless of whether or not the observed electrophoretic differences between these populations are biologically important, they demonstrate that these populations are genetically distinct.

While it is recognized that many of the differences between these populations observed in the morphological and meristic analyses are probably the result of environmental influences, the high degree of population differentiation as demonstrated by allozyme variation, makes it likely that at least some of the observed morphological and meristic differences are the result of genetic differentiation. The planting of hatchery reared lake charr into lakes in Ontario has been so extensive that few lakes in the populated areas of the province have not been stocked (staff MNR personal communication). These study populations are some of the few in the southern part of the province that we know have not been

stocked and, as a result, contain only indigenous lake charr gene pools. On the basis of the results of this analysis and the fact that these lakes contain only indigenous lake charr genes, it is recommended that until we have a better understanding of the basis of the morphological and meristic variation in these populations, they be treated as unique genetic strains or "stocks" and all activity such as the stocking of hatchery reared lake charr, that might affect the genetic structure of these populations be avoided.

McLean et al. (1981) demonstrated that the survival success of planted lake charr is to some extent dependent on the environmental similarity of the lake of origin of the planted lake charr strain and the lake into which the fish are stocked. The populations of these study lakes could be considered as sources of strains of lake charr for the rehabilitation of environmentally similar lakes where the native populations of lake charr have been lost. One of the main factors to be considered when choosing an appropriate strain would be whether the indigenous population had been piscivorous or planktonivorous. In cases where the biological characteristics of the original population are not known, or where the environmental conditions are very broad, it might be better to maximize the amount of genetic variation by developing a hatchery strain from stocks of diverse genetic origins. These

populations could be used as a source of genetic variability to aid in developing these hatchery stocks. These populations could also be used as a source of electrophoretic variants to be used as genetic markers to genetically "tag" hatchery strains (Moave et al. 1976). These genetically tagged strains could be used to measure the reproductive success of planted lake charr of different genetic origins. Although there are data available on the survival of planted lake charr, there is little information available on the reproductive success of these fish.

CONCLUSIONS

1. I found significant morphological differences as estimated by linear measurements, between the six study populations. Differences in head shape and fin sizes were evident.
2. Significant differences in meristic characters as estimated by the counts of 9 serially repeating anatomical structures were found between the six study populations.
3. Standardizing the linear measurements by dividing by fork length gave results that were insignificantly different from those obtained using more sophisticated allometric correction methods.
4. Low levels of electrophoretically detectable genetic variation were found. Whether this is an accurate estimate of the total genetic variation in these populations is not known but the electrophoretic results did demonstrated significant differences in allozyme frequencies between populations.
5. The morphological and meristic variation appear, to a large extent, to be the result of environmental influences, but the possibility that the observed differences might be, at least in part, the result of genetic differences could not be eliminated.

6. Until the amount of biological differentiation between these populations is clarified by further research, these populations should be considered as genetically distinct subunits or "stocks" and managed from that perspective.

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Table 1. Location and codes of the six study lakes.

Lake	Code No.	Code	Location		Watershed
			Lat.	Long.	
Merchant Lake	1	Merch	45 46	78 32	Petawawa
Happy Isle Lake	2	Hisle	45 45	78 30	Opeongo
Lake Louisa	3	Louisa	45 28	78 30	Madawaska
Big Trout Lake	4	Btrout	45 46	78 30	Petawawa
Wilkins Lake	5	Wilkins	45 41	78 37	Bonnechere
Lake la Muir	6	laMuir	45 50	77 55	Little Madawaska

Table 2. List of morphological measurements and mnemonics.

Mnemonic	Character
ADFH	Height of adipose fin at its insertion
ADFL	Distance from the insertion of the adipose fin to fork length
AFIH	Height of the anal fin at its insertion
AFLG	Length of the base of the anal fin
AFOH	Length of the anal fin at its origin
AFSL	Distance from the insertion of the anal fin to standard length
AXSH	Height of axillary scale
AXSL	Length of axillary scale
BWDF	Width of body at the origin of the dorsal fin
CDPF	Height of caudal peduncle
DFAD	Distance from the insertion of the dorsal fin to the origin of the adipose fin
DFIF	Height of dorsal fin at its insertion
DFLG	Length of the base of the dorsal fin
DFOH	Height of dorsal fin at its origin
DFSL	Distance from the insertion of the dorsal fin to standard length
INOW	Interorbital width
FKLG	Fork length
LADF	Length of adipose fin
LJPF	Distance from the anterior tip of lower jaw to the insertion of the pectorial fin
LGR	Length of longest gill raker
LJVF	Distance from the anterior tip of lower jaw to the origin of the pelvic fin
LJWL	Length of lower jaw

Table 2. Cont.

MAXH	Height of maxilla
MAXL	Length of maxilla
OPOV	Distance from the origin of the pectoral fin to the origin of the pelvic fin
OPFL	Distance from the anterior upper end of the opercle to the fork of the tail
OVOA	Distance from the origin of the pelvic fin to the origin of the anal fin
PCFH	Height of the pectoral fin at its origin
PMXL	Length of premaxilla
PFBD	Height of body at the origin of the pectoral fin
PMXO	Distance from the anterior end of the premaxilla to the end of the opercle
PMXY	Distance from the anterior end of the premaxilla to the anterior margin of the orbit of the eye
SNDE	Distance from the anterior end of the premaxilla to the origin of the dorsal fin
SNLL	Distance from the anterior end of the snout to the finish of scales on the lateral line
STLG	Standard length
TTLG	Total length
UJWL	Length of upper jaw
VFOH	Height of the pelvic fin at its origin
YDIA	Diameter of the eye
YOPR	Distance from the posterior margin of the orbit of the eye to the end of opercle
YPRO	Distance from the posterior margin of the orbit to the upper edge of the pre-opercle

Table 3. List of meristic counts and mnemonics.

NAFR	Number of anal fin rays
NDFR	Number of dorsal fin rays
NGR	Number of gill rakers
NLBR	Number of left branchiostegal rays
NMP	Number of mandibular pores
NPCFR	Number of pectorial fin rays
NPVFR	Number of pelvic fin rays
NRBR	Number of right branchiostegal rays
NVERT	Number of vertebrae

Table 4. Summary of samples showing mean fork length (mm), mean fresh weight (g), mean age (yr) and the sex ratio of the samples.

