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SPATIAL GENETIC STRUCTURE WITHIN FOUR TAMARACK (*Larix laricina* (Du Roi) K. Koch) POPULATIONS IN NORTHWESTERN ONTARIO

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A Graduate Thesis
submitted in partial fulfillment of the requirements
for the degree of Masters of Science in Forestry

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A CAUTION TO THE READER

This M.Sc.F. thesis has been through a formal process of review and comment by several members of the faculty of the School of Forestry, Lakehead University, as well as an external examiner.

It is made available for loan by the faculty for the purpose of advancing the practice of professional and scientific forestry.

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MAJOR ADVISOR'S COMMENTS

ABSTRACT

Foster, H.A. 1989. Spatial genetic structure within four tamarack (Larix laricina (Du Roi) K. Koch) populations in northwestern Ontario. 153pp. Advisor: Dr. P. Knowles

Key Words: isozymes, Larix laricina (Du Roi) K. Koch, Moran's I, population structure, spatial genetic structure, spatial autocorrelation, tamarack.

This study was conducted to test the null hypothesis that tamarack (Larix laricina (Du Roi) K. Koch) populations are random assemblages of genotypes, and that this absence of pattern can be observed on sites with differing ecological and demographic characteristics. A total of 1715 trees in four populations with distinct ecological and demographic characteristics were surveyed and sampled for isozyme analysis. These trees were mapped for later plotting and spatial autocorrelation analysis. Seven variable and three monomorphic allozyme loci were resolved. Visual examination of the distribution of single alleles over space revealed pattern in 22.2 percent of the 36 plots. Spatial autocorrelation analysis resulted in calculation of 313 Moran's I autocorrelation coefficients, 8.9 percent of which were significant (95 percent confidence level). In addition, results of tests of the correlograms constructed from these 313 coefficients revealed that 38.9 percent of the correlograms were significant using Bonferroni's criterion (90 percent confidence level). These results suggested that the null hypothesis be rejected for a modest, but still important proportion of the tests. The spatial pattern that was observed, both by eye and through statistical tests, was manifested mainly as a tendency for similar genotypes to occur in trees that were near to each other.

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H.F.

INTRODUCTION

Tamarack (Larix laricina (Du Roi) K. Koch) is a widely distributed boreal conifer exhibiting excellent growth under low competition and high light on well drained sites. Unfortunately, the level of understanding of the genetics of this species is rudimentary. However, since tamarack has potential for use in alleviating periodic wood supply shortages, interest in deployment of this species in tree improvement programs is rising.

As genetic improvement programs are developed for tree species, the need for information on their population genetics becomes apparent. The various aspects of a species' ecology that influence gene flow and recruitment are of particular interest because of their potential roles in the development of population genetic structure. In addition to being a fundamental aspect of a species' genecology, population genetic structure may be important in the development of successful management and breeding programs (Sluder, 1969; Guries and Ledig, 1977; Yeh, 1979; Hamrick, 1982; Park and Fowler, 1982). The population structure of native tree populations should be considered in the design of a number of components of tree breeding programs, including seed collection and production strategies (Linhart et al., 1981), plus tree selection methods (Ledig, 1973; Guries and Ledig, 1977), evaluation and testing methods (Coles and Fowler, 1976; Linhart et al., 1981; Cheliak et al., 1985), and genetic conservation strategies (Sakai and Park, 1971).

This study was designed to examine the null hypotheses:

1. tamarack populations in the vicinity of Thunder Bay are random assemblages of genotypes, and,
2. this randomness can be observed in populations of different ages and on different sites.

The objectives of this study were:

1. to use electrophoretic techniques to infer the genotypes of a large, contiguous group of tamarack within a population,
2. to map these population members,
3. to test for the presence of any within - population spatial genetic pattern, and finally,
4. to observe possible relationships between the ecological and demographic characteristics of populations, and spatial genetic pattern, by repeating the above procedures on four sites with different ecological and demographic characteristics.

LITERATURE REVIEW

SILVICS AND ECOLOGY OF TAMARACK

The range of tamarack extends along the treeline from Newfoundland to the Yukon, and south to northeastern British Columbia and northern Maine (Fowells, 1965). It pioneers under many conditions, but most often is encountered on wet sites (Henry et al., 1973; Morgenstern et al., 1984). Tamarack has high tolerance for soil moisture, needing a wet but not flooded seedbed for seedling establishment (Henry et al., 1973; Mead, 1978; Morgenstern et al., 1984). This species also is very tolerant of the cold growing conditions prevalent on these sites (Morgenstern et al., 1984).

Tamarack is the most intolerant conifer, requiring full overhead light for successful establishment (Henry et al., 1973; Park and Fowler, 1983). On uplands or lowlands, given sufficient light, it outgrows most other boreal tree species (Fowells, 1965; Logan, 1966; Henry et al., 1973; Mead, 1978; Reimenschneider and Neinstaedt, 1983; Hall, 1986).

Reproduction in the southern part of tamarack's range is primarily sexual, but layering occurs occasionally, particularly in the forest-tundra ecotone (Duncan, 1954; Henry et al., 1973; Elliott, 1979;). Tamarack also produces sprouts from its spreading root system. These sprouts can occur up to 10 meters from the tree's base (Henry et al., 1973).

Tamarack flowers at an early age (seven to ten years) (Fowells, 1965). However, it is notorious for its irregular cone crops, low seed production, poor seed quality and rapid seed dispersal (Duncan, 1954; Fowells, 1965; Morgenstern et al., 1984; Fowler, 1986). The small seed generally is dispersed over distances of less than two tree heights (Duncan, 1954). Cone and seed insects often damage substantial portions of the crop (Duncan, 1964; Fowler, 1986).

Occasional widespread epidemics of larch sawfly (Pristiphora erichsonii Hartig) cause severe reductions in growth and mortality in tamarack (Fowells, 1965). More recently, concern has arisen for tamarack's vulnerability to attacks of European larch canker (Lachnellula willkommi Hartig). This disease, which is a serious pest in Europe, has been reported in eastern Canada and the United States (Magasi and Pond, 1982; Ostaff and Newell, 1986).

In addition to exhibiting very high growth rates, tamarack is suitable for use as pulp and lumber (Einspahr et al., 1984; Hall, 1986; Yang and Hazenberg, 1987). Therefore, it is a species with potential for ameliorating wood supply problems that have been predicted for eastern Canada and the United States (Morgenstern et al., 1984; Carter and Simpson, 1985; Hall, 1986; OMNR, 1987). This has led to interest in the use of tamarack in relatively large regeneration and breeding programs (Carter and Simpson, 1985; Fowler, 1986). Recent studies have investigated the practicality of using vegetative propagation for stock production. Tamarack appears to root easily from soft or slightly lignified cuttings (Carter, 1984; Morgenstern et al., 1984; Farmer et al., 1986).

GENETICS OF TAMARACK

Literature on the genetics of tamarack is limited (Park and Fowler, 1982; Morgenstern et al., 1984). Investigations of patterns of genetic variation indicate that levels of intrapopulation variation are relatively high (Rehfeldt, 1970; Jeffers, 1975; Park and Fowler, 1982), as is the case for many other conifers (e.g. Neinstaedt and Teich, 1972; Morgenstern, 1978; Rudolph and Yeatman, 1981).

Interpopulation variation in tamarack has not been the subject of much study. Rauter and Graham (1983) suggested that genetic variation across the species' wide geographic range may be clinal. Knowles and Perry's (1986) examination of allozyme variation in populations across northwestern Ontario found little interpopulation variation. Rehfeldt (1970), Cech _et_ _al_. (1977), and Reimenschneider and Jeffers (1983) observed clinal variation in provenance trials of tamarack in the northeastern United States.

Franklin (1970) found that species of the genus _Larix_ exhibited more deleterious effects of inbreeding than did most species in the family Pinaceae. Rehfeldt (1970), and Park and Fowler (1982) observed inferior performance in selfed progeny of tamarack. Knowles _et_ _al_. (1987) found that natural populations of tamarack in northern Ontario have lower outcrossing rates than those reported for other conifers. While significant heterozygote deficiencies occurred in most embryo populations, these deficiencies were observed in few adult populations.

Park and Fowler (1982) found very high variances for specific combining ability of seedling height. In another improvement-oriented study, Morgenstern _et_ _al_. (1984) observed significant clonal differences in rootability of tamarack.

Cheliak and Pitel (1985) investigated the inheritance and linkage of allozymes in tamarack. Their examination of variation in 12 enzyme systems showed that the segregation ratios generally agreed with those expected under single gene Mendelian control.

Western larch (_Larix_ _occidentalis_ Nutt.) is one of the two other north American members of the genus _Larix_.

Fins and Seeb (1986) found that most of the variation in allozymes of this species occurred within, rather than among, populations. Also, Rehfeldt (1982) and Joyce (1985) found low levels of interpopulation variation in patterns of growth, phenology and cold hardiness.

The genetics of alpine larch (Larix lyalli Parl.) has received very little study. This western timberline species shows limited differentiation among populations, with less phenotypic variation (e.g. in needle and cone traits) than western larch (Bakowsky, 1989).

GENE FLOW AND SPATIAL GENETIC STRUCTURE

The results of work in the last two decades suggest that some species of seed plants are composed of fairly isolated and heterogeneous breeding units (Bradshaw, 1972; Levin and Kerster, 1974; Schaal, 1974; Allard, 1975; Linhart et al., 1981). This spatial genetic structure appears to develop as a result of a number of factors, including restrictions on gene flow, the action of selection (e.g. microhabitat adaptation) and chance effects (e.g. availability of new colonization opportunities) (Levin and Kerster, 1974; Hamrick, 1982; Loveless and Hamrick, 1984).

Gene flow includes all the mechanisms that result in the movement of genes among populations (Slatkin, 1985). The extent of this flow depends on a number of aspects of a species' ecology, including breeding system, mating system, population size, population density, population spatial structure, phenology, and characteristics of pollen and seed production and dispersal (Levin and Kerster, 1974; Hamrick, 1982; Loveless and Hamrick, 1984). Some studies suggest that the majority of pollen and seed are dispersed relatively short distances (Bradshaw, 1972; Tigerstedt, 1973; Levin and Kerster, 1974). However, recent studies based on electrophoretic analysis suggest that gene flow in some species may be quite extensive (Friedman and Adams, 1985; Neale and Adams, 1985).

Selective forces acting on pollen and seed, and on other life cycle stages, may modify the effects that gene flow ultimately has on the spatial genetic structure of populations. Results of some studies of microhabitat adaptations (e.g. Antonovics _et al_., 1971; Turkington and Harper, 1979) and of changes in genetic composition of populations over time (e.g. Schaal and Levin, 1976; Linhart _et al_., 1981; Tigerstedt _et al_., 1982) suggest that the action of selection (and the ecology of reproduction and establishment) may itself contribute to the development of spatial genetic structure.

Spatial genetic structure may develop due to limited gene flow, localized selection or patchy colonization. These factors may restrict the genetic diversity of the neighborhood, thereby facilitating consanguineous mating and further development of spatial genetic structure (Guries and Ledig, 1981; Hamrick, 1982; Huenneke, 1985).

SPATIAL GENETIC STRUCTURE IN POPULATIONS

Herb and Shrub Species

Recently, investigations of spatial population genetic structure have been reported for a number of herb and shrub species. Many of these studies used electrophoretic techniques. While the evolutionary significance of allozyme variation is of some debate (Lewontin, 1974; Clark, 1975; Koehn, 1978; Merrell, 1981), electrophoresis does provide genetic markers that can be used to study variation patterns in plant populations (Yeh, 1979; Hamrick, 1982).

Schaal (1975) reported on an investigation of spatial population genetic structure in Liatris cylindracea Michx., an entomophilous perennial herb. This investigation used electrophoretic techniques to sample a population that was growing on an identifiable environmental gradient. Schaal examined variation in allele frequencies for 27 loci resolved from samples taken from quadrats distributed along a series of transects. She examined the relationship between genetic and environmental variation, and found a significant correlation between gene frequencies and edaphic factors in two of fifteen loci. Analysis of population stucture using gene frequencies and Wright's _F_-statistics (Nei, 1977) suggested that the population was genetically substructured. Inbreeding presumably was occurring, although this was inconsistent with the fact that the species is an obligate outcrosser.

Huenneke (1985) reported on spatial genetic structure in _Alnus rugosa_ (Du Roi) Spreng., a clonal shrub. The distribution of alleles at one electrophoretically resolved locus was mapped across four different populations. Nearest-neighbor analysis (Pielou, 1977) and examination of the genotype maps revealed no departure from randomness in their distribution.

Epperson and Clegg (1986) found spatial genetic structure within populations of _Ipomoea purpurea_ following completion of spatial autocorrelation analysis (Cliff and Ord, 1973) using colour polymorphism data. Waser (1987) investigated spatial population genetic structure in _Delphinium nelsonii_ Greene, again using spatial autocorrelation analysis. This study used allelic frequencies for five polymorphic allozyme loci. No overall structure was found in this population. Further details regarding these studies are reported in the spatial autocorrelation analysis summary, later in this paper.

Tree Species

Investigations of spatial genetic structure in tree populations have taken a variety of approaches, but most have used allozyme variation in conjunction with mapping of sample trees or population subdivisions.

A number of investigations of spatial genetic structure in tree populations have failed to find evidence of this structure. Tigerstedt (1973) found no evidence of family structure when he mapped the distribution of allozymes in two Picea abies (L.) Karst stands in Finland.

Similarly, Guries and Ledig (1977) mapped allozyme patterns for 15 loci in four populations of Pinus rigida Mill. Their examination of variation patterns within the populations, which ranged in size from 61 to 152 trees, revealed no significant clustering of genotypes. However, differences were found between populations.

Roberds and Conkle (1984) studied population genetic structure in Pinus taeda L. populations. They examined allele frequencies at eight polymorphic loci in two related old field stands. Examination of variation between and within stands through analysis using *F*-statistics and allele frequencies revealed no spatial genetic structure.

Spatial autocorrelation analyses of Psychotria nervosa (Dewey and Heywood, 1988) and Pinus contorta ssp. latifolia (Epperson and Allard, 1989) also revealed no evidence of spatial genetic structure. These studies are reported in further detail in the following section on spatial autocorrelation analysis.

Conversely, several other studies have found evidence suggesting the existence of spatial genetic structure in forest stands. Linhart *et al*. (1981) investigated genetic structure in *Pinus ponderosa* Laws. populations, again mapping results of electrophoretic analyses. Three subpopulations, containing up to 200 trees each, were sampled. Differences in gene frequencies were found between nearby clusters of trees and between different age-classes.

Tigerstedt *et al*. (1982) reported on the results of electrophoretic analysis of a *Pinus sylvestris* L. stand in which parent and regeneration clusters were identified. Examinations of Wright's *F*-statistics and comparisons with Hardy-Weinberg expectations led the authors to suggest that seeds tend to disperse and land in cohorts, though not necessarily under their maternal parent. Gene frequency differences were found between different generations and different regeneration clusters.

Knowles (1984) noted the non-random distribution of some alleles at four loci mapped in an electrophoretic study of genetic variability between and within closely spaced *Pinus contorta* Dougl. populations. The results of the analyses, which included calculation of *F*-statistics, measures of genetic variability and tests of allelic heterogeneity, suggested that there was genetic heterogeneity among and within the populations.

Shea (1985) examined population structure in *Picea engelmanni* (Parry) Engelm. and *Abies lasiocarpa* (Hook.) Nutt. Trees were sampled for electrophoresis from along transects, and then populations were divided into equally - sized subdivisions. The analyses included testing for allelic heterogeneity, and evaluating Nei's genetic distances and Wright's *F*-statistics. The results of this study suggested that there was significant spatial genetic variation in both species at the microhabitat level.

Sproule (1988) reported on the results of work examining spatial population genetic structure in *Picea mariana* (Mill.) B.S.P. His analyses were based on ten electophoretically resolved loci sampled from individual trees located along transects. He conducted runs tests (Sokal and Rohlf, 1981) for non-random sequences of alleles along transects, cluster analysis of genotypes, comparison of geographic distance and genetic dissimilarity, and examination of distribution of rare genotypes. Sproule's conclusion was that the populations studied were subdivided into groups of related trees, with the groups overlapping in a series of intermingling clusters.

In related studies, but using much different methodology, Coles and Fowler (1976), and Park and Fowler

(1982) examined inbreeding patterns in Picea glauca (Moench) Voss and Larix laricina, respectively. Using controlled crossing techniques, Coles and Fowler found a strong relationship between proximity of parent trees and genetic load. They suggested that parent trees located less than 100 m apart likely were related. Park and Fowler's controlled crossing work with tamarack did not reveal significant differences among crosses with neighbors, distant neighbors or polymix pollen. However, the percentage of sound seed did increase as distance between parents increased. This likely was due to decreased relatedness and genetic load with increased geographic separation between trees.