Lake	N	Fork length			Fresh weight			Age		Sex Ratio
		Mean	SD	Range	Mean	SD	Mean	SD	Range	
Merchant Lake	24	392.3	80.8	132-512	772.1	404.6	6.8	2.39	2-11	1.13:1
Happy Isle Lake	25	350.0	78.1	236-589	538.7	546.0	5.5	1.54	4-10	0.87:1
Lake Louisa	54	347.5	66.8	167-481	531.0	302.2	6.2	2.33	2-12	0.74:1
Big Trout Lake	30	506.8	104.0	261-646	1613.0	762.0	10.0	3.32	5-15	1.03:1
Wilkins Lake	64	312.5	57.6	132-465	372.7	183.0	5.3	1.31	2-9	1.32:1
Lake la Muir	31	470.8	132.4	184-770	1536.5	1435.4	10.9	4.60	4-23	1.48:1
Total	228	380.4	108.9	132-770	793.0	815.5	6.9	6.88	2-23	0.85:1

Table 5. Regression coefficients (b) from the analysis of covariance of log transformed measurements against log fork length showing differences among lakes. (**, Significant at 1% level; *, Significant at 5% level; NS, nonsignificant at the 5% level). a=not significantly different from 1.

Variable	Merch	Hisle	Louisa	Btrout	Wilk	laMuir	Pooled Within-lake
1 YDIA	0.59	0.65	0.61	0.76	0.68	0.73	*
2 INOW	1.33	0.87	1.22	1.44	1.22	1.22	**
3 PMXY	1.28	1.51	1.20	1.45	1.23	1.24	**
4 YPRO	1.31	1.22	1.21	1.25	1.22	1.25	NS
5 YOPR	1.12	1.06	1.07	1.14	1.06	1.02	NS
6 MAXH	1.05	0.88	0.84	1.04	0.93	1.03	NS
7 PMXL	1.06	1.64	1.24	1.33	1.27	1.28	**
8 MAXL	1.03	1.15	1.03	1.22	1.09	1.09	*
9 UJWL	1.17	1.22	1.11	1.26	1.17	1.19	NS
10 LJWL	1.11	1.19	1.06	1.22	1.08	1.14	**
11 DFIH	0.99	0.91	0.65	1.04	0.81	1.05	**
12 DFLG	0.97	1.01	0.98	1.00	0.99	1.02	NS
13 DFOH	1.01	0.88	0.84	0.96	0.88	0.92	*
14 ADFH	0.85	0.55	0.55	0.70	0.78	0.94	**
15 LADF	0.81	0.53	0.66	0.93	0.57	0.88	NS
16 AFIH	1.02	0.95	0.86	1.07	1.04	1.06	NS
17 AFLG	1.02	0.96	0.98	1.10	1.00	1.14	NS
18 AFOH	1.06	0.97	1.00	1.09	0.89	1.07	*
19 VFOH	1.01	1.02	1.06	1.08	0.94	1.08	*
20 PCFH	1.15	1.00	1.07	1.16	0.99	1.11	**
21 OPOV	1.00	0.99	1.06	1.07	1.00	1.03	NS
22 OVOA	1.02	1.01	1.00	0.97	1.03	0.99	NS
23 DFAD	0.97	0.85	1.01	0.94	0.99	0.87	**
24 AXSL	0.95	1.01	0.88	1.00	0.82	1.23	NS

Table 5. Cont.

Variable	Merch	Hisle	Louisa	Brout	Wilk	laMuir	Pooled Within-lake
25 AXSH	1.21	0.84	0.90	0.94	0.90	1.10	NS 1.00 a
26 CDPH	0.98	0.90	1.01	0.94	0.92	0.99	NS 0.96 a
27 AFSL	0.93	0.81	0.97	0.92	1.02	0.96	NS 0.94
28 ADFL	1.01	0.99	0.94	0.98	0.95	0.98	NS 0.97
29 DFSL	0.94	0.90	1.00	0.95	1.00	0.92	NS 0.95
30 LJPF	1.03	1.13	0.99	1.09	0.99	1.01	** 1.03
31 PMXO	1.02	1.10	0.98	1.15	1.01	1.04	** 1.04
32 SNDF	1.02	1.09	1.04	1.04	1.04	1.06	NS 1.05
33 LJVF	1.01	1.02	1.03	1.07	1.00	1.03	NS 1.03 a
34 TTLG	0.99	0.98	0.98	0.98	1.00	0.99	NS 0.99
35 STLG	1.02	1.01	1.02	1.00	1.01	0.99	** 1.01
36 SNLL	1.01	1.00	1.01	0.99	1.00	0.99	NS 1.00 a
37 OPFL	0.99	0.99	1.00	0.98	1.02	0.97	NS 0.99 a
38 PFBD	1.02	1.12	1.15	1.15	0.99	1.22	** 1.12
39 BWDF	1.41	1.24	1.41	1.10	1.12	1.63	** 1.36
40 LGR	0.94	0.69	0.84	0.60	0.88	0.79	* 0.80

Table 6. Univariate summary statistics of size adjusted morphological variables.

Merchants Lake							
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value	
1 YDIA	24	19.3	1.35	0.070	17.5	22.5	
2 INOW	24	20.2	1.79	0.089	17.5	24.7	
3 PMXY	24	20.2	1.62	0.080	18.3	23.5	
4 YPRO	24	24.1	1.71	0.071	21.5	27.2	
5 YOPR	24	44.0	1.84	0.042	40.9	47.4	
6 MAXH	24	6.4	0.86	0.134	3.9	8.1	
7 PMXL	24	10.5	1.50	0.143	7.9	15.9	
8 MAXL	24	37.7	3.07	0.082	33.6	45.5	
9 UJWL	24	46.2	3.35	0.073	41.4	53.4	
10 LJWL	24	56.2	3.45	0.061	51.3	63.8	
11 DFIH	23	18.6	1.89	0.102	14.9	22.5	
12 DFLG	24	36.7	1.97	0.054	32.4	40.4	
13 DFOH	24	57.3	3.48	0.061	52.3	66.9	
14 ADFH	23	12.1	1.65	0.136	8.9	15.6	
15 LADF	23	6.6	0.86	0.129	5.2	8.3	
16 AFIH	24	14.5	1.59	0.109	12.1	18.9	
17 AFLG	24	29.2	1.89	0.065	25.5	32.6	
18 AFOH	24	53.7	1.98	0.037	50.9	58.5	
19 VFOH	24	50.0	2.53	0.051	45.5	55.3	
20 PCFH	24	61.8	2.60	0.042	57.7	67.5	
21 OPOV	24	120.8	5.72	0.047	110.0	130.6	
22 OVOA	24	72.8	4.00	0.055	62.7	80.5	
23 DFAD	23	83.4	4.98	0.060	72.6	92.2	
24 AXSL	24	5.0	1.13	0.225	2.9	8.1	
25 AXSH	24	10.8	1.95	0.180	7.8	15.0	
26 CDPH	24	27.1	0.99	0.037	25.2	29.3	
27 AFSL	24	54.1	2.70	0.050	48.6	58.8	
28 ADFL	23	81.4	3.32	0.041	74.3	89.2	
29 DFSL	24	139.3	4.32	0.031	131.7	149.3	
30 LJPF	24	80.3	3.84	0.048	73.8	89.4	
31 PMXO	24	87.7	3.75	0.043	82.1	95.5	
32 SNDF	24	178.7	3.29	0.018	171.6	184.0	
33 LJVF	24	199.8	4.57	0.023	192.5	207.6	
34 TTLG	24	413.0	4.03	0.010	405.6	419.3	
35 STLG	24	348.2	2.64	0.008	343.2	352.5	
36 SNLL	24	358.6	3.12	0.009	349.9	362.8	
37 OPFL	24	314.1	7.26	0.023	284.9	322.6	
38 PFBD	24	63.5	3.14	0.049	59.1	72.7	
39 BWDF	24	43.0	3.56	0.083	34.4	49.8	
40 LGR	24	7.4	0.75	0.101	5.8	8.6	

Table 6. Cont.

Happy Isle Lake							
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value	
1 YDIA	25	19.5	0.99	0.051	17.8	21.6	
2 INOW	25	26.7	2.54	0.095	21.7	31.5	
3 PMXY	25	19.8	1.46	0.074	15.6	22.8	
4 YPRO	25	23.5	1.18	0.050	21.3	26.0	
5 YOPR	25	43.5	3.42	0.078	30.5	49.8	
6 MAXH	25	6.2	0.74	0.120	4.5	7.5	
7 PMXL	25	10.1	1.48	0.146	6.3	12.5	
8 MAXL	25	37.5	1.92	0.051	34.3	42.7	
9 UJWL	25	46.3	2.34	0.050	42.9	52.4	
10 LJWL	25	56.7	2.09	0.037	52.9	63.6	
11 DFIH	25	17.7	1.86	0.105	13.8	21.2	
12 DFLG	25	38.1	2.23	0.058	34.0	44.2	
13 DFOH	25	58.1	2.37	0.041	51.3	61.5	
14 ADFH	25	11.0	1.43	0.129	8.3	13.8	
15 LADF	25	7.0	1.18	0.170	4.6	9.8	
16 AFIH	25	14.8	1.48	0.100	12.0	18.2	
17 AFLG	25	30.2	1.77	0.059	27.5	33.8	
18 AFOH	25	52.8	1.81	0.034	49.2	56.9	
19 VFOH	25	50.2	2.43	0.048	44.3	54.9	
20 PCFH	25	60.5	3.40	0.056	47.7	65.3	
21 OPOV	25	119.8	4.04	0.034	112.1	128.0	
22 OVOA	25	72.8	2.61	0.036	67.4	77.1	
23 DFAD	25	82.1	3.95	0.048	75.1	89.4	
24 AXSL	25	3.9	1.06	0.274	2.1	5.9	
25 AXSH	25	9.2	1.60	0.174	6.4	12.0	
26 CDPH	25	26.1	1.42	0.055	23.5	30.3	
27 AFSL	25	56.6	3.41	0.060	48.2	62.2	
28 ADFL	25	81.4	2.54	0.031	74.7	85.4	
29 DFSL	25	140.7	4.09	0.029	129.7	148.0	
30 LJPF	25	83.5	3.46	0.041	78.3	94.8	
31 PMXO	25	88.7	2.71	0.031	83.5	97.5	
32 SNDF	25	177.1	3.45	0.020	169.9	184.4	
33 LJVF	25	198.9	6.31	0.032	177.8	209.2	
34 TTLG	25	414.1	4.28	0.010	405.3	423.7	
35 STLG	25	348.8	3.38	0.010	343.4	356.7	
36 SNLL	25	358.5	3.88	0.011	353.1	367.5	
37 OPFL	25	314.0	4.02	0.013	304.6	322.2	
38 PFBD	25	59.3	2.86	0.048	53.4	65.7	
39 BWDF	25	42.3	5.69	0.134	26.3	57.2	
40 LGR	25	7.7	0.75	0.097	6.6	9.3	

Table 6. Cont.

Lake Louisa

	Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1	YDIA	54	18.9	0.97	0.051	16.5	20.9
2	INOW	54	18.6	1.71	0.092	14.3	22.2
3	PMXY	54	20.7	1.43	0.069	18.0	25.5
4	YPRO	54	24.0	1.50	0.062	21.1	28.0
5	YOPR	54	42.9	1.65	0.039	38.3	46.1
6	MAXH	54	6.3	0.70	0.111	4.2	7.8
7	PMXL	54	10.2	0.95	0.093	7.7	12.2
8	MAXL	54	38.2	2.16	0.056	30.9	42.9
9	UJWL	54	42.2	1.94	0.041	39.6	52.2
10	LJWL	54	56.5	2.10	0.037	52.2	63.4
11	DFIH	53	16.2	2.06	0.127	8.7	22.9
12	DFLG	54	36.0	1.78	0.049	32.2	38.9
13	DFOH	54	55.5	3.00	0.054	46.5	63.2
14	ADFH	51	10.7	1.64	0.153	7.1	14.6
15	LADF	52	6.0	0.99	0.164	3.8	7.7
16	AFIH	54	14.2	1.64	0.116	11.4	18.1
17	AFLG	54	28.8	1.76	0.061	24.6	33.3
18	AFOH	52	49.5	2.76	0.056	38.9	54.0
19	VFOH	54	45.8	3.10	0.068	29.5	51.5
20	PCFH	54	58.5	3.29	0.056	46.5	66.1
21	OPOV	54	120.1	3.98	0.033	108.9	127.8
22	OVOA	54	75.4	4.82	0.064	66.2	87.2
23	DFAD	53	84.4	3.37	0.040	75.2	94.5
24	AXSL	54	4.8	1.09	0.229	3.1	8.1
25	AXSH	54	9.2	1.76	0.192	5.4	13.6
26	CDPH	54	25.7	1.32	0.051	23.1	29.2
27	AFSL	54	53.4	2.94	0.055	47.8	60.6
28	ADFL	52	81.6	2.79	0.034	74.1	87.0
29	DFSL	54	140.2	3.81	0.027	128.2	146.4
30	LJPF	54	81.1	2.73	0.034	76.1	89.8
31	PMXO	54	87.6	2.46	0.028	82.8	95.1
32	SNDF	54	178.1	3.93	0.022	167.9	196.2
33	LJVF	54	198.3	3.94	0.020	188.8	207.9
34	TTLG	54	409.2	6.60	0.016	394.3	425.9
35	STLG	54	350.7	2.54	0.007	339.4	355.2
36	SNLL	54	358.6	2.49	0.007	347.4	362.7
37	OPFL	54	317.4	2.78	0.009	312.4	325.3
38	PFBD	54	57.9	4.28	0.074	51.4	72.5
39	BWDF	54	41.8	3.42	0.082	35.0	50.4
40	LGR	54	7.8	0.60	0.077	6.1	8.9

Table 6. Cont.