SPATIAL AUTOCORRELATION ANALYSIS

Spatial autocorrelation analysis is a technique that has been used to test for spatial patterns in surfaces. Spatial autocorrelation tests the dependence of the value of a variable on the values of that variable at neighboring localities (Sokal and Oden, 1978a). Cliff and Ord (1973) described how this technique could be used to test for geographical patterns in point and areal data, and explained the underlying theories, procedures and tests associated with the technique. This was expanded on in their monograph on spatial processes (Cliff and Ord, 1981).

In spatial autocorrelation analysis, pairs of points or areas in a plane are considered to be joined or neighbors on the basis of some predetermined criteria. The joins or connections may be based on geographic distance between the pairs of points or areas, or on other criteria (e.g. Gabriel joins; Gabriel and Sokal, 1969). Cliff and Ord (1981), Sokal and Oden (1978a, 1978b) and Jumars *et al*. (1977) discussed some of the considerations in construction of matrices of connections between point pairs. For each of these matrices, an autocorrelation coefficient, either Moran's *I* statistic (Moran, 1950) or Geary's *c* (Geary, 1954), is calculated. Often, in geographic variation work, autocorrelation coefficients are constructed for a series of matrices which correspond to pairs of points or areas that are separated by increasingly large distances. Then a correlogram, a graph of the autocorrelation coefficients by distance class, is constructed. Positive autocorrelation occurs when high scores of a variable at one locality are associated with high scores of that variable at adjacent localities; negative autocorrelation occurs when high and low values of a variable alternate from locality to locality.

Sokal and Oden (1978a, 1978b) illustrated how spatial autocorrelation could be applied to biological data, particularly in the areas of population genetics and ecology. Sokal and Wartenberg (1983) showed the use of this technique in examining geographic variation patterns in biological data, and discussed inferences that may be made from these analyses.

Sokal and Wartenberg (1981) reported results of their tests of many of the assumptions associated with use of spatial autocorrelation in population genetics studies. They tested the use of spatial autocorrelation with the isolation-by-distance model (Wright, 1969). This model suggests that there is random mating within defined neighborhoods, but that more distant individuals cannot mate because of limitations in dispersal. This type of model could account for the development of spatial population genetic structure under some conditions.

The authors tested, among others, the assumptions that isolation-by-distance results in spatial autocorrelation, and that changes in the generating processes included in the model (e.g. vagility) result in changes in the correlograms resulting from analysis. Using a Monte Carlo simulation, gene frequency surfaces of isolation-by-distance models with different parameters were generated, and then subjected to spatial autocorrelation analysis. The results of the simulations showed that isolation-by-distance leads to spatial autocorrelation and that changes in model parameters are detectable in the autocorrelation results. In addition, examination of the simulated changes in the populations over time showed that significant autocorrelation had developed by generation five.

Sakai and Oden (1983) used spatial autocorrelation analysis in a study of the spatial pattern of sex expression in Acer saccharinum L. All the mature trees (490) in a 200 by 100 m area were mapped. Then spatial autocorrelation analysis was used to test whether neighboring trees were more similar than expected, in respect to size and sex. All possible tree pairs were divided into five meter distance classes. Moran's I values were computed, and correlograms were constructed. Results of the analysis showed that both sex and tree size were spatially autocorrelated. This study showed the technique's potential for use in examining microgeographic patterns.

More commonly, spatial autocorrelation analysis has been used to examine macrogeographic variation. Jensen (1986) used the technique to examine variation in the size and shape of acorns in Quercus ellipsoidalis among 36 localities in the United States. Pairs of localities were linked by Gabriel connections. Distance classes were chosen to have approximately equal frequencies of joins in each distance class or adjacency matrix. Moran's I values were calculated and correlograms were constructed. The shape characters showed little pattern, but the size characters generally showed a trend ranging from positive to negative autocorrelation with increasing distance. For extremely distant join classes, the autocorrelation coefficients tended to become positive again.

Sokal _et_ _al_. (1986b) completed a similar study of macrogeographic variation in _Populus_ _deltoides_ Bartr. ex Marsh. ssp. _deltoides_. Here, variation in 10 vegetative characters from 522 individuals distributed over 302 localities was evaluated. Pairs of localities were joined on the basis of geographic distance. Pairs of joins were grouped into 10 distance classes which had approximately equal numbers of joins in each. Computation of autocorrelation coefficients and construction of correlograms revealed a high number of significant coefficients. There was an overall trend from positive to negative autocorrelation with increasing geographic distance between locality pairs.

Sokal _et_ _al_. (1986a) reported on a study of geographic variation among populations of Yanomama Indians in South America. Spatial autocorrelation analysis was used to examine spatial variation in blood groups and allozyme polymorphisms among 50 villages. One of the two alleles from each enzyme system was dropped from analysis. Matrices of point pairs were based on Gabriel connections and again, distance classes were devised to yield approximately equal numbers of joins in each. Generally, results showed declining genetic similarity with increasing distance. Mean correlograms by distance class showed the strongest trends. The authors suggested that mean correlograms may be better indicators of trends in genetic similarity than those constructed from single allele frequencies, because of the tendency for single allele variations to cancel each other out.

Epperson and Clegg's (1986) study of flower colour polymorphisms in Ipomoea purpurea populations incorporated microgeographic spatial autocorrelation analysis. Nominal data on flower colour was sampled along regularly spaced lattices or transects in 17 populations and converted to genotypes for two colour loci. Examination of autocorrelation statistics and correlograms based on geographic distances between sample points showed that the phenotypes for the two colour loci occurred in patches. In addition, the patches for the two loci were of different sizes.

Waser (1987) reported on a study of microgeographic population structure in Delphinium nelsonii. This study used spatial autocorrelation to examine variation in allozyme frequencies in plants sampled along transects. Pairs of sample points were joined in a matrix based on geographic distance and then separated into 20 m distance classes. Only the more common alleles at a locus were used. One of the 40 Moran's I values calculated was significant. A mean correlogram also was constructed.

This correlogram showed that the mean autocorrelation coefficients deviating the most from expectations were negative coefficients in the 0-20 m and the 100-120 m distance classes. This suggested the existence of extremely localized spatial heterogeneity.

Dewey and Heywood (1988) reported on another recent microgeographic application of spatial autocorrelation analysis. This study examined spatial genetic structure within a Psychotria nervosa population. The data used were allozyme scores from two polymorphic loci for 245 trees sampled along transects. The connectivity matrix for autocorrelation was based on Gabriel joins between tree pairs. Analysis included all the allozyme variants that were resolved. No evidence of spatial genetic structure was observed.

Epperson and Allard (1989) reported on the results of their study of microgeographic spatial genetic structure in two Pinus contorta ssp. latifolia populations. Pollen and maternal genotype data based on seven and fourteen allozyme loci, respectively, was collected from 200 trees per population. The sample trees were located in regularly spaced lattice patterns. Connectivity matrices were based on geographic distances between tree pairs. The autocorrelation analyses used single and multi-locus genotypes for maternal trees and pollen. Very few of the autocorrelation statistics were significant, suggesting that microgeographic genetic pattern was absent.

The simulations done by Sokal and Wartenberg (1981) and these recent applications reported for spatial autocorrelation analysis suggest its potential for application to analysis of spatial genetic population structure. Spatial population genetic structure in tree populations has been observed in a few cases, using a number of techniques; and spatial autocorrelation analysis has been used to test for microgeographic and macrogeographic variation in a variety of characteristics, including allozyme frequencies.

METHODS

FIELD METHODS

Four natural populations of tamarack were selected for study near Thunder Bay, Ontario (Figure 1). One of the four populations, the Twin City population, previously was used in studies by Farmer _et_ _al_. (1986), and Yang and Hazenberg (1987).

In each population, all the tamarack located in the main portion of the stand were sampled and mapped. The number of trees sampled and mapped per stand ranged from 196 to 573, for a total of 1715. The sample collected from each tree consisted of a twig containing expanding spring buds, which were used for electrophoretic analysis.

Information on the texture and drainage of the associated soils, the composition of associated vegetation, and the ages, diameters and heights of the tamarack populations was collected. Tamarack that due to proximity or similar allozyme scores were provisionally identified as members of a clone were excavated. Then clones which were formed either by layering or root suckering were treated as one individual, and were mapped either at the position of the largest stem, or the center of the clone.

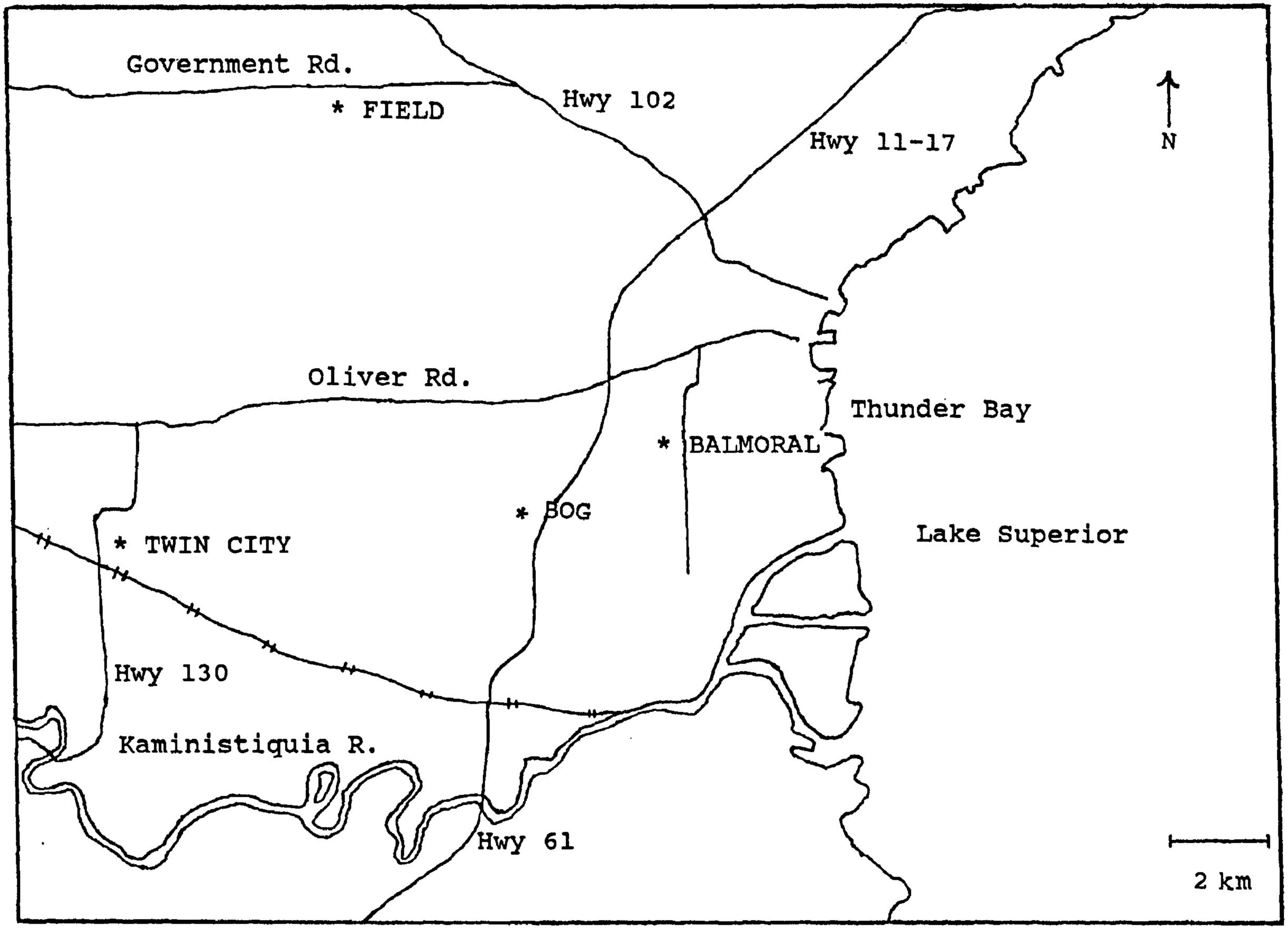

Figure 1. Location of four tamarack populations studied near Thunder Bay, Ontario.

SITE DESCRIPTIONS

In the Balmoral population, trees ranged in age from under 5 to 20 years. The dominant trees averaged 15 years, with mean heights and diameters of 5.5 m and 8 cm, respectively. The area occupied by the population (*n*=465, excluding clones) was 2.02 hectares. This site had a weakly decomposed organic soil (greater than two meters deep) with evidence of previous disturbance by logging and fire. The associated vegetation in this community included: *Picea mariana* (Mill.) B.S.P., *Betula papyrifera* Marsh., heavy cover of *Ledum groenlandicum* L., *Chamaedaphne calyculata* (L.) Moench and *Myrica gale* L., *Smilacina trifolia* (L.) Desf., *Pleurozium schreberi* (B.S.G.) Mitt. and *Sphagnum* spp.

The second population, the Thunder Bay Bog population, was a very stagnant stand that was part of a large wetland complex. The tree ages ranged from less than 7 to 75 years. The central area of this stand was characterized by a very wet, hummocky area predominantly vegetated by grasses and sedges. In this portion of the stand the tamarack were either very old and stunted, or very young. Towards the perimeter, which was characterized by larger trees and more shrub cover, the dominant tamarack had average ages of 55 years, and mean heights and diameters of 4 m and 5 cm, respectively. This population (*n*=481, excluding clones) covered 0.15 hectares. The deep organic soil on this site was saturated, and weakly to moderately decomposed. The associated vegetation included: *Picea mariana*, *Betula glandulosa* Michx., *Ledum groenlandicum*, *Andromeda glaucophylla* Link., *Sarracenia purpurea* L., *Drosera rotundifolia* L., *Eriophorum* sp., *Pleurozium schreberi* and *Sphagnum* spp.

The third population was located in an abandoned hay field. The average dominants in this young Field population were 9 m tall, with diameters of 12 cm at 13 years. Some seedlings were present. The tree sizes and ages decreased across the stand from the edge of the field towards the center. This population (*n*=573, excluding clones) covered 0.22 hectares. The soil was loamy and associated vegetation included: *Picea mariana*, *Populus balsamifera* L., *Salix* sp., *Rubus idaeus* var. *strigosus* (Michx.) Maxim., *Rosa acicularis* Lindl., *Aster macrophyllus* L., *Rubus pubescens* Raf., *Solidago canadensis* L., *Clintonia borealis* (Ait.) Raf. and assorted grass species.

The fourth and final population was a mature, relatively productive tamarack stand near Twin City Crossroads. This Twin City stand was characterized by average dominants 54 years old, with average heights and diameters of 14 m and 20 cm, respectively. The population (*n*=196, excluding clones) covered about 0.20 hectares. The soil was a deep, moderate to well decomposed organic which supported a variety of associates: Abies balsamea (L.) Mill., Picea mariana, Populus balsamifera, Fraxinus nigra Marsh., Acer spicatum Lam., Cornus stolonifera Michx., Aralia nudicaulis L., Trientalis borealis Raf., Mitella nuda L., Pleurozium schreberi, Hylocomium splendens (Hedw.) B.S.G., and Mnium sp.

The reduction in population numbers due to identification of clones was: Balmoral, 6.6 percent; Bog, 1.0 percent; Field, 2.4 percent; and Twin City, 2.9 percent. Clones on the three organic sites (Balmoral, Bog and Twin City) were formed by layering; on the upland Field site, they were formed by root sprouts.

ELECTROPHORETIC PROCEDURES

The buds collected from each tree were stored, refrigerated, for up to ten days. Electrophoretic methods generally followed those of Cheliak and Pitel (1984). The basal portions of two to four buds from each tree were placed in a five milliliter sample cup with two drops of extraction buffer (Extraction Buffer #10; Cheliak and Pitel, 1984) and refrigerated overnight. See Table 1 for the eight enzyme system stains, and gel and buffer systems used. Ten loci consistently were resolved and subsequently were used in analysis. Inheritance in eight of these loci

Table 1. Enzyme systems used for electrophoretic procedures with tamarack buds.

Enzyme System[a]	Loci	Buffer[b]
Aspartate aminotransferase (AAT)(E.C.2.6.1.1)	*Aat1*, *Aat2*	A
Aldolase (ALD)(E.C.4.1.2.13)	*Ald2*, *Ald3*	B
Fumarase (FUM)(E.C.4.2.1.2)	*Fum*	B
Glutamate dehydrogenase (GDH)(E.C.1.4.1.2)	*Gdh*	A
Hexokinase (HK)(E.C.2.7.1.1)	*Hk*	B
Isocitrate dehydrogenase (IDH)(E.C.1.1.1.42)	*Idh*	B
Phosphoglucose isomerase (PGI)(E.C.5.3.1.9)	*Pgi2*	A
Phosphoglucomutase (PGM)(E.C.2.7.5.1)	*Pgm*	B

[a] All stain and buffer systems from Cheliak and Pitel (1984)

[b] Buffer systems: A - Tris-citrate pH 8.5 gel buffer, lithium borate pH 8.1 electrode buffer; B - L-Histidine - tris pH 7.0 gel buffer, Tris-citrate pH 7.0 electrode buffer

previously was described by Cheliak and Pitel (1985). These eight loci were: *Aat1*, *Aat2*, *Ald2*, *Ald3*, *Pgi2*, *Pgm*, *Gdh*, and *Idh*. The *Ald2* locus included in this study corresponds to the *Ald1* locus described by Cheliak and Pitel (1985). Similarly, *Ald3* corresponds to *Ald2*; and *Pgi2* corresponds to *Pgi* (Cheliak and Pitel, 1985). In addition, this study included the *Fum* and *Hk* loci, which were not included in Cheliak and Pitel's study.

DATA ANALYSIS

Population Genetic Characteristics

For each population, basic genetic descriptors based on the allozyme data were summarized. These included: allele frequencies, genotype frequencies, the average number of alleles per locus, and the percentage of loci that were polymorphic. Expected heterozygosity, the proportion of heterozygotes expected under panmixia (H_e), was calculated for each locus using the formula:

$$H_e = 1 - \sum p_k \quad ,$$

where p is the estimated frequency of the kth allele at the locus (Nei, 1977). Observed heterozygosity, the proportion of heterozygotes observed for each locus (H_o), also was recorded.

Deviations of each population from Hardy-Weinberg equilibrium were tested using a Chi-square test. In addition, Wright's (1965) F_{IS} statistic also was used to examine the deviation of each population from equilibrium genotypic proportions. F_{IS} values are measures of the correlation of uniting gametes between individuals within the four populations and were calculated for each locus in each population using the formula:

$$F_{IS} = (H_S - H_O) / H_S$$

where H_S and H_O are the expected and observed heterozygosities, respectively, of the *i*th locus in the population.

Among-Population Variation

A row-by-column test of independence, based on the *G* -statistic, was used to test for allelic heterogeneity among populations (Sokal and Rohlf, 1981). Genetic distances between populations also were calculated. Each single-locus genetic distance (D_N) was calculated using the formula:

$$D_N = -\ln (I_N) ,$$

where

$$I_N = J_{xy} / \ (J_x J_y) \ ,$$

$$J_{xy} = \ \sum p_{x(i)} p_{y(i)} ,$$

$$J_x = \ \sum p_{x(i)} p_{x(i)} ,$$

and

$$J_y = \ \sum p_{y(i)} p_{y(i)}$$

(Nei, 1972). I_N is the normalized identity, for the locus, of genes between populations x and y. J_x is the probability of identity of two randomly chosen genes in population x. J_y is the probability of identity of two randomly chosen genes in population y. J_{xy} is the probability of identity of one randomly chosen gene from each of populations x and y, respectively. Here, $p_{x(i)}$ and $p_{y(i)}$ are the frequencies of the ith allele in populations x and y, respectively.

The multilocus version of Nei's genetic distance ($\bar{D}_N$) was calculated as:

$$\bar{D}_N = -\ln \ (\bar{I}_N) \ ,$$

where

$$\bar{I}_N = \bar{J}_{xy} / \ (\bar{J}_x \bar{J}_y)$$

(Nei, 1972). $\bar{I}_N$ is the normalized identity, over all loci, of genes between populations x and y; $\bar{J}_{xy}$, $\bar{J}_x$ and $\bar{J}_y$ are the arithmetic means over all loci of $\underline{J}_{xy}$, $\underline{J}_{x}$ and $\underline{J}_{y}$, respectively.

Spatial Genetic Structure Within Populations

For each of the four populations studied, the spatial distribution of each allele at each polymorphic locus was mapped onto the tree location map. The Lakehead University Geographic Information System (ARC/INFO) was used to generate plots of these maps. One plot was produced for each allele in each population. These plots were examined for any visible departures from randomness.

Spatial autocorrelation analysis also was completed for each of the four populations. Analysis was done with SAAP 3.2 (written by D. Wartenberg) on IBM - compatible microcomputers. Within each of the four populations, the geographic distances joining all possible tree pairs were calculated. Then these tree pairs or 'joins' were grouped into distance classes. For each population, a maximum of ten distance classes (the limits of the software) were used. The distance classes were constructed to balance a number of considerations. Five meter increments were used in initial (proximal) classes in order to allow detection of relatively fine grained pattern (e.g. pattern associated with near neighbors). The more distant classes were greater in size (e.g. 45-78 m) in order to accommodate the longer joins necessarily constucted between trees in the larger stands. These longer joins were considered less likely to reveal information concerning any underlying spatial genetic structure. Finally, the number of joins was distributed as evenly as possible over the distance classes. Table 2 shows the distance classes used and the numbers of joins in each class.

For each distance class, Moran's I, an autocorrelation coefficient, was calculated. Because of the variation in number of tree joins among the different distance classes, the significance of the autocorrelation coefficients in the different distance classes did not necessarily vary in strict proportion with magnitude of the coefficients calculated. Moran's I is calculated as:

$$I = n \sum w_{ij} z_i z_j / W \sum z_i ,$$

where

$$z_i = Y_i - \bar{Y} ,$$

$$z_j = Y_j - \bar{Y} ,$$

and

$$W = \sum w_{ij}$$

(Sokal and Oden, 1978a). Here, n is the number of trees in the population; $w_{ij}$is the weight given to the join made between tree i and tree j. The weight for the join is '1' if the join falls within the distance class for which the autocorrelation coefficient is being calculated, and '0' if

Table 2. Summary of spatial autocorrelation distance classes and numbers of joins by population for four tamarack populations.

Balmoral (n=465)		Bog (n=481)		Field (n=573)		Twin City (n=196)	
Distance Class (m)	Number Of Joins	Distance Class (m)	Number Of Joins	Distance Class (m)	Number Of Joins	Distance Class (m)	Number Of Joins
0 - 5	743	0 - 5	7 120	0 - 5	7 668	0 - 5	1 006
5 - 10	1 594	5 - 10	17 481	5 - 10	14 997	5 - 10	2 037
10 - 15	2 329	10 - 15	22 984	10 - 15	15 923	10 - 15	2 675
15 - 20	2 905	15 - 20	23 343	15 - 20	16 688	15 - 20	3 128
20 - 25	3 400	20 - 25	18 310	20 - 25	18 320	20 - 25	3 117
25 - 30	4 129	25 - 30	13 056	25 - 30	20 793	25 - 30	2 723
30 - 35	4 596	30 - 35	8 143	30 - 35	20 125	30 - 35	2 024
35 - 65	31 438	35 - 50	5 003	35 - 40	17 429	35 - 40	1 362
65 -110	39 641	-	-	40 - 45	13 153	40 - 57	1 038
110 -200	17 105	-	-	45 - 78	18 782	-	-
Total Joins	107 880		115 440		163 878		19 110

it does not. Y_i and Y_j are the values of the variable (transformed genotype) for trees i and j, respectively. $\bar{Y}$ is the mean value of the variable (transformed genotype) for all the trees in the population.

The tree genotypes (as determined by electrophoresis) were transformed using the method of Smouse and Neel (1977). This transformation converted each single - locus genotype to a series of vectors showing the contribution of each allele to the genotype.

For each locus in each population, the most common allele was dropped from analysis. The only exception occurred when an allele was encountered only once in a population. Then, for that population and locus only, the unique allele was dropped and all the other alleles (including the most common) were analysed.

Moran's I is asymptotically normally distributed as n increases, and is tested for significance as a standard normal deviate (Cliff and Ord, 1981). For this analysis, I was evaluated under the randomisation assumption. This assumption is based on the premise that the observations (transformed genotypes or scores) are random, independent drawings from a population with an unknown distribution function. This assumption is more appropriate than that of normality (which assumes that the observations are random, independent drawings from a normal population), because the transformed tree genotypes do not follow a normal distribution.

Moran's *I* was chosen over Geary's *c*, a similar autocorrelation coefficient, because the variance of Moran's *I* seems to be less affected by the distribution of the sample data than is Geary's *c* (Cliff and Ord, 1981). Each autocorrelation tested the hypothesis:

> H_0: the probability that a tree has a particular score for a given variable (allele at a locus) is the same for each tree, and the score of a given tree is fixed independently of the others. Therefore, the distribution of alleles over tree positions is random.

The alternate hypothesis was:

> H_1: the probability that a tree has a particular score is not the same for each tree, and the scores are not fixed independently. Therefore, the distribution of alleles over tree positions is not random.

Positive autocorrelation occurred when tree pairs joined in a distance class had more similar scores than would have been expected if the alleles were randomly distributed. Negative autocorrelation occurred when tree pairs in a distance class had more dissimilar scores than would have been expected if the alleles were randomly distributed. Since both positive and negative autocorrelation were of interest ecologically, the region of rejection of the test statistic (standard normal deviate) was two-tailed.

Spatial correlograms were constructed by graphing the calculated autocorrelation coefficients (Moran's *I* values) against the distance classes for which they were calculated. Correlograms were constructed for the series of *I* values for each allele in each population, and for the average *I* values over all alleles for each population. Correlograms for individual alleles also were tested for significance using the Bonferroni procedure (Neter *et al.*, 1985; Oden, 1984; Sakai and Oden, 1983). This test was used to indicate whether the null hypothesis (that of random distribution of alleles) was valid for individual correlograms, each of which was constructed from a series of non-independent *I* values.

The secondary hypothesis of this thesis, that random spatial genetic structure can be observed in populations with differing demographic and ecological characteristics, was examined by completing the analyses using data from four populations.

RESULTS

POPULATION GENETIC CHARACTERISTICS

Table 3 summarizes the observed allozyme frequencies by population. The raw data are presented in Appendices I-IV. Three of the ten loci consistently resolved were monomorphic. Three other loci were variable only in the Field population. Generally, the frequency of the most common allele at each locus was very high. The average number of alleles per locus, by population, ranged from 1.7 to 2.2, with an overall mean of 2.0 (Table 4). The percentage of loci over all populations that were polymorphic was 47.5 percent ($\underline{p} < 1.0$). By population, between 40.0 and 70.0 percent of loci were polymorphic ($\underline{p} < 1.0$). However, only 10 percent of the loci were polymorphic using the criteria $\underline{p} < 0.95$ (Table 4).

The expected heterozygosities ($\underline{H}_e$) generally were relatively small (Table 5). The overall mean $\underline{H}_e$ was only 0.066. The observed heterozygosities generally were close to the expected. The results of the Chi-square tests for departure of genotype frequencies from Hardy-Weinberg equilibrium showed that loci differed significantly from expectations in only two cases. These exceptions were

Table 3. Allele frequency estimates for allozyme loci observed in four tamarack populations.

Locus	Allele	Population			
		Balmoral	Bog	Field	Twin City
Aat1	*1*	1.0000	1.0000	1.0000	1.0000
Aat2	*1*	1.0000	1.0000	1.0000	1.0000
Ald2	*1*	1.0000	1.0000	1.0000	1.0000
Ald3	*1*	0.9871	0.9958	0.9869	0.9949
	2	0.0129	0.0042	0.0131	0.0051
Fum	*1*	0.9828	0.9927	0.9825	0.9949
	2	0.0172	0.0073	0.0175	0.0051
Gdh	*1*	1.0000	1.0000	0.9939	1.0000
	2	0.0000	0.0000	0.0061	0.0000
Hk	*1*	1.0000	1.0000	0.9991	1.0000
	2	0.0000	0.0000	0.0018	0.0000
Idh	*1*	1.0000	1.0000	0.9939	1.0000
	2	0.0000	0.0000	0.0061	0.0000
Pgi2	*1*	0.5699	0.5489	0.6143	0.5663
	2	0.1624	0.1674	0.1710	0.1301
	3	0.2086	0.2235	0.1920	0.2347
	4	0.0538	0.0561	0.0201	0.0638
	5	0.0043	0.0042	0.0017	0.0051
	6	0.0011	0.0000	0.0009	0.0000
Pgm	*1*	0.9903	0.9896	0.9913	0.9872
	2	0.0065	0.0042	0.0061	0.0128
	3	0.0011	0.0000	0.0000	0.0000
	4	0.0011	0.0052	0.0000	0.0000
	5	0.0011	0.0010	0.0026	0.0000

Table 4. Levels of genetic variation observed in four tamarack populations.

Population	Alleles Per Locus	Percent Polymorphic	
		$p^{a}<1.0$	$p<0.95$
Balmoral	2.1	40.0	10.0
Bog	1.9	40.0	10.0
Field	2.2	70.0	10.0
Twin City	1.7	40.0	10.0
Mean	1.98	47.5	10.0

[a] Frequency of most common allele.

Table 5. Analysis of heterozygosity levels in four tamarack populations.

Population	Locus	Heterozygosity	
		Expected ($\underline{H}_e$)	Observed ($\underline{H}_o$)
Balmoral	*Ald3*	0.025	0.022
	Fum	0.034	0.034
	Pgi2	0.602	0.591
	Pgm	0.019	0.019
	Mean	0.068	0.067
Bog	*Ald3*	0.008	0.008
	Fum	0.014	0.015
	Pgi2	0.618	0.624
	Pgm	0.021	0.021
	Mean	0.066	0.067
Field	*Ald3*	0.026	0.026
	Fum	0.034	0.035
	Gdh	0.003	0.003
	Hk	0.002	0.002
	Idh	0.012	0.012
	Pgi2	0.556	0.553
	Pgm	0.017	0.017
	Mean	0.065	0.065
Twin City	*Ald3*	0.010	0.010
	Fum	0.010	0.010
	Pgi2	0.603	0.658
	Pgm	0.025	0.015
	Mean	0.065	0.069
Overall	Mean	0.066	0.067

Ald3 in the Balmoral population, and Pgm in the Twin City population (Table 6). The F_{IS} statistics showed that both of these population/locus combinations had excess homozygotes (Table 7). Otherwise, most of the F_{IS} statistics by locus in each population were very small and negative in sign. This indicated slight excesses of heterozygotes.

AMONG-POPULATION VARIATION

The test for allelic heterogeneity among populations (G-statistic) showed that there was significant allelic heterogeneity among populations in three loci (50 percent of those tested), Pgi2, Fum and Idh (Table 8). The genetic distances among populations were very small (mean multilocus distance = 0.0002) (Table 9).

SPATIAL GENETIC STRUCTURE WITHIN POPULATIONS

Visual examination of the plots of the spatial distribution of alleles in the four populations (one plot for each allele at each variable locus in each population) revealed that most of the alleles apparently were randomly distributed over the population members. However, for 8 of the 36 allele/population plots examined (22.2 percent), there appeared to be some pattern or departure from

Table 6. Results of Chi-square test of deviations from Hardy-Weinberg equilibrium for variable allozyme loci observed in four tamarack populations.

Population	Locus	Chi-square	Degrees of Freedom
Balmoral	Ald3	11.283*	1
	Fum	0.142	1
	Pgi2	16.733	15
	Pgm	0.044	10
Bog	Ald3	0.008	1
	Fum	0.026	1
	Pgi2	6.538	10
	Pgm	0.053	6
Field	Ald3	0.101	1
	Fum	0.181	1
	Gdh	0.002	1
	Hk	0.000	1
	Idh	0.022	1
	Pgi2	1.718	15
	Pgm	0.044	3
Twin City	Ald3	0.005	1
	Fum	0.005	1
	Pgi2	9.856	10
	Pgm	30.156*	1

* Significant at 95 percent confidence level.

Table 7. $\underline{F}_{IS}$ statistics for four tamarack populations.

Locus	$\underline{F}_{IS}$ Population Balmoral	Bog	Field	Twin City	Mean
Ald3	0.156	-0.004	-0.013	-0.005	0.051
Fum	-0.018	-0.007	-0.018	-0.005	-0.015
Gdh	nv[a]	nv	-0.002	nv	-0.002
Hk	nv	nv	-0.001	nv	-0.001
Idh	nv	nv	-0.006	nv	-0.006
Pgi2	0.018	-0.010	0.005	-0.091	-0.020
Pgm	-0.007	-0.007	-0.007	0.392	0.115
Mean	0.037	-0.007	-0.006	0.073	0.017

[a] No variation.

Table 8. Results of test for allelic heterogeneity among four tamarack populations.