Big Trout Lake

	Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1	YDIA	30	19.6	1.36	0.069	17.2	22.7
2	INOW	30	20.3	2.30	0.113	12.3	23.2
3	PMXY	30	22.6	1.46	0.065	19.3	25.2
4	YPRO	30	24.3	1.73	0.071	20.2	27.4
5	YOPR	30	47.1	2.53	0.054	42.4	53.8
6	MAXH	30	6.2	0.70	0.114	4.5	8.2
7	PMXL	30	11.3	1.14	0.101	8.2	13.6
8	MAXL	30	39.6	2.29	0.057	34.6	43.4
9	UJWL	30	49.2	2.85	0.058	43.5	54.0
10	LJWL	30	61.0	2.63	0.043	56.4	65.1
11	DFIH	30	18.9	1.84	0.097	14.7	22.3
12	DFLG	30	37.9	2.69	0.070	32.9	46.7
13	DFOH	30	56.7	3.30	0.058	48.5	62.7
14	ADFH	29	11.8	1.50	0.126	8.4	14.8
15	LADF	29	5.5	1.26	0.227	3.7	8.4
16	AFIH	30	14.1	1.25	0.088	11.6	17.1
17	AFLG	30	29.4	1.75	0.060	25.9	32.4
18	AFOH	30	50.6	2.78	0.055	43.9	56.0
19	VFOH	30	45.1	2.65	0.059	40.3	52.0
20	PCFH	30	57.1	3.15	0.055	51.8	64.2
21	OPOV	30	118.1	5.40	0.045	107.1	127.9
22	OVOA	30	73.5	3.41	0.046	65.6	81.8
23	DFAD	29	80.7	3.81	0.047	69.3	88.0
24	AXSL	30	13.8	1.02	0.268	1.8	6.4
25	AXSH	30	8.6	2.32	0.268	5.0	13.3
26	CRPH	30	26.1	1.40	0.054	22.2	28.3
27	AFSL	30	53.1	3.58	0.067	45.2	61.1
28	ADFL	29	81.6	3.29	0.040	73.1	88.0
29	DFSL	30	137.2	5.06	0.037	125.3	150.7
30	LJPF	30	87.5	3.21	0.037	81.9	94.2
31	PMXO	30	93.5	4.06	0.043	84.0	100.5
32	SNDF	30	174.6	3.87	0.022	166.8	180.9
33	LJVF	30	201.9	9.82	0.049	188.1	211.2
34	TTLG	30	407.9	4.51	0.011	400.8	422.4
35	STLG	30	347.2	3.17	0.009	339.8	351.0
36	SNLL	30	356.2	3.87	0.011	344.3	361.8
37	OPFL	30	311.1	4.60	0.015	303.8	319.3
38	PFBD	30	64.3	4.09	0.064	57.9	75.5
39	BWDF	30	37.6	3.95	0.105	31.2	49.3
40	LGR	30	6.5	0.80	0.123	4.9	8.2

Table 6. Cont.

Wilkins Lake						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 YDIA	64	18.9	0.91	0.048	16.4	21.3
2 INOW	64	22.7	1.23	0.054	20.4	26.3
3 PMXY	64	20.5	1.45	0.071	18.1	24.4
4 YPRO	64	22.2	1.35	0.061	19.5	25.7
5 YOPR	64	41.3	1.44	0.035	36.6	43.7
6 MAXH	64	5.1	0.62	0.123	3.3	6.5
7 PMXL	64	10.2	1.52	0.149	7.5	17.1
8 MAXL	64	34.9	1.64	0.047	31.2	39.1
9 UJWL	64	43.3	1.92	0.044	39.8	50.6
10 LJWL	64	54.4	1.90	0.035	50.0	59.2
11 DFIH	64	20.4	1.50	0.073	17.2	24.1
12 DFLG	64	37.2	2.15	0.058	30.8	41.3
13 DFOH	64	60.0	2.19	0.037	53.3	64.2
14 ADFH	63	12.0	1.23	0.103	9.5	14.2
15 LADF	64	5.8	0.82	0.141	4.1	8.2
16 AFIH	64	14.6	1.30	0.089	11.4	18.1
17 AFLG	64	27.4	2.04	0.074	21.8	33.2
18 AFOH	64	49.4	3.76	0.076	26.8	54.4
19 VFOH	64	48.1	2.17	0.045	42.4	53.4
20 PCFH	63	59.2	2.43	0.041	54.2	65.8
21 OPOV	63	118.6	5.54	0.047	106.1	130.3
22 OVOA	64	79.7	14.40	0.181	67.6	188.3
23 DFAD	64	85.1	4.33	0.051	75.8	97.3
24 AXSL	62	4.2	0.77	0.098	2.7	6.1
25 AXSH	62	10.8	1.72	0.158	7.4	14.3
26 CDPH	64	26.4	1.09	0.041	23.7	28.8
27 AFSL	64	54.6	2.85	0.052	48.3	63.8
28 ADPL	63	80.8	2.78	0.034	72.0	89.3
29 DFSL	64	138.7	7.41	0.053	90.0	152.5
30 LJPF	63	78.6	3.05	0.039	68.2	85.3
31 PMXO	64	84.3	2.19	0.026	79.4	88.6
32 SNDF	64	173.3	3.44	0.020	167.1	181.9
33 LJVF	64	194.3	5.68	0.029	178.4	204.8
34 TTLG	64	408.0	4.30	0.011	397.1	418.9
35 STLG	64	349.1	2.10	0.006	343.5	353.0
36 SNLL	64	359.8	2.24	0.006	350.6	363.9
37 OPFL	64	316.6	6.01	0.019	278.0	324.4
38 PFBD	64	61.4	4.56	0.074	53.8	89.3
39 BNDF	64	47.9	4.27	0.089	38.2	61.5
40 LGR	64	7.7	0.74	0.097	5.9	9.1

Table 6. Cont.