Locus	_G_-statistic	Degrees of Freedom
Ald3	7.094	3
Fum	8.148*	3
Gdh	4.387	3
Idh	15.379*	3
Pgi2	39.063*	12
Pgm	0.492	3

* Significant at 95 percent confidence level.

Table 9. Estimates of Nei's genetic distances among all pairs of the tamarack populations.

Locus	Population	Bog	Field	Twin City
<u>Ald3</u>	Balmoral	0.0000	0.0000	0.0000
	Bog		0.0000	0.0000
	Field			0.0000
<u>Fum</u>	Balmoral	0.0001	0.0000	0.0001
	Bog		0.0001	0.0000
	Field			0.0001
<u>Gdh</u>	Balmoral	0.0000	0.0000	0.0000
	Bog		0.0000	0.0000
	Field			0.0000
<u>Hk</u>	Balmoral	0.0000	0.0000	0.0000
	Bog		0.0000	0.0000
	Field			0.0000
<u>Idh</u>	Balmoral	0.0000	0.0000	0.0000
	Bog		0.0000	0.0000
	Field			0.0000
<u>Pgi2</u>	Balmoral	0.0007	0.0026	0.0023
	Bog		0.0052	0.0022
	Field			0.0077
<u>Pgm</u>	Balmoral	0.0000	0.0000	0.0000
	Bog		0.0000	0.0001
	Field			0.0000
Multi-locus Genetic Distance				
	Balmoral	0.0001	0.0002	0.0001
	Bog		0.0004	0.0001
	Field			0.0004

randomness. Figures 2-9 show these plots. The patterns that appeared were in:

1. the Balmoral population, <u>Pgi2-4</u> and <u>Ald3-2</u>,
2. the Bog population, <u>Pgi2-4</u>, <u>Pgm-2</u> and <u>Pgm-4</u>, and
3. the Twin City population, <u>Ald3-2</u>, <u>Fum-2</u> and <u>Pgi2-5</u>.

Generally, this pattern was manifested as alleles that occurred in near-neighbors.

Spatial autocorrelation analysis was completed for between seven and eleven alleles, and from eight to ten distance classes in each population (Tables 10, 11, Figures 10-13). In total, 313 individual autocorrelation coefficients (Moran's <u>I</u> values) were calculated (Appendices V-VIII). Twenty-eight (8.9 percent) of these values were significant (95 percent confidence level) (Tables 10, 11). This indicated the null hypothesis was not supported in a small proportion of the tests. Of the 36 correlograms constructed for single alleles, 14 (38.9 percent) were significant using Bonferroni's criterion (90 percent

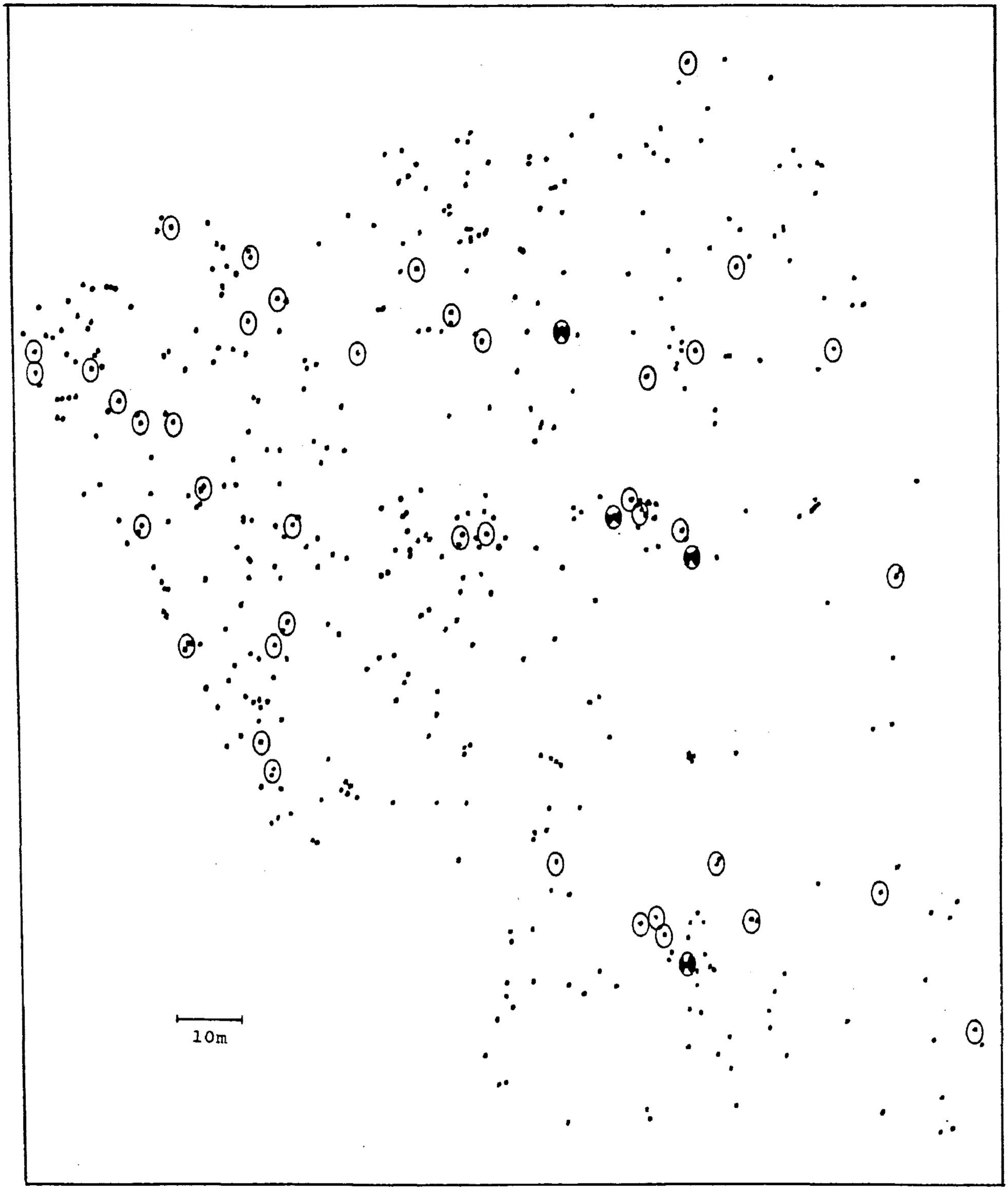

Figure 2. Spatial distribution of Pgi2-4 allele in Balmoral population. (individual with: no Pgi2-4 allele - '•' ; one Pgi2-4 allele - '⊙' ; two Pgi2-4 alleles - '●')

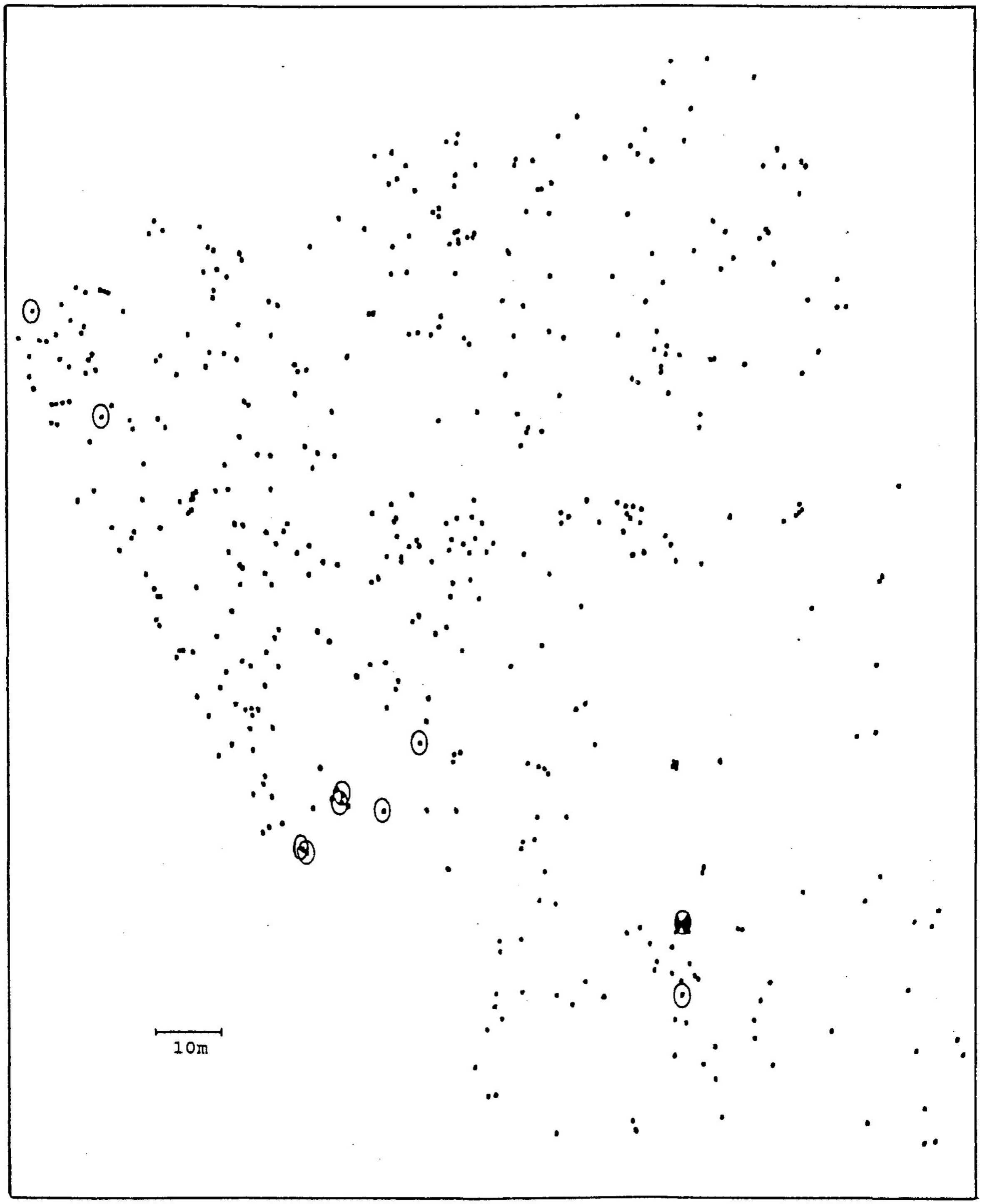

Figure 3. Spatial distribution of <u>Ald3-2</u> allele in Balmoral population. (individual with: no <u>Ald3-2</u> allele - '•' ; one <u>Ald3-2</u> allele - '⊙' ; two <u>Ald3-2</u> alleles - '8')

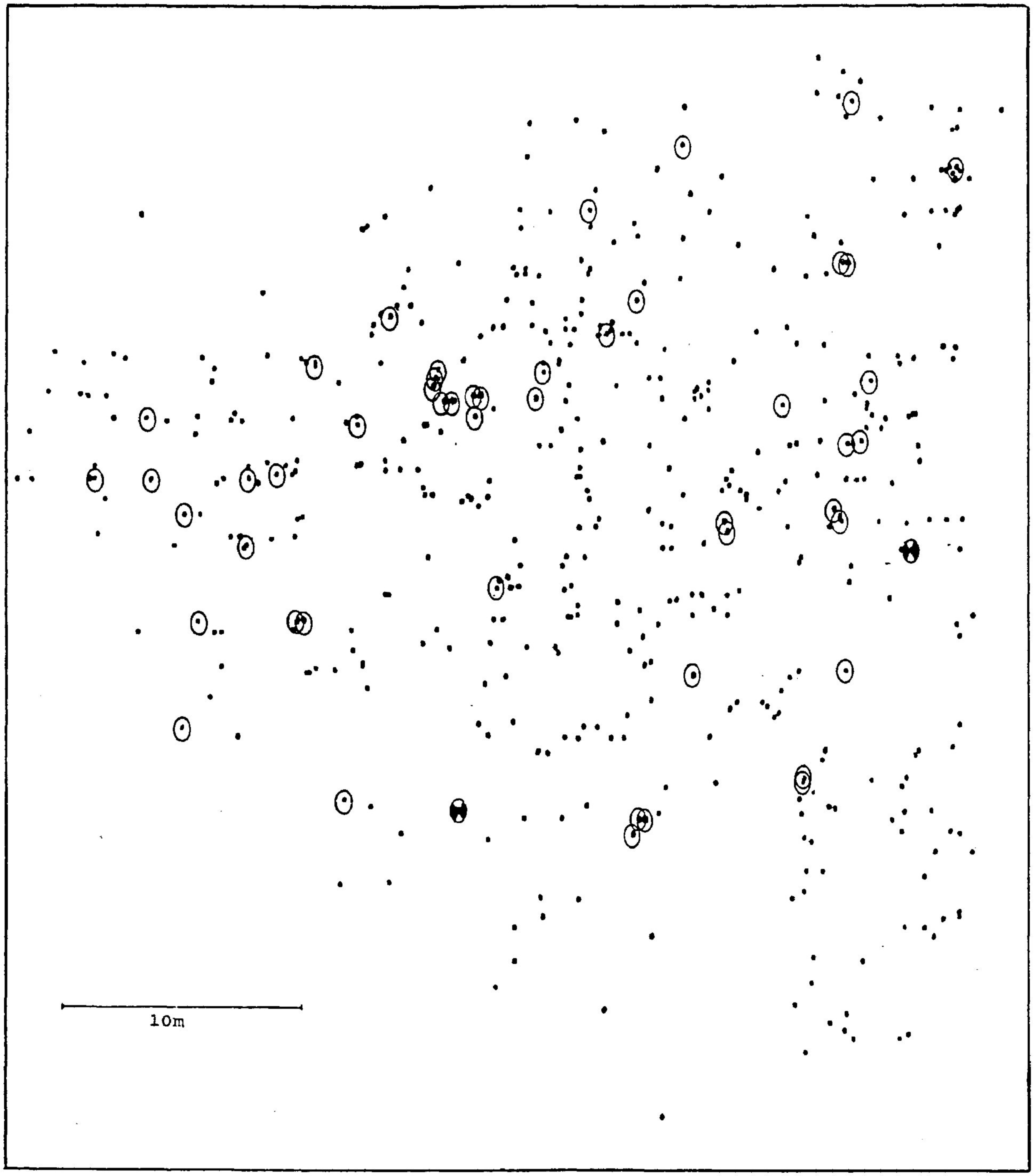

Figure 4. Spatial distribution of Pgi2-4 allele in Bog population. (individual with: no Pgi2-4 allele - '•' ; one Pgi2-4 allele - '⨀' ; two Pgi2-4 alleles - '●')

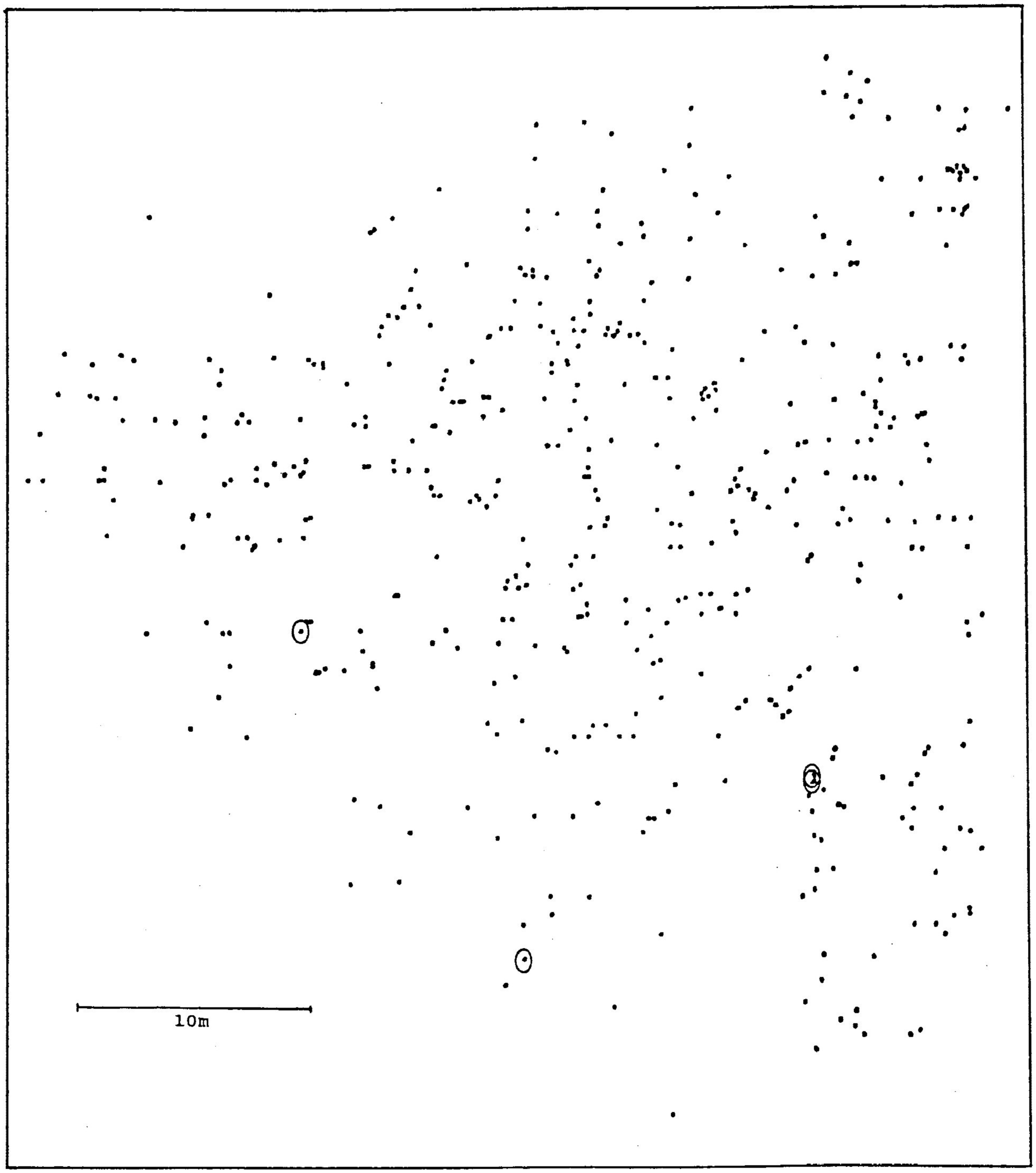

Figure 5. Spatial distribution of Pgm-2 allele in Bog population. (individual with: no Pgm-2 allele - '•' ; one Pgm-2 allele - '⊙')

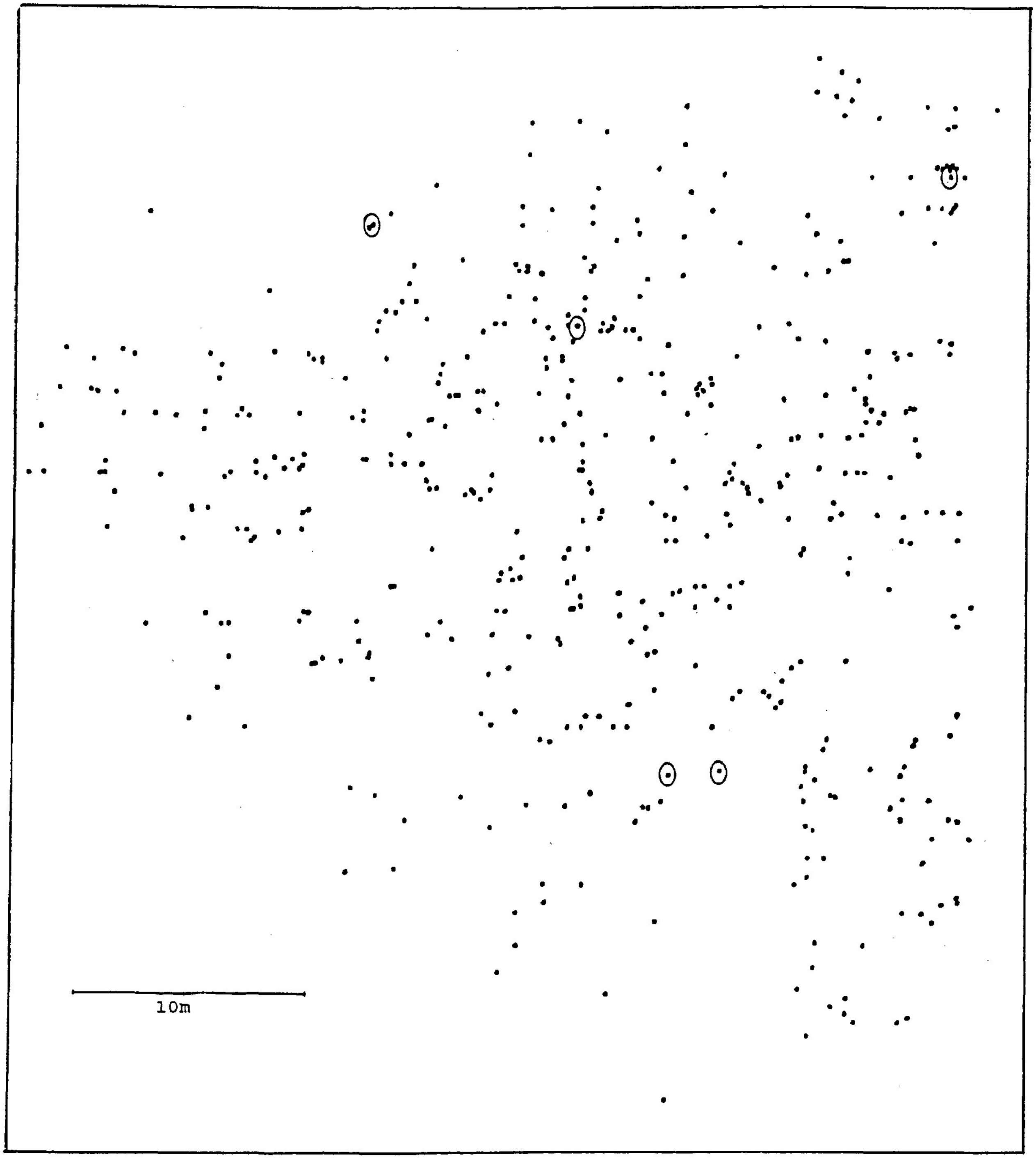

Figure 6. Spatial distribution of Pgm-4 allele in Bog population. (individual with: no Pgm-4 allele - '•' ; one Pgm-4 allele - '⊙')

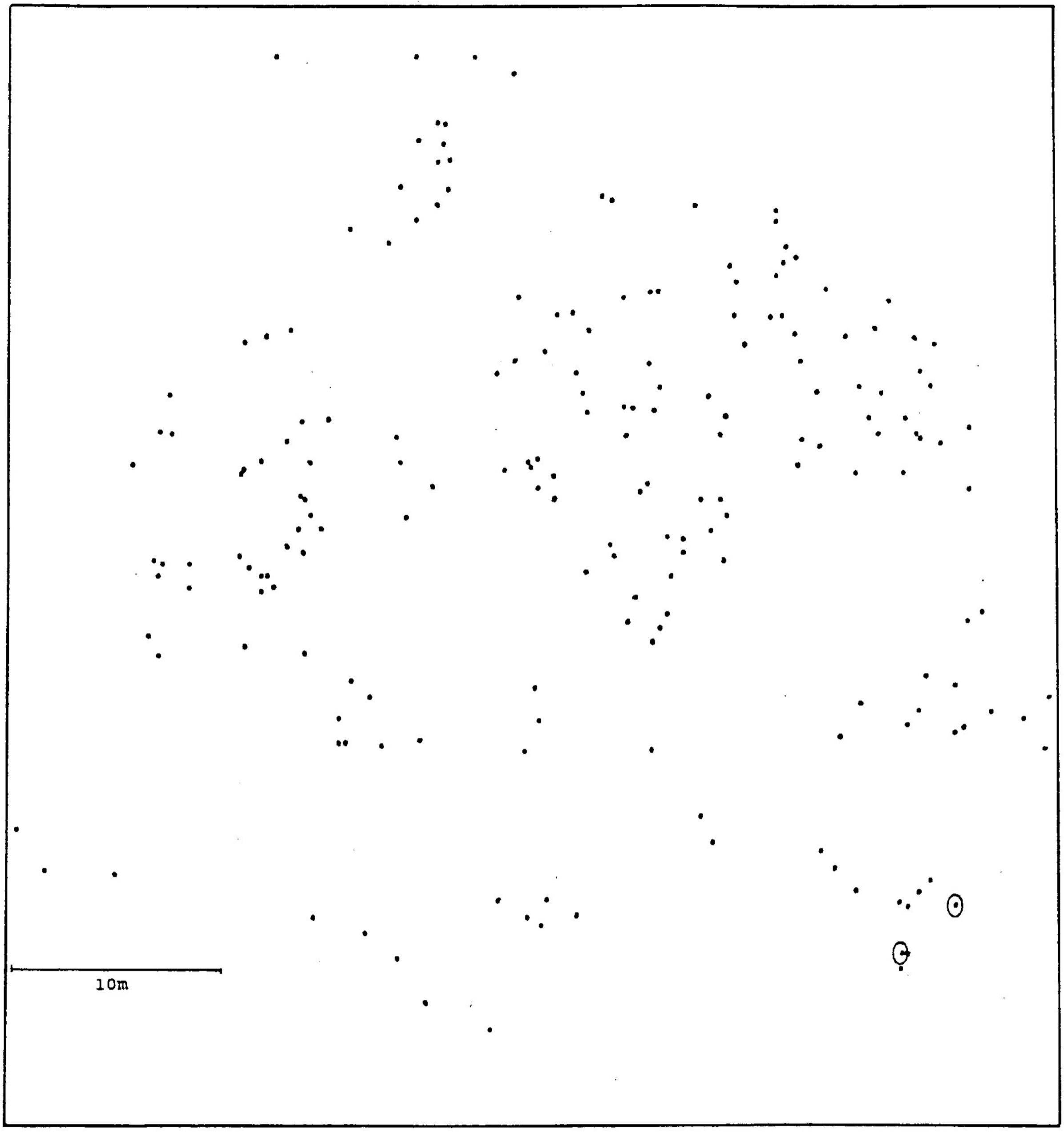

Figure 7. Spatial distribution of Fum-2 allele in Twin City population. (individual with: no Fum-2 allele - '•' ; one Fum-2 allele - '⊙')

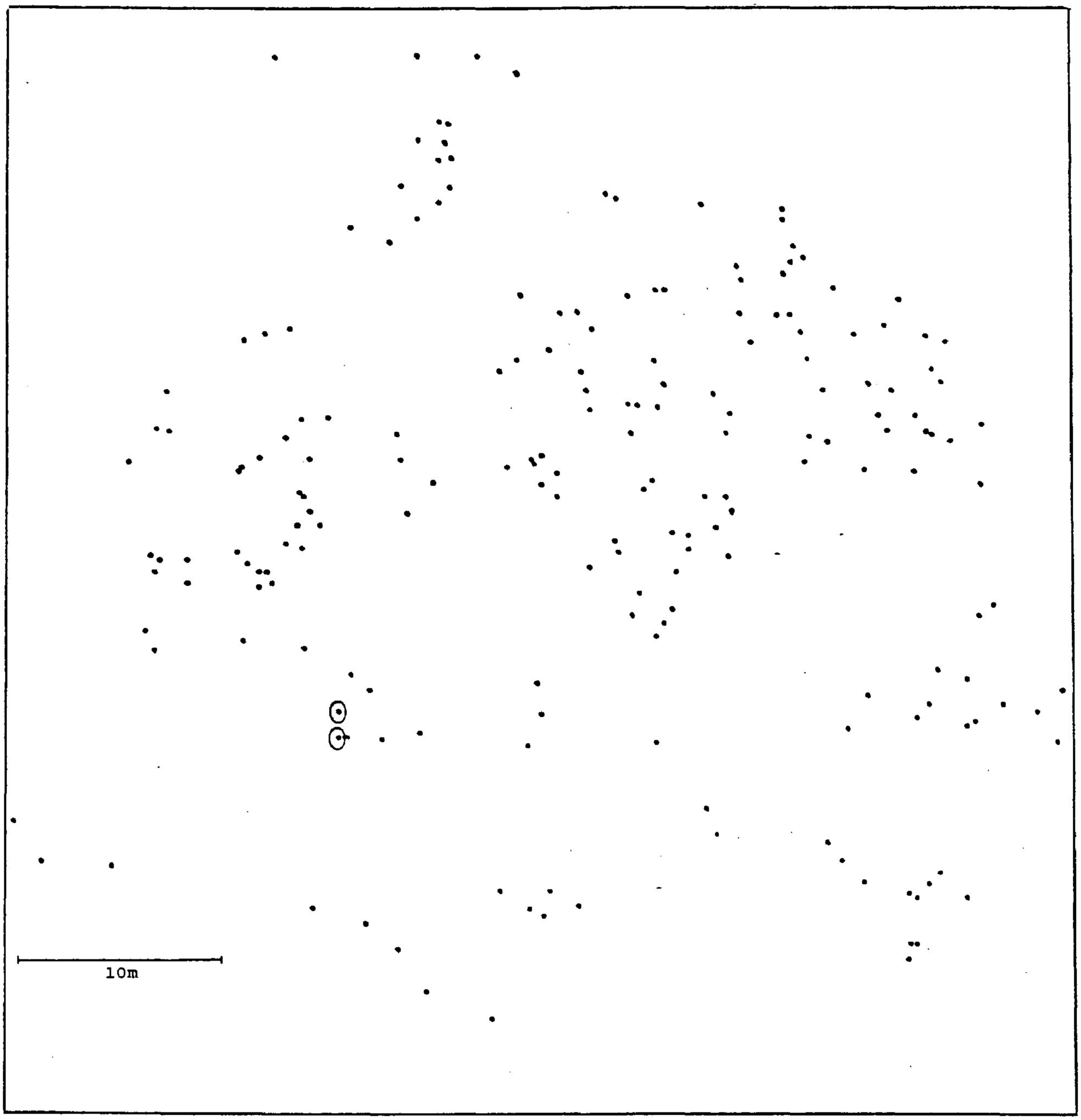

Figure 8. Spatial distribution of Pgi2-5 allele in Twin City population. (individual with: no Pgi2-5 allele - '•' ; one Pgi2-5 allele - '⊙')

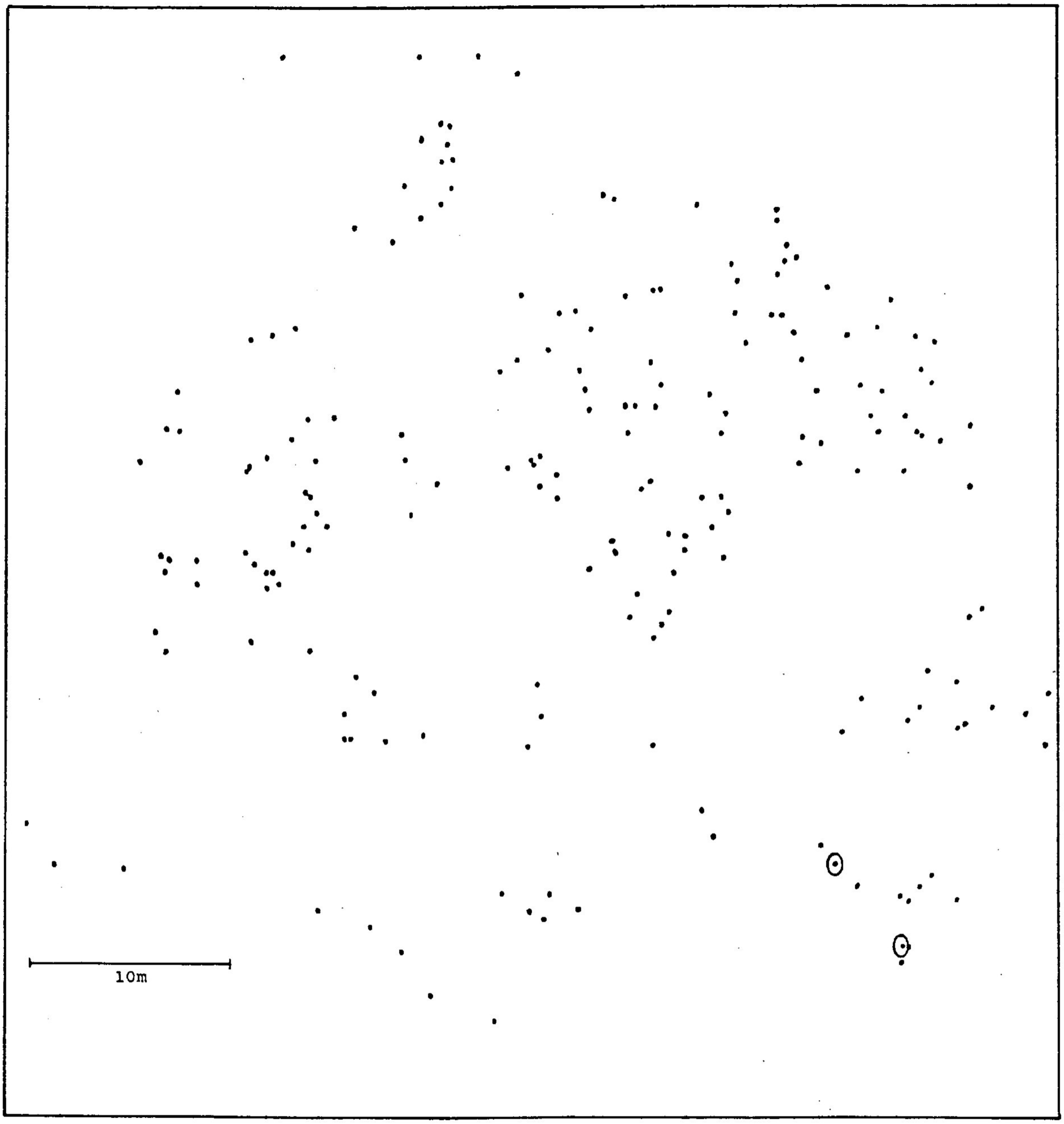

Figure 9. Spatial distribution of Ald3-2 allele in Twin City population. (individual with: no Ald3-2 allele - '•' ; one Ald3-2 allele - '⊙')

Table 10. Summary of spatial autocorrelations completed for four tamarack populations.