Lake la Muir

	Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1	YDIA	31	19.4	0.98	0.051	16.8	21.5
2	INOW	31	20.3	1.16	0.057	18.6	22.5
3	PMXY	31	21.7	1.60	0.074	18.8	26.4
4	YPRO	31	23.0	1.31	0.057	21.2	25.9
5	YOPR	31	45.3	2.21	0.049	41.7	51.7
6	MAXH	31	6.3	0.58	0.092	4.8	7.8
7	PMXL	31	11.7	1.09	0.094	9.7	14.0
8	MAXL	31	39.4	1.64	0.042	36.6	43.6
9	UJWL	31	48.9	1.98	0.041	45.6	53.4
10	LJWL	31	57.8	2.34	0.040	54.2	64.1
11	DFIH	29	19.1	2.33	0.122	14.5	24.1
12	DFLG	31	38.0	1.78	0.047	34.2	40.3
13	DFOH	31	55.9	2.86	0.051	49.7	61.3
14	ADFH	30	14.7	1.56	0.106	11.5	17.7
15	LADF	31	4.3	0.54	0.125	2.9	5.6
16	AFIH	31	14.3	1.13	0.079	12.0	16.2
17	AFLG	31	29.4	2.31	0.078	25.0	35.8
18	AFOH	31	50.1	2.49	0.049	43.7	54.3
19	VFOH	31	45.2	2.04	0.045	42.0	51.9
20	PCFH	31	55.7	2.54	0.045	50.5	60.1
21	OPOV	31	115.9	8.02	0.069	93.2	130.8
22	OVOA	31	71.1	3.37	0.047	64.5	77.7
23	DFAD	31	81.3	4.05	0.050	73.9	87.8
24	AXSL	31	3.2	0.73	0.131	1.8	4.8
25	AXSH	31	8.4	1.58	0.188	5.6	12.3
26	CDPH	31	25.6	1.16	0.045	23.4	28.2
27	AFSL	31	52.7	2.41	0.046	47.2	57.3
28	ADFL	31	83.1	2.51	0.030	78.9	88.4
29	DFSL	31	134.1	3.97	0.030	125.5	139.1
30	LJPF	31	82.5	3.48	0.042	75.1	88.9
31	PMXO	31	91.4	2.38	0.026	85.4	95.6
32	SNDF	31	175.5	4.10	0.023	166.8	181.1
33	LJVF	31	195.9	7.40	0.038	174.5	213.6
34	TTLG	31	407.7	4.31	0.011	396.7	417.1
35	STLG	31	346.7	3.49	0.010	339.9	359.1
36	SNLL	31	359.3	3.15	0.009	355.6	372.4
37	OPFL	31	321.8	23.50	0.037	307.8	387.5
38	PFBD	31	60.7	3.83	0.063	54.3	68.5
39	BWDF	31	39.7	6.05	0.152	13.7	49.5
40	LGR	31	6.5	0.60	0.092	5.1	8.3

Table 7. Univariate summary statistics of the size adjusted morphological variables of all lakes combined. F-values from ANOVA showing differences among lakes. (**, Significant at 1% level; *, Significant at 5% level; NS, Nonsignificant at 5% level).

	Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value	F-value
1	YDIA	228	19.2	1.08	0.056	16.4	22.7	3.50 *
2	INOW	228	21.3	2.98	0.140	12.3	31.5	85.58/ **
3	PMXY	228	20.9	1.70	0.085	15.6	26.4	16.01 **
4	YPRO	228	23.3	1.67	0.072	19.5	28.0	13.30 **
5	YOPR	228	43.5	2.81	0.065	30.5	53.8	36.39 **
6	MAXH	228	5.9	0.89	0.147	3.3	8.2	26.21 **
7	PMXL	228	10.6	1.40	0.093	6.3	17.1	11.55 **
8	MAXL	228	37.5	2.70	0.072	30.9	45.6	31.69 **
9	UJWL	228	46.4	3.16	0.068	39.6	54.0	43.41 **
10	LJWL	228	56.7	3.08	0.054	50.0	65.1	34.40 **
11	DFIH	224	18.6	2.44	0.131	8.7	24.1	27.10 **
12	DFLG	228	37.2	2.21	0.059	30.8	46.7	5.09 **
13	DFOH	228	57.4	3.28	0.057	48.5	66.9	15.01 **
14	ADFH	221	11.9	1.90	0.160	7.1	17.7	29.38 **
15	LADF	224	5.8	1.19	0.205	2.9	9.8	25.89 **
16	AFIH	228	14.4	1.42	0.098	11.4	18.9	1.79 NS
17	AFLG	228	28.8	2.13	0.074	21.8	35.8	10.73 **
18	AFOH	226	50.5	3.25	0.064	26.8	58.5	12.45 **
19	VFOH	228	47.2	3.15	0.067	29.5	55.3	29.31 **
20	PCFH	227	58.7	3.35	0.057	46.5	67.5	16.23 **
21	OPOV	227	118.9	5.62	0.047	93.2	130.8	3.01 *
22	OVOA	228	75.2	8.84	0.117	62.7	188.3	15.72 **
23	DFAD	225	83.3	4.33	0.052	69.3	97.3	7.41 **
24	AXSL	226	4.2	1.10	0.263	1.8	8.1	12.93 **

Table 7. Cont.

	Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value	F-value
25	AXSH	226	9.6	2.05	0.213	5.0	15.0	11.75 **
26	CDPH	228	26.1	1.29	0.049	22.2	30.3	4.57 **
27	AFSL	228	54.0	3.14	0.058	45.2	63.8	5.69 **
28	ADFL	223	81.5	2.90	0.036	72.0	89.3	2.58 *
29	DFSL	228	138.5	5.64	0.040	90.0	152.5	5.43 **
30	LJPF	227	81.6	4.22	0.052	68.2	94.8	34.50 **
31	PMXO	228	88.1	4.17	0.047	79.4	100.5	54.99 **
32	SNDF	228	175.9	4.21	0.024	166.8	186.2	13.87 **
33	LJVF	228	197.1	7.5	0.038	129.5	213.6	3.15 **
34	TTLG	228	409.4	5.37	0.013	394.3	425.9	9.35 **
35	STLG	228	348.8	3.07	0.009	339.4	359.1	9.93 **
36	SNLL	228	358.7	3.13	0.009	344.3	372.4	6.61 **
37	OPFL	228	316.2	10.20	0.032	278.1	387.5	3.92 **
38	PFBD	228	60.8	4.56	0.075	51.4	89.3	10.86 **
39	BWDF	228	42.9	5.64	0.134	13.7	61.5	27.77 **
40	LGR	228	7.4	0.87	.118	4.9	9.3	23.36 **

Table 8. F-matrix from canonical variate analysis of size
adjusted morphological measurements.
(P 0.01,1.88; P 0.05,1.57)

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	13.72				
Louisa	8.29	29.82			
Btrout	16.76	29.43	17.37		
Wilkins	17.41	23.15	41.81	37.77	
laMuir	23.55	39.60	30.63	14.63	48.35

Table 9. Classification matrix from canonical variate analysis of size adjusted morphological measurements.