	Population				
	Balmoral	Bog	Field	Twin City	Total
Number of distance classes (*I* values)	10	8	8	9	35
Number of correlograms (alleles analyzed)	9	9	11	7	36
Number of correlograms significant[a]	3 (33.3%)	5 (55.6%)	3 (27.3%)	3 (42.9%)	14 (38.9%)
Number of *I* values calculated	90	72	88	63	313
Number of *I* values significant[b]	7 (7.8%)	11 (15.3%)	3 (3.4%)	7 (11.0%)	28 (8.9%)

[a] 90 percent confidence level.

[b] 95 percent confidence level.

Table 11. Significant spatial autocorrelations by allele for four tamarack populations.

		Population			
		Balmoral	Bog	Field	Twin City
Locus	Allele	Number of I Values Calculated for Each Allele			
		10	8	8	9
		Number of Significant[a] I Values			
Ald3	2	4 *[b]	0	0	1 *[b]
Fum	2	0	1 *	0	2 *[b]
Gdh	2	-[c]	-	1 *	-
Idh	2	-	-	1 *	-
Pgi2	1	1 *	-	0	-
	2	1	1	0	0
	3	0 [b]	3 * [b]	0	0
	4	0	1	0	0
	5	1 *	2 *	1 *	2 *[b]
	6	-	-	-	-
Pgm	1	0	0	-	-
	2	0	2 *[b]	0	2
	3	-	-	-	-
	4	-	1 *[b]	-	-
	5	-	-	0	-

[a] 95 percent confidence level.

* Significant correlogram (90 percent confidence level).

[b] Spatial pattern detected visually.

[c] Insufficient variation for analysis.

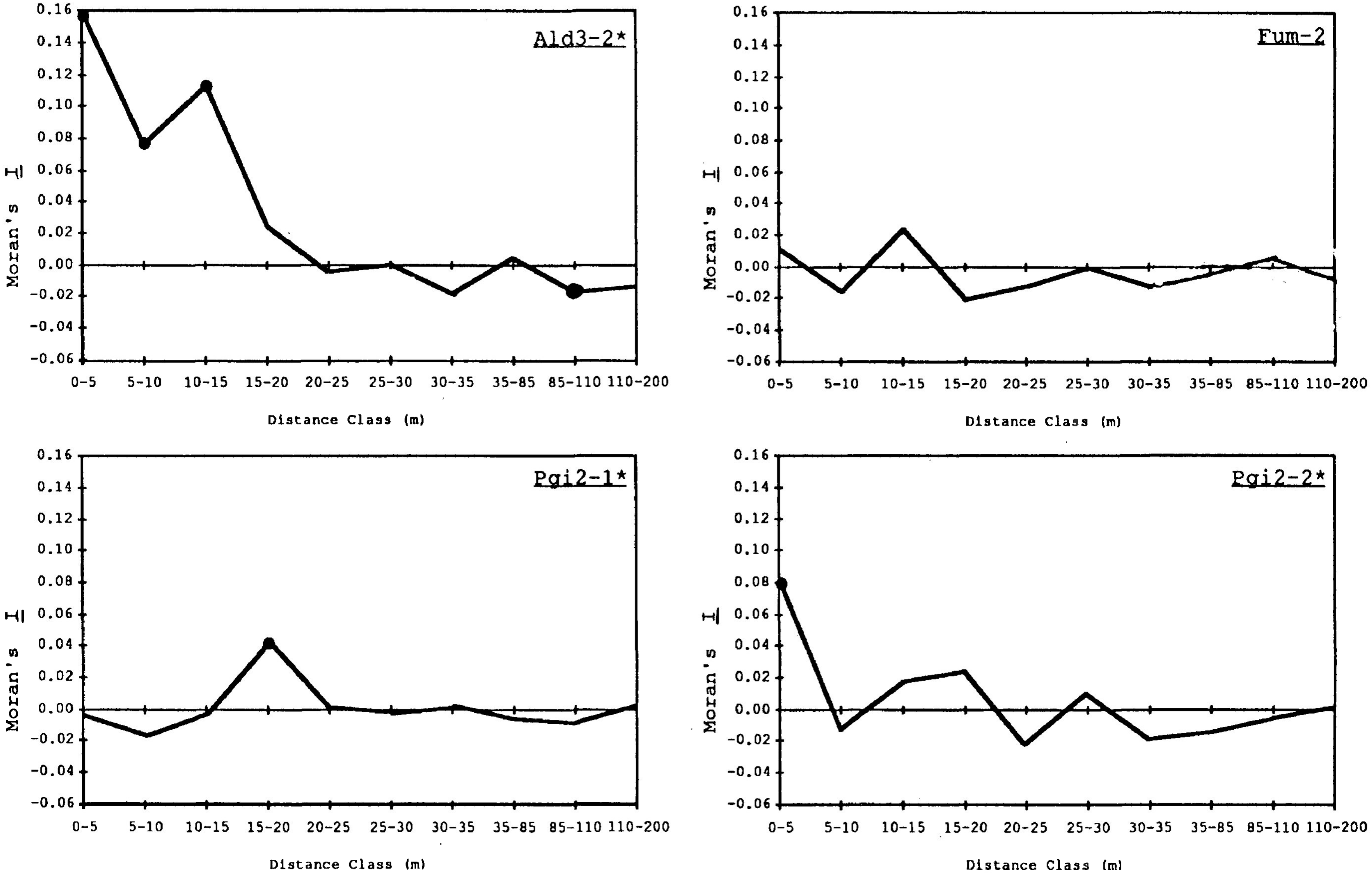

Figure 10. Correlograms for Balmoral population. ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

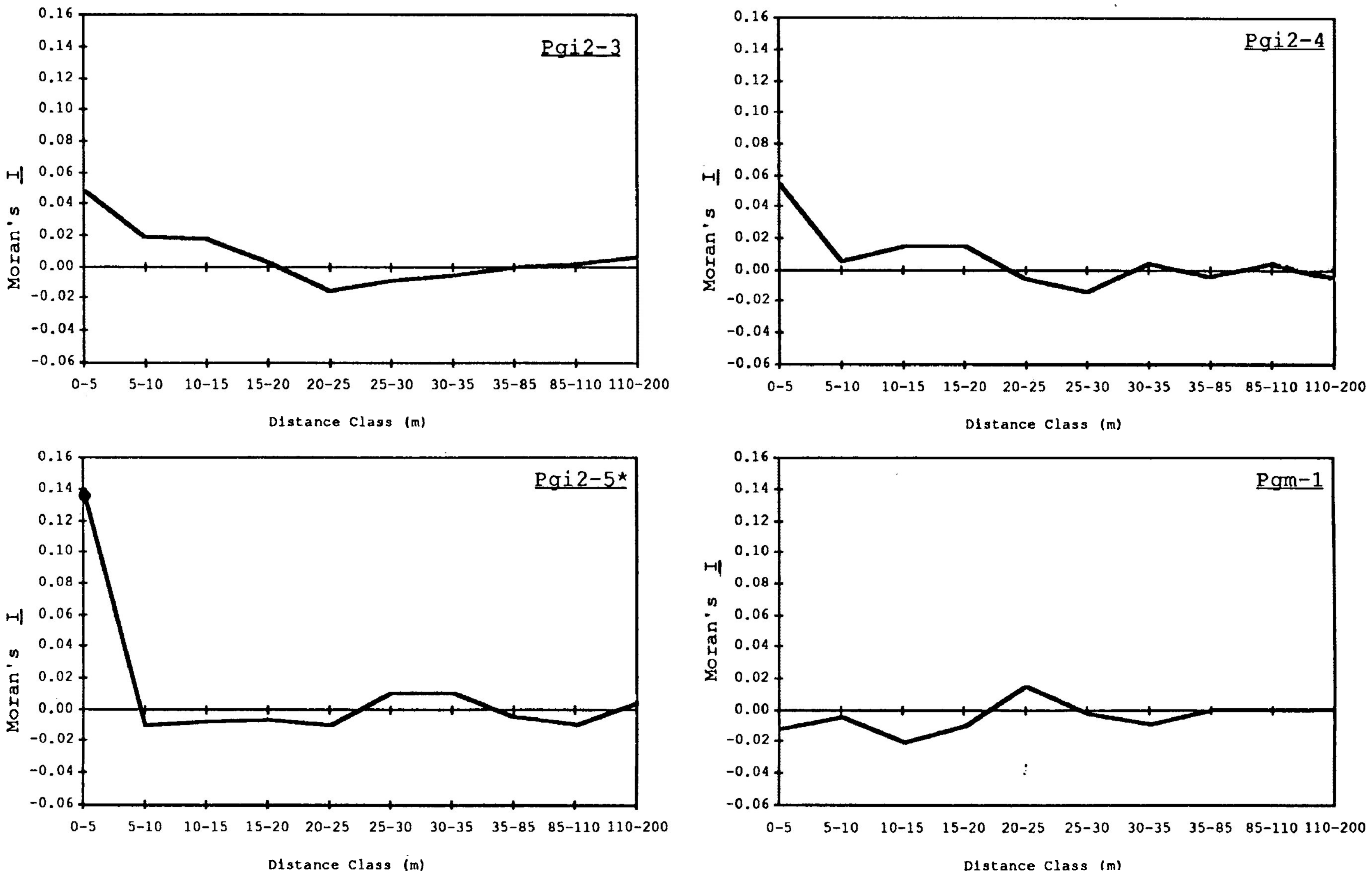

Figure 10. (Continued) (Balmoral). ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

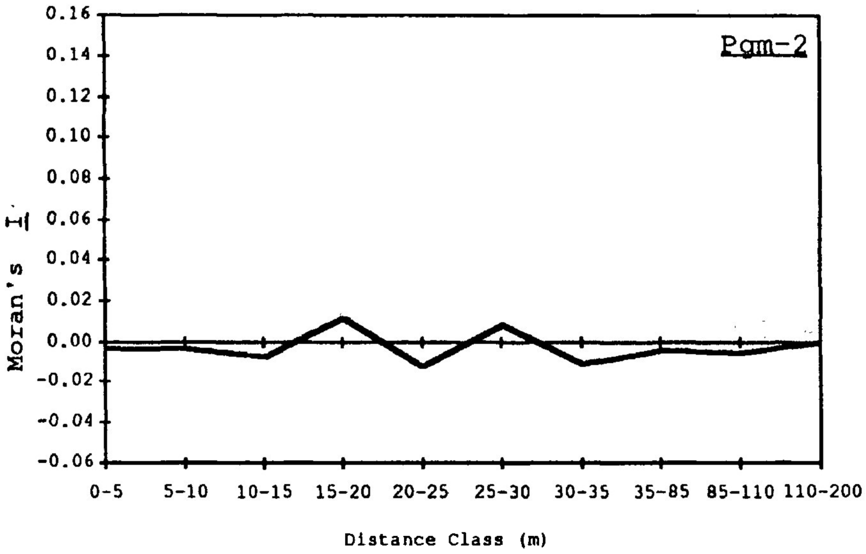

Figure 10. (Continued) (Balmoral).

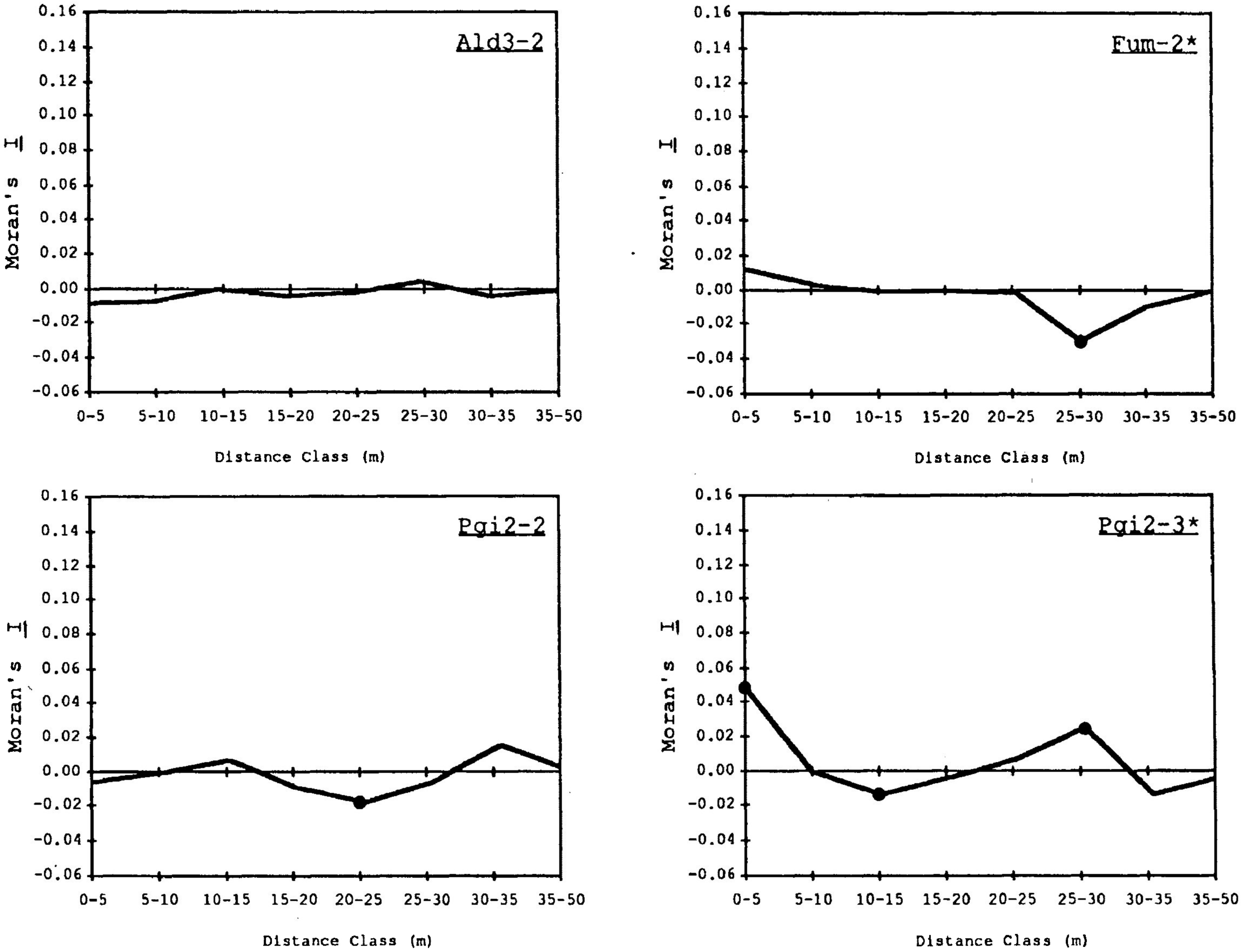

Figure 11. Correlograms for Bog population. ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

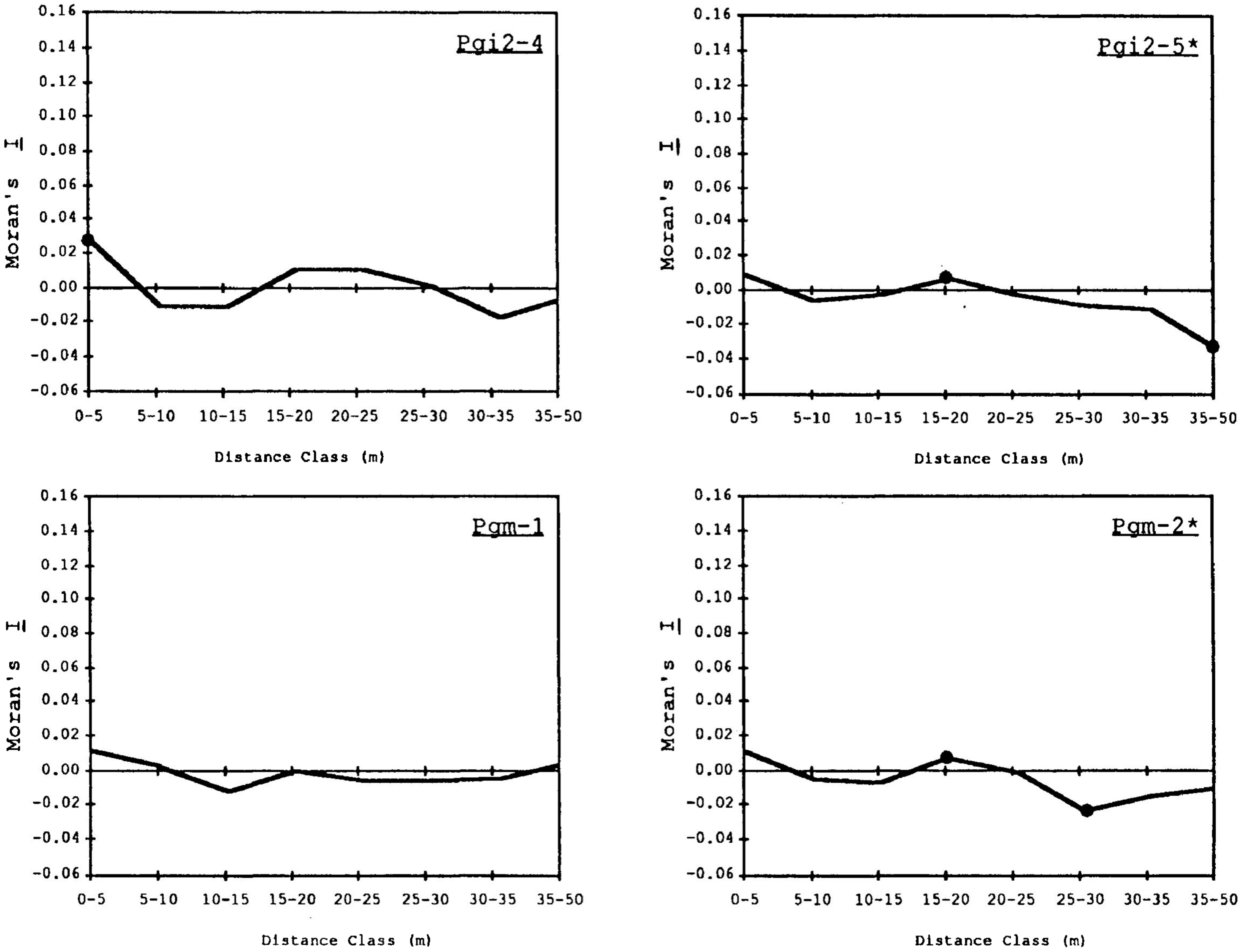

Figure 11. (Continued) (Bog). ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

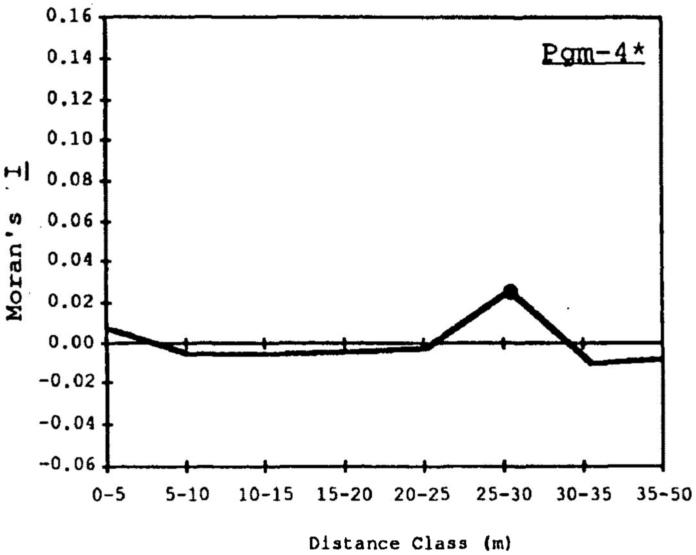

Figure 11. (Continued) (Bog). ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

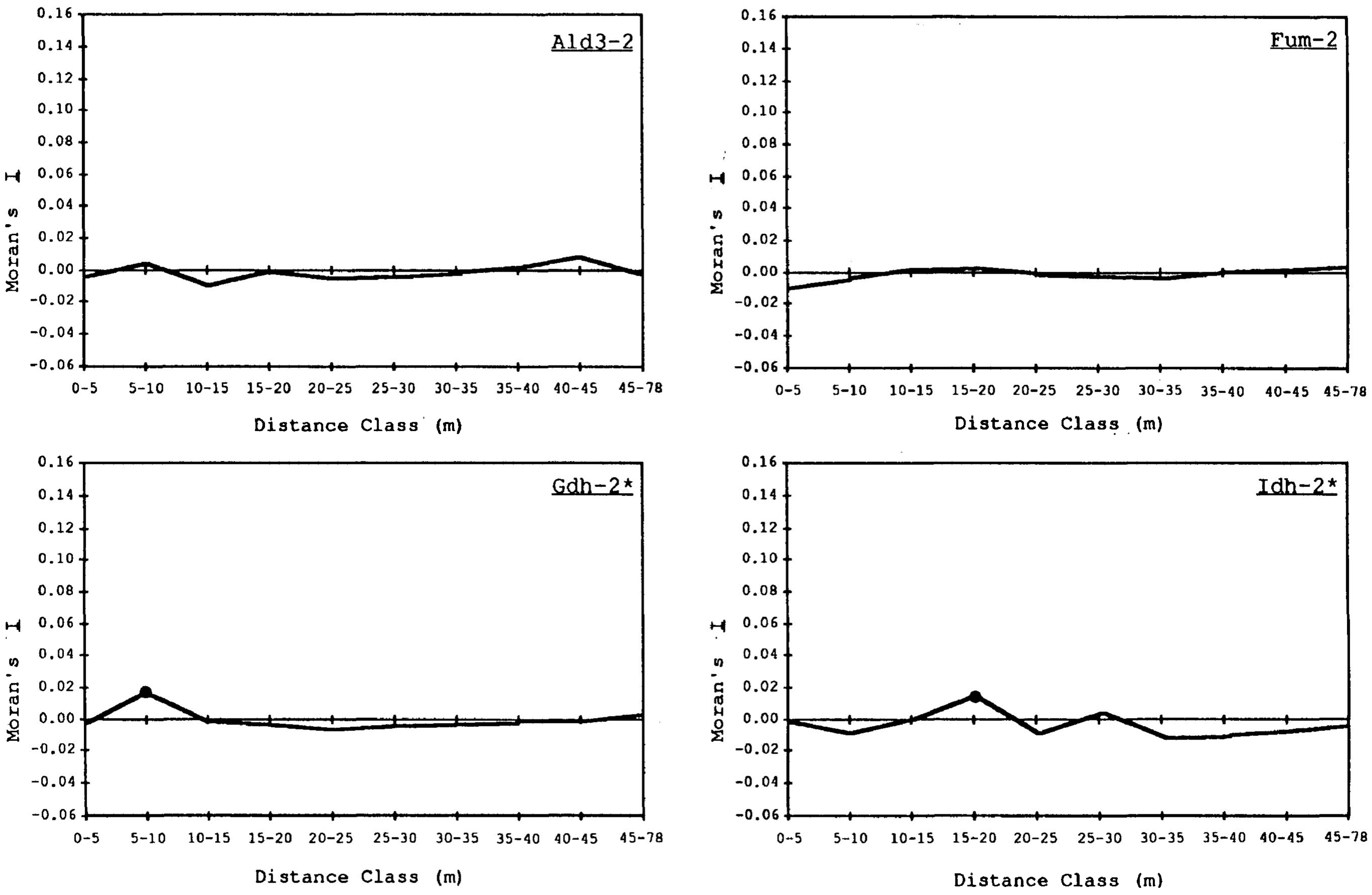

Figure 12. Correlograms for Field population. ('*' correlogram significant at percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

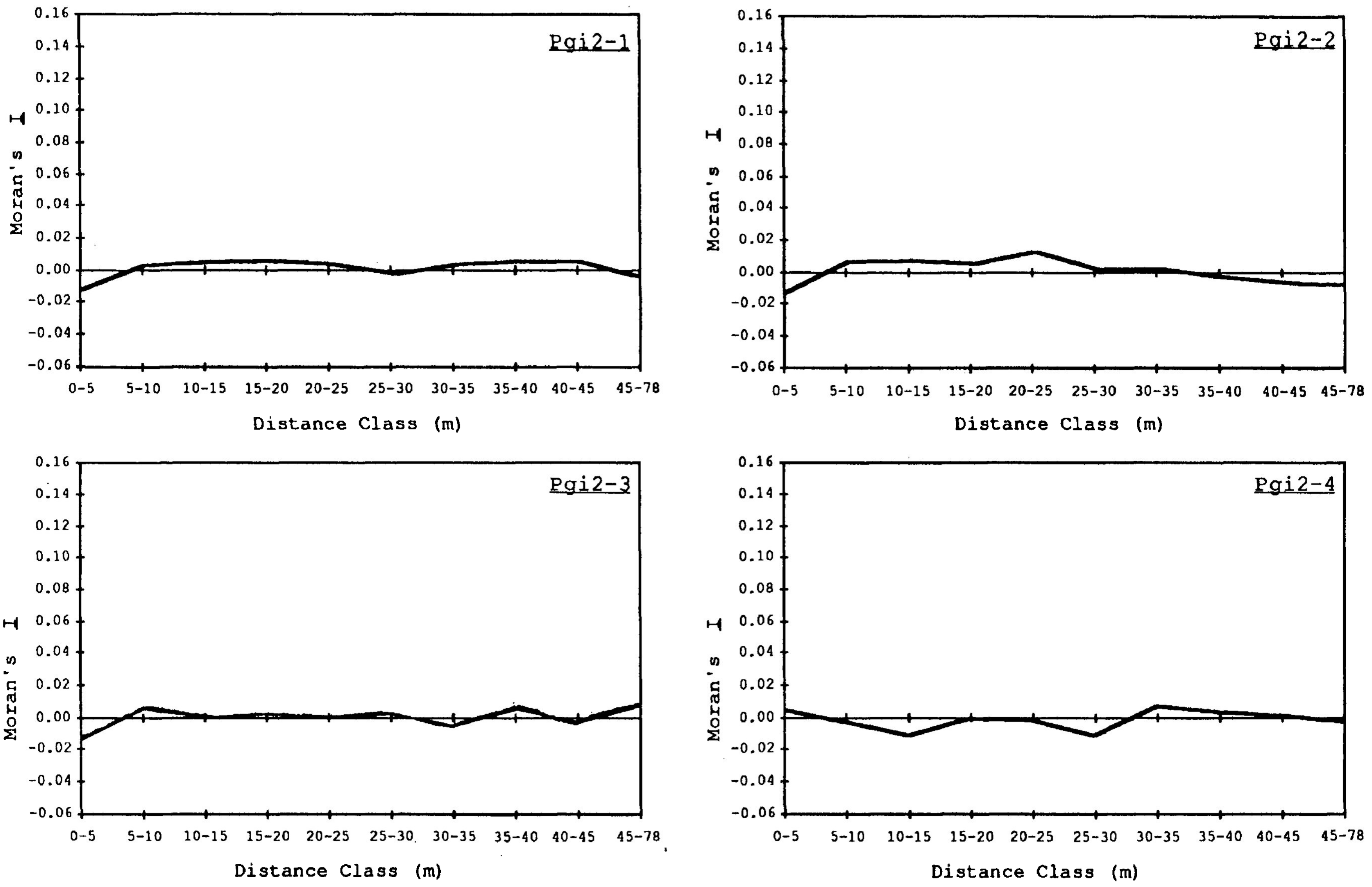

Figure 12. (Continued) (Field).

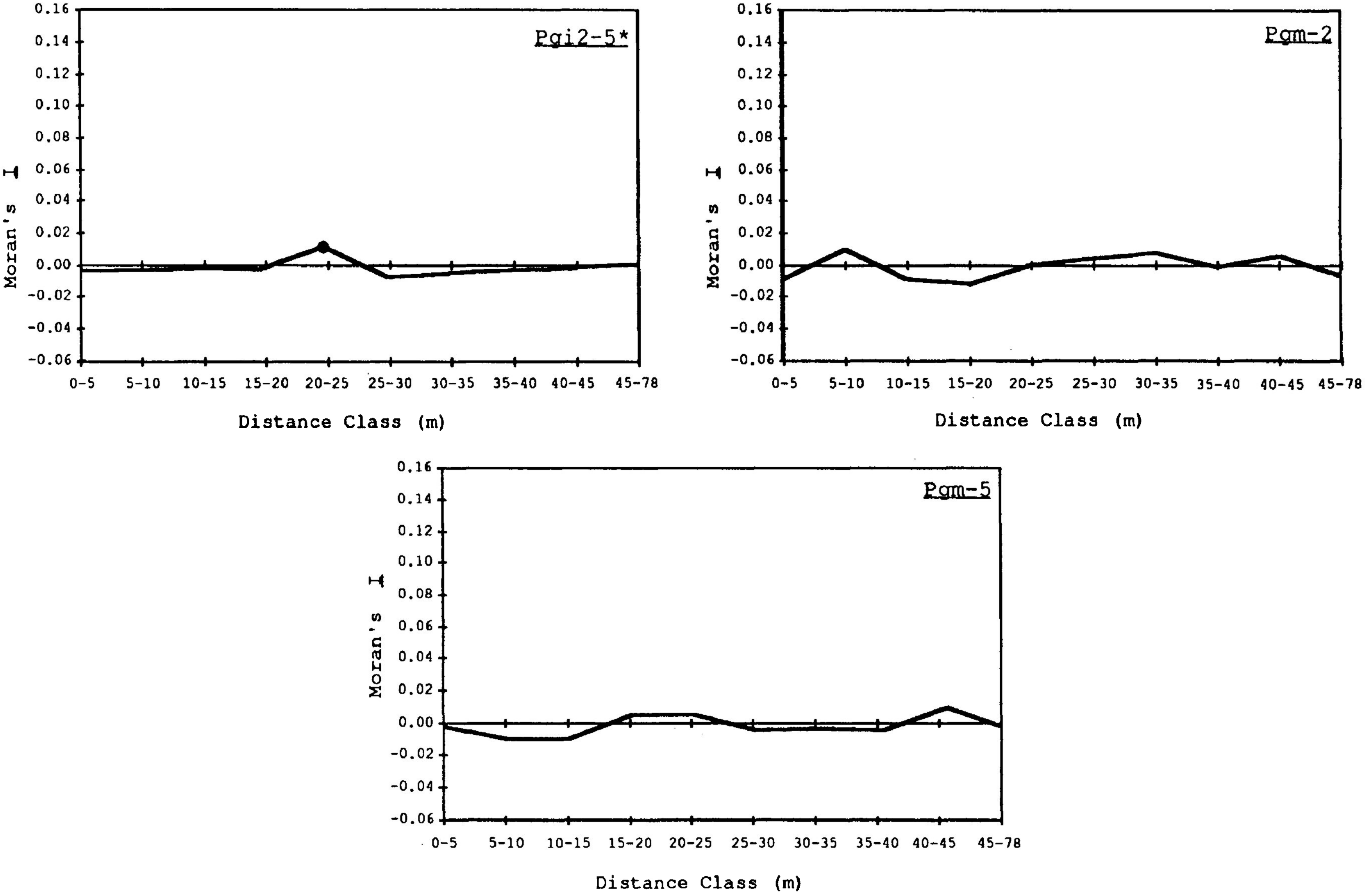

Figure 12. (Continued) (Field). ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