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir	Percent Correct
Merch	20	0	1	1	0	0	90.9
Hisle	0	24	0	1	0	0	96.0
Louisa	3	0	45	0	0	0	93.8
Btrout	0	0	0	28	0	1	96.6
Wilkins	0	0	0	0	60	0	100.0
laMuir	0	0	0	1	0	27	96.4

Jackknifed classification

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir	Percent Correct
Merch	19	0	2	1	0	0	86.4
Hisle	0	22	0	1	1	1	88.0
Louisa	6	0	40	2	0	0	83.3
Btrout	0	0	2	26	0	1	89.7
Wilkins	0	0	0	0	60	0	100.0
laMuir	0	0	0	1	0	27	96.4

Table 10. The amount of overlap between populations in per cent based on the jackknifed classification of morphometrics.

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	0				
Louisa	11.6	0			
Btrout	1.8	1.9	5.3		
Wilkins	0	1.2	0	0	
laMuir	0	2.0	0	3.3	0

Table 11. Mahalanobis distance matrix for morphometric variables.

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	4.52				
Louisa	2.82	14.41			
Btrout	11.91	25.20	8.98		
Wilkins	14.02	4.70	28.43	29.12	
laMuir	30.92	45.48	27.90	5.22	41.71

Table 12. Coefficients of the classification function based on the measurements expressed as a ratio of fork length and then scaled by overall mean fork length.

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir
INOW	-6.98	-4.52	-7.59	-7.12	-5.77	-6.94
PMXY	-6.76	-7.84	-6.33	-6.33	-5.18	-5.73
YOPR	6.26	5.92	5.66	6.37	5.63	6.50
MAXH	57.42	55.91	56.82	55.86	53.91	57.20
UJWL	4.58	4.10	4.82	3.98	3.72	5.40
LJWL	7.28	7.20	7.26	7.94	7.03	6.27
DFIH	-1.52	-1.76	-2.05	-1.76	-0.65	-1.61
DFOH	-0.88	-0.65	-0.64	-0.75	0.18	-0.79
ADFH	-1.59	-2.06	-1.55	-0.82	-1.55	0.93
LADF	24.53	25.44	24.61	24.24	24.07	22.21
AFOH	-2.49	-2.89	-2.93	-2.82	-3.48	-2.94
VFOH	-0.89	-0.81	-1.71	-2.31	-0.99	-2.07
AXSL	1.52	1.01	2.10	0.78	1.12	-0.37
LJPF	1.77	2.30	1.81	2.10	1.73	1.42
PMXO	8.71	9.06	9.20	9.56	8.42	9.93
TLTG	10.83	10.89	10.65	10.72	10.50	10.56
STLG	20.80	20.91	21.62	21.12	21.14	20.27
SNLL	29.58	29.31	29.12	29.19	29.32	30.22
PFBD	5.29	4.94	5.01	5.28	5.08	4.87
LGR	26.65	26.57	28.04	25.22	27.15	25.47
Constant	-12321.08	-12313.53	-12330.61	-12275.59	-12143.63	-12253.61

Table 13. Coefficients of the classification functions based on the 5 linear measurements expressed as a ratio of fork length and then scaled by overall mean fork length that gave the best separation among groups.

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir
INOW	-0.32	1.25	-0.87	-0.30	0.49	-0.09
DFIH.	-1.24	-1.35	-1.74	-1.45	-0.29	-1.64
ADPH	6.58	6.64	6.42	6.83	6.48	8.06
VFOH	4.04	3.87	3.20	2.46	3.67	2.48
PMXO	9.56	9.30	10.00	10.93	8.83	10.72
Constant	-546.91	-550.97	-524.49	-595.88	-501.33	-593.86

Table 14. Univariate summary statistics for meristic variables.

Merchants Lake						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	24	12.6	0.50	0.040	12	13
2 NRBR	23	12.1	0.52	0.043	11	13
3 NGR	24	21.8	1.31	0.060	20	24
4 NAFR	24	14.3	0.53	0.037	13	15
5 NDFR	24	14.3	0.48	0.034	14	15
6 NPVFR	24	10.6	0.50	0.047	10	11
7 NPCFR	24	14.0	0.55	0.039	13	15
8 NMP	22	18.5	1.54	0.083	16	21
9 NVERT	24	61.3	1.82	0.030	55	63
Happy Isle Lake						
Variable	N	Mean	Standard Deviation	Coefficient	Smallest	Largest
1 NLBR	25	12.5	0.65	0.052	11	14
2 NRBR	25	12.2	0.65	0.053	11	13
3 NGR	25	22.1	1.75	0.079	18	25
4 NAFR	25	14.3	0.79	0.055	13	16
5 NDFR	25	14.9	0.60	0.040	14	16
6 NPVFR	25	10.2	0.58	0.057	9	12
7 NPCFR	25	14.4	0.50	0.035	14	15
8 NMP	25	19.9	1.55	0.078	17	22
9 NVERT	25	62.0	1.24	0.020	59	64

Table 14. Cont.

Lake Louisa						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	54	12.4	0.69	0.056	11	14
2 NRBR	54	12.2	0.59	0.048	11	13
3 NGR	54	23.1	1.24	0.053	20	27
4 NAFR	54	13.9	0.71	0.051	12	15
5 NDFR	54	14.2	0.60	0.042	13	15
6 NPVFR	54	10.2	0.38	0.037	10	11
7 NPCFR	54	13.7	0.60	0.044	11	15
8 NMP	54	18.0	1.11	0.061	16	20
9 NVERT	53	61.6	1.33	0.022	57	63
Big Trout Lake						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	30	12.6	0.63	0.050	11	14
2 NRBR	30	12.3	0.64	0.052	11	13
3 NGR	30	21.2	1.30	0.061	19	24
4 NAFR	30	14.1	0.69	0.049	13	15
5 NDFR	30	14.5	0.57	0.039	14	16
6 NPVFR	30	10.5	0.68	0.065	9	12
7 NPCFR	30	14.3	0.80	0.056	12	16
8 NMP	30	19.5	1.55	0.080	16	24
9 NVERT	30	62.3	0.92	0.015	60	64

Table 14. Cont.