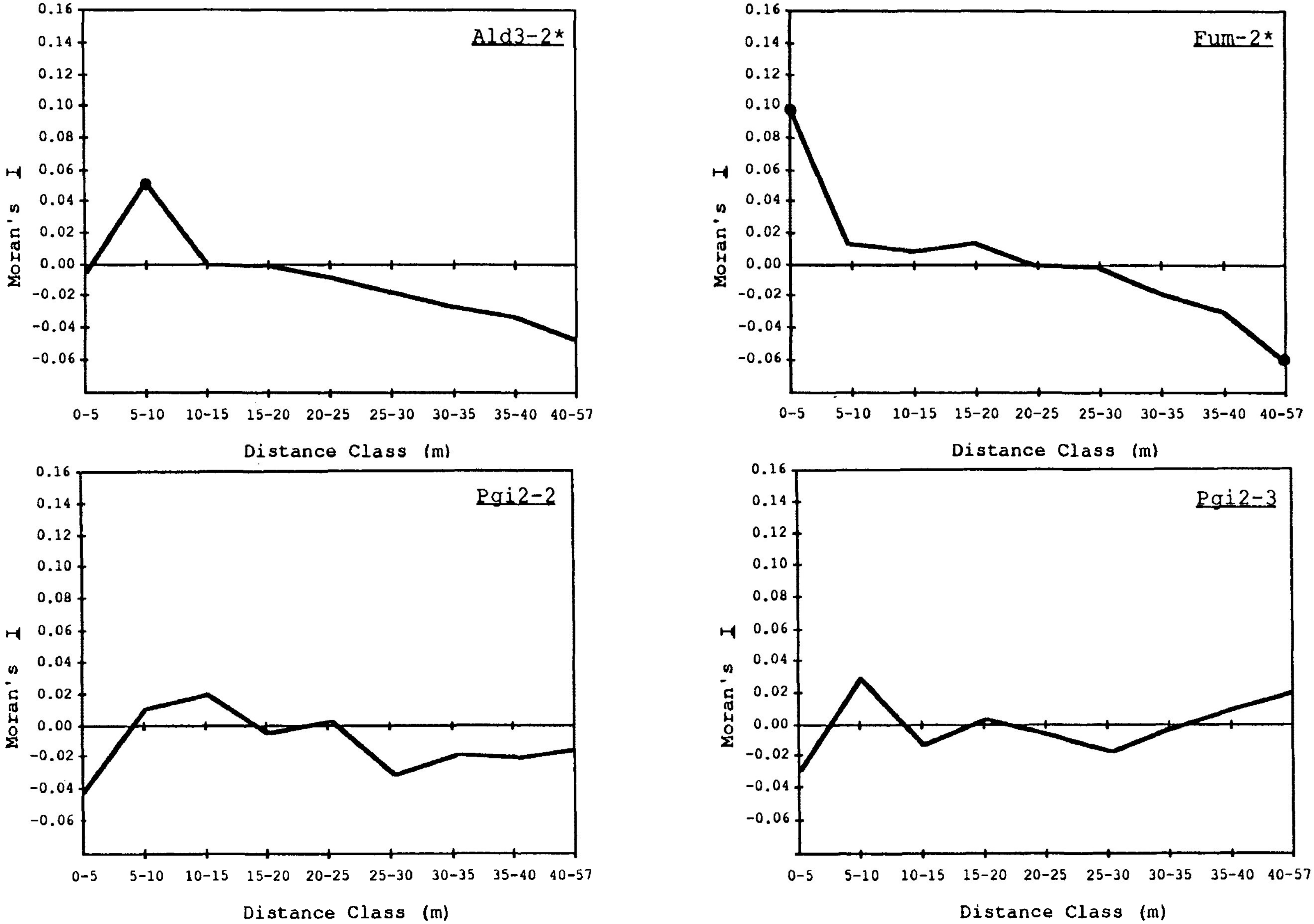

Figure 13. Correlograms for Twin City population. ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

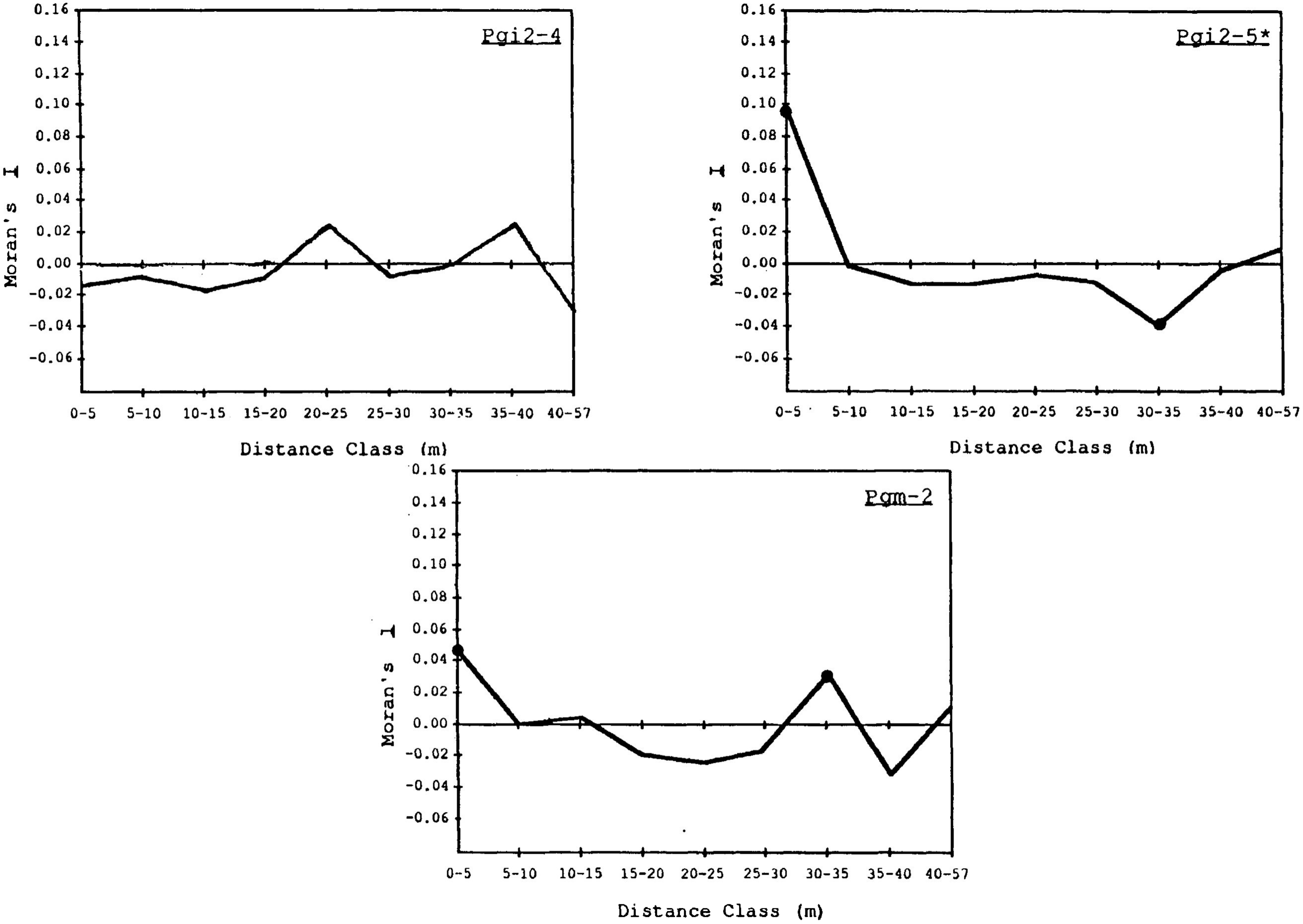

Figure 13. (Continued) (Twin City). ('*' correlogram significant at 90 percent confidence level; '●' Moran's I value significant at 95 percent confidence level)

confidence level). Therefore, when the series of autocorrelation coefficients (one I value for each distance class) was considered for each allele, a considerable proportion of the Bonferroni tests did not support the null hypothesis. Figure 14 shows the average correlograms that were constructed for each population. A summary of the distribution of significant autocorrelation coefficients over the distance classes by population is presented in Figure 15.

Overall, the correlograms were characterized by fluctuations in the magnitude and direction of the autocorrelation from distance class to distance class. This occurred in both significant and non-significant correlograms. Most, but not all, of the significant coefficients were part of correlograms that also were significant (Table 11). Trends in the significant correlograms were weak, but similar to those suggested by the mean correlograms and the overall frequency distribution of significant coefficients. In the Balmoral and Twin City populations, most of the significant correlograms showed positive autocorrelation at closer distance classes. In the significant Bog correlograms, it

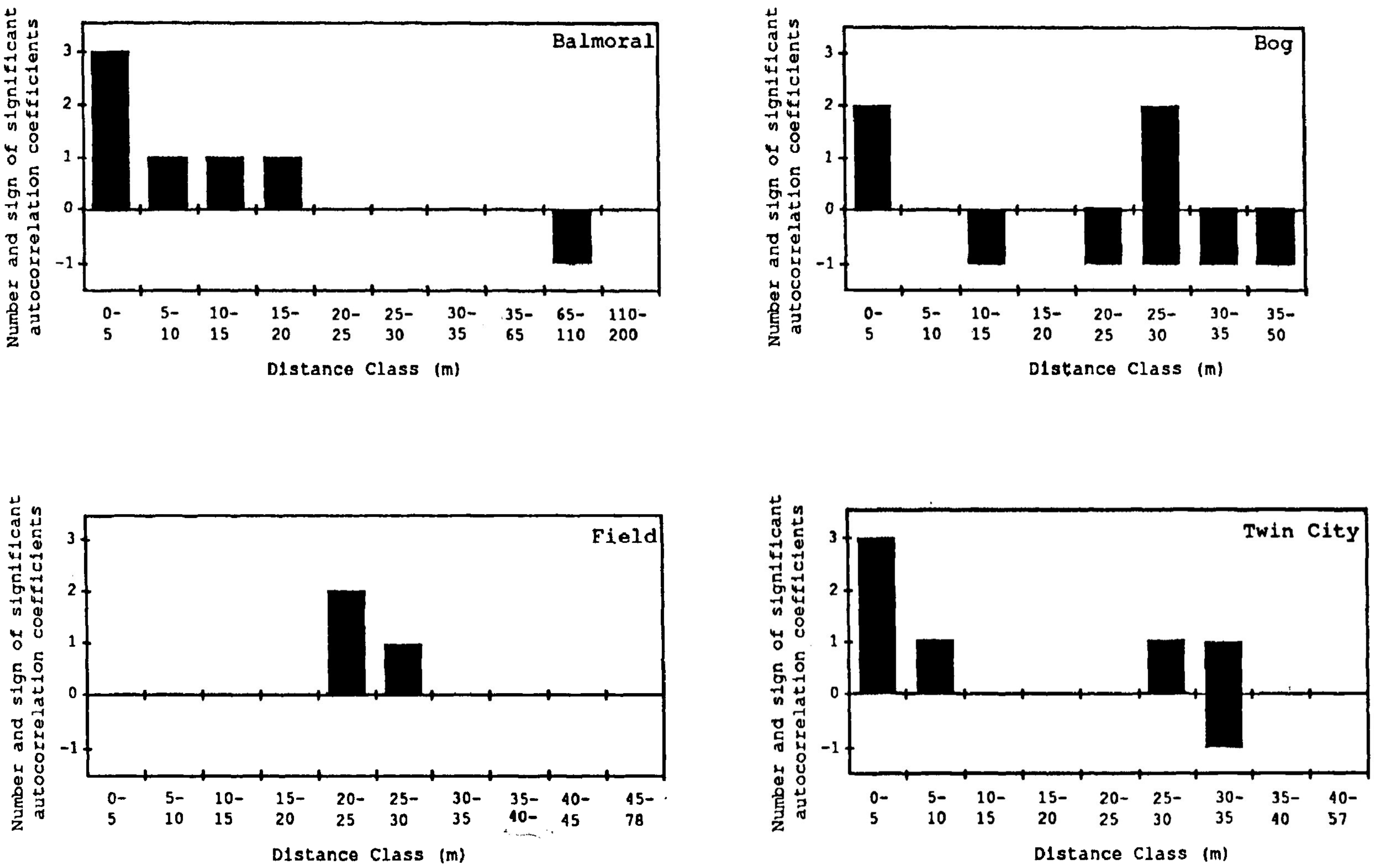

Figure 14. Frequency distribution of significant autocorrelation coefficients (Moran's I values) over distance classes for each of four tamarack populations.

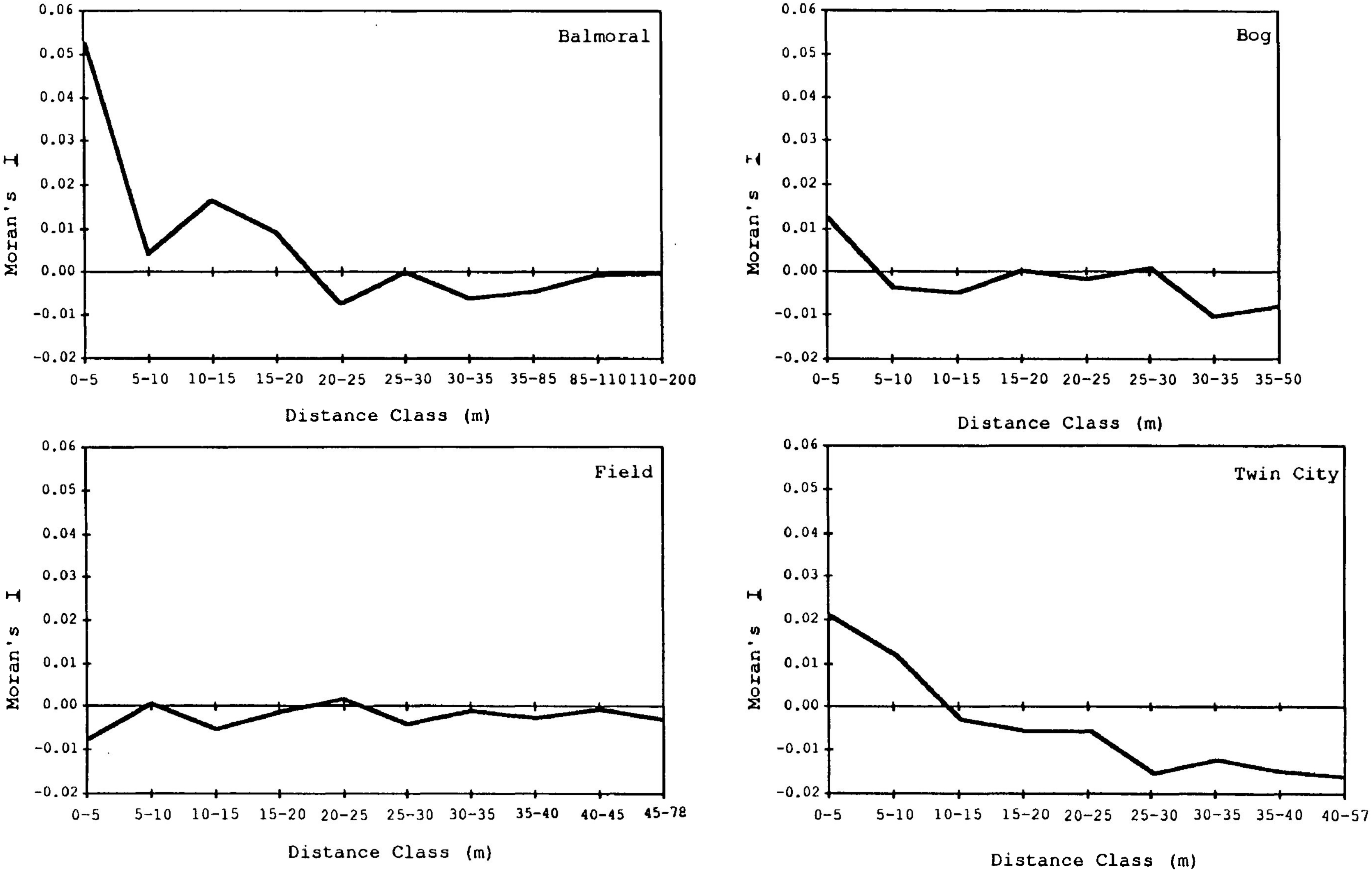

Figure 15. Mean correlograms by population for four tamarack populations.

was difficult to detect any trends. Finally, the significant correlograms in the Field population showed significant positive autocorrelation at middle distance classes.

The mean correlograms constructed for each population (Figure 14) also showed positive autocorrelation in close distance classes in the Balmoral and Twin City, and to a lesser extent, the Bog stand. The Field population correlogram showed a very weak trend in the reverse direction, with a small positive peak in the middle classes.

The frequency distribution of significant autocorrelation coefficients tended to show similar trends. As shown in Figure 15, in the Balmoral, Bog and Twin City populations, the first (0-5 m) distance classes had relatively high frequencies of significant, positive autocorrelation coefficients. Significant negative autocorrelation tended to occur in the more distant classes. In the Field population, the few significant autocorrelation coefficients that were present were positive coefficients that occurred in the middle distance classes (e.g. 20-25, 25-30 m).

DISCUSSION

POPULATION GENETIC CHARACTERISTICS

The levels of within-population variation observed in these four tamarack populations were relatively low compared