Wilkins Lake						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	64	12.4	0.64	0.051	11	14
2 NRBR	64	12.0	0.68	0.056	11	13
3 NGR	64	22.3	1.10	0.049	18	25
4 NAFR	64	13.5	0.78	0.057	12	15
5 NDFR	64	14.6	0.53	0.036	14	16
6 NPVFR	64	10.1	0.43	0.043	9	11
7 NPCFR	63	14.1	0.64	0.046	13	15
8 NMP	63	19.3	1.44	0.075	16	22
9 NVERT	63	61.3	0.91	0.015	58	63

Lake la Muir						
Variable	N	Mean	Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	31	13.3	0.68	0.051	12	14
2 NRBR	31	12.6	0.61	0.048	12	14
3 NGR	31	19.7	1.70	0.086	16	24
4 NAFR	31	14.2	0.62	0.043	13	15
5 NDFR	31	14.4	0.72	0.050	13	16
6 NPVFR	31	10.0	0.18	0.018	9	10
7 NPCFR	31	14.1	0.63	0.045	13	15
8 NMP	31	19.8	1.43	0.072	17	23
9 NVERT	31	61.5	0.93	0.015	60	63

Table 14. Cont.

Variable	N	Mean	Overall			
			Standard Deviation	Coefficient of Variation	Smallest Value	Largest Value
1 NLBR	239	12.6	0.70	0.056	11	14
2 NRBR	238	12.2	0.66	0.054	11	14
3 NGR	239	21.9	1.68	0.077	16	27
4 NAJR	239	14.0	0.78	0.055	12	16
5 WDPR	239	14.5	0.61	0.042	13	16
6 NPVFR	239	10.2	0.49	0.048	9	12
7 NPCFR	238	14.1	0.67	0.047	11	16
8 NMP	236	19.1	1.56	0.082	16	24
9 NVERT	237	61.6	1.22	0.020	55	64

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Table 15. ANOVA of group means for meristic variables.

Analysis of variance of NLBR				
Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	17.72	3.54	8.55
Error	222	92.02	.41	
Analysis of variance of NRBR				
Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	8.76	1.75	4.50
Error	221	85.92	.39	
Analysis of variance of NGR				
Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	259.85	51.97	28.46
Error	222	405.28	1.83	

Table 15. Cont.

Analysis of variance of NAFR

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	18.87	3.77	7.51
Error	222	111.59	.50	

Analysis of variance of NDFR

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	8.82	1.76	5.16
Error	222	75.96	.34	

Analysis of variance of NPVFR

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	8.30	1.66	7.79
Error	222	47.29	.21	

Table 15. Cont.

Analysis of variance of NPCFR

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	12.40	2.48	6.20
Error	221	88.47	.40	

Analysis of variance of NMP

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	107.93	21.59	10.94
Error	219	432.06	1.97	

Analysis of variance of NVERT

Source of variance	Df	Sum of squares	Mean square	F-value
Equality of cell means	5	29.51	5.90	4.22
Error	220	307.52	1.39	

Table 16. Results of Scheffe multiple range test,
 * denotes pairs of lakes significantly different
 at the 5% level.

Number of left branchiostegal rays

		W	L	H	B	M	l
		i	o	i	t	e	a
		l	u	s	r	r	M
		k	i	l	o	c	u
		i	s	e	u	h	i
		n	a	t			r
		s					
Mean	Lake						
12.4	Wilkins						
12.4	Louisa						
12.5	Hisle						
12.6	Btrout						
12.6	Merch						
13.3	laMuir	*	*	*	*	*	*

Number of right branchiostegal rays

		W	M	L	H	B	l
		i	e	o	i	t	a
		l	r	u	s	r	M
		k	c	i	l	o	u
		i	h	s	e	u	i
		n	a		t		r
		s					
Mean	Lake						
12.0	Wilkins						
12.1	Merch						
12.2	Louisa						
12.2	Hisle						
12.3	Btrout						
12.6	laMuir	*					

Table 16 Cont.

Number of gill rakers

		l	B	M	H	W	L
		a	t	e	i	i	O
		M	r	r	s	l	u
		u	o	c	l	k	i
		i	u	h	e	i	s
		r	t			n	a
						s	
Mean	Lake						
19.7	laMuir						
21.2	Btrout	*					
21.8	Merch	*					
22.1	Hisle	*					
22.3	Wilkins	*	*				
23.1	Louisa	*	*	*			

Number of anal fin rays

		W	L	B	l	M	H
		i	o	t	a	e	i
		l	u	r	M	r	s
		k	i	o	u	c	l
		i	s	u	i	h	e
		n	a	t	r		
		s					
Mean	Lake						
13.5	Wilkins						
13.9	Louisa						
14.1	Btrout	*					
14.2	laMuir	*					
14.3	Merch	*					
14.3	Hisle	*					

Table 16 Cont.

Number of dorsal fin rays

	L	M	l	B	W	H
	o	e	a	t	i	i
	u	r	M	r	l	s
	i	c	u	o	k	l
	s	h	i	u	i	e
	a		r	t	n	s

Mean	Lake	
14.2	Louisa	
14.3	Merch	
14.4	laMuir	
14.5	Btrout	
14.6	Wilkins	
14.9	Hisle	*

Number of ventral fin rays

	l	W	L	H	B	M
	a	i	o	i	t	e
	M	l	u	s	r	r
	u	k	i	l	o	c
	i	i	s	e	u	h
	r	n	a		t	
	s					

Mean	Lake			
10.0	laMuir			
10.1	Wilkins			
10.2	Louisa			
10.2	Hisle			
10.5	Btrout	*		
10.6	Merch	*	*	*

Table 16 Cont.

Number of pectoral fin rays

		L	M	l	W	B	H
		o	e	a	i	t	i
		u	r	M	l	r	s
		i	c	u	k	o	l
		s	h	i	i	u	e
		a		r	n	t	
					s		
Mean	Lake						
13.7	Louisa						
14.0	Merch						
14.1	laMuir						
14.1	Wilkins	*					
14.3	Btrout	*					
14.4	Hisle	*					

Number of mandibular pores

		L	M	W	B	l	H
		o	e	i	t	a	i
		u	r	l	r	M	s
		i	c	k	o	u	l
		s	h	i	u	i	e
		a		n	t	r	
				s			
Mean	Lake						
18.0	Louisa						
18.5	Merch						
19.3	Wilkins	*					
19.5	Btrout	*					
19.8	laMuir	*					
20.0	Hisle	*	*				

Table 16 Cont.

95

Number of vertebrae

		M	W	l	L	H	B
		e	i	a	O	i	t
		r	l	M	u	s	r
		c	k	u	i	l	o
		h	i	i	s	e	u
			n	r	a		t
			s				
Mean	Lake						
61.3	Merch						
61.3	Wilkins						
61.5	laMuir						
61.6	Louisa						
62.0	Hisle						
62.3	Btrout		*				

Table 17. Summary of Scheffe multiple range test showing the number of pairwise comparisons between populations that were significant at the 5% level.

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	1				
Louisa	2	3			
Btrout	0	0	2		
Wilkins	2	1	2	4	
laMuir	3	2	3	3	4

Table 18. F-matrix from canonical variate analysis of meristic variables.
(P. 0.01, 2.66; P. 0.05, 2.02).

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	5.85				
Louisa	5.10	9.34			
Btrout	3.63	2.81	11.56		
Wilkins	8.38	4.31	9.93	8.07	
laMuir	11.20	12.49	26.34	8.71	21.66

Table 19. Classification matrix from canonical variate analysis of meristic variables.

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir	Percent Correct
Merch	11	1	3	4	2	1	50.0
Hisle	1	14	1	2	5	2	56.0
Louisa	8	7	32	1	4	1	60.4
Btrout	3	6	2	13	3	3	43.3
Wilkins	4	10	8	1	36	2	59.0
laMuir	0	1	1	1	1	27	87.1

Jackknifed classification

	Merch	Hisle	Louisa	Btrout	Wilkins	laMuir	Percent Correct
Merch	9	1	4	5	2	1	40.9
Hisle	1	11	1	3	7	2	44.0
Louisa	8	7	31	1	5	1	58.5
Btrout	4	8	2	8	4	4	26.7
Wilkins	5	11	10	1	32	2	52.5
laMuir	0	1	1	2	1	26	83.9

Table 20. The amount of overlap between populations in percent based on the jackknifed classification of meristics.

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	4.3				
Louisa	16.0	10.3			
Btrout	17.3	20.0	3.6		
Wilkins	8.4	23.7	14.4	5.5	
laMuir	1.9	5.4	2.4	9.8	3.3

Table 21. Mahalanobis distance matrix for meristic variables.

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	2.83				
Louisa	1.20	3.59			
Btrout	1.49	0.76	3.75		
Wilkins	3.14	0.34	2.64	1.79	
laMuir	5.23	5.73	10.99	2.60	8.50

Table 22. Tissues, enzyme and buffer systems used in the electrophoretic analysis. See methods for buffer and tissue designations.

Enzyme System	Locus	Tissue	Buffer
Alcohol dehydrogenase	ADH	L	R (TC)
Aspartate aminotransferase	AAT-(1,2) AAT-3 AAT-4	H(M) E L	R R R
Creatine kinase	CPK-(1,2) CPK-3	M E	R R
Glucose phosphate isomerase	GPI-(1,2) GPI-3	M M	R R
Glycerol-3-phosphate dehydrogenase	G-3-PDH-(1,2) G-3-PDH-3	M M	TC CT
Isocitrate dehydrogenase	IDH-(1,2) IDH-(3,4)	M L	CT CT
Lactate dehydrogenase	LDH-(1,2) LDH-3 LDH-4 LDH-5	M M L E	R R R R
Malate dehydrogenase	MDH-(1,2) MDH-(3,4)	E M	R R
Malic enzyme	ME -(1,2) ME-(3,4)	M M	CT CT
Mannosephosphate isomerase	MPI	E	MF
4-Methylumbelliferyl phosatate	MUP	L	CT
Phosphoglucomutase	PGM-1 PGM-2 PGM-(3,4)	L M L	CT R CT
Phosphogluconate dehydrogenase	6-PDGH	L	CT
Sorbitol dehydrogenase	SDH	L	R
Superoxide dismutase	SOD	L	R

Table 23. Distribution of genotypes and gene frequencies for polymorphic loci.

		MUP					
Population	N	-100/-100	-100/-170	-170/-170	p(-100)	p(-100)	
Merch	24	24	0	0	1.00	1.00	
Hisle	25	11	10	4	0.64	0.64	
Louisa	17	8	8	1	0.71	0.71	
Btrout	31	31	0	0	1.00	1.00	
Wilkins	64	64	0	0	1.00	1.00	
laMuir	30	20	9	1	0.82	0.82	

		MDH					
Population	N	100/100	100/100	100/100	100/170	170/170	p(100)
Merch	16	14	2	0	0	0	0.97
Hisle	25	25	0	0	0	0	1.00
Louisa	54	54	0	0	0	0	1.00
Btrout	21	13	7	1	0	0	0.89
Wilkins	64	64	0	0	0	0	1.00
laMuir	31	23	8	0	0	0	0.94

Table 24. Frequency of most common allele and the contingency chi-square for overall homogeneity. The average heterozygosity (H) and the percent polymorphism (%P).

Population	MUP	MDH(3,4)	H	%P
Merch	1.00	0.97	0.0016	2.6%
Hisle	0.64	1.00	0.0121	2.6%
Louisa	0.71	1.00	0.0108	2.6%
Brout	1.00	0.89	0.0052	2.6%
Wilkins	1.00	1.00	0.0000	0%
laMuir	0.82	0.94	0.0107	5.3%
Chi-square	105.23	55.82	df=5 P<.001	

Table 25. Standard genetic distances (Nei 1973).

	Merch	Hisle	Louisa	Btrout	Wilkins
Hisle	0.0477				
Louisa	0.0304	0.0019			
Btrout	0.0034	0.0615	0.0426		
Wilkins	0.0004	0.0445	0.0278	0.0062	
laMuir	0.0100	0.0158	0.0074	0.0145	0.0100

Figure 1. Map of the Algonquin Park region showing the location of the study lakes and the drainage pattern of the area.

1. Merchant Lake
2. Happy Isle Lake
3. Lake Louisa
4. Big Trout Lake
5. Wilkins Lake
6. Lake la Muir

Figure 2. Plot of the first and second canonical variates obtained from the analysis of the size corrected linear measurements. The centroids of the populations are plotted and the limits of the populations are outlined.

1. Merchant Lake
2. Happy Isle Lake
3. Lake Louisa
4. Big Trout Lake
5. Wilkins Lake
6. Lake la Muir

Figure 3. Dendrogram produced by UPGMA cluster analysis of the Mahalanobis generalized distances obtained from the canonical variate analysis of the size adjusted linear measurements.

Figure 4. Plot of the first and second canonical variates obtained from the analysis of the meristic variables. The population centroids are plotted and the limits of the populations are outlined.

1. Merchant Lake
2. Happy Isle Lake
3. Lake Louisa
4. Big Trout Lake
5. Wilkins Lake
6. Lake la Muir

Figure 5. Dendrogram produced by UPGMA cluster analysis of the Mahalanobis generalized distances obtained from the canonical variate analysis of the meristic variables.

Figure 6. Map showing the distribution of malate dehydrogenase (Mdh 3-4) allelic frequencies.

MDH

100

170

Figure 7. Map showing the distribution of
4-methylumbelliferyl phosphate (Mup) allelic frequencies.

Figure 8. Dendrogram produced by UPGMA cluster analysis of Nei's genetic distance obtained from the electrophoretic analysis.

END

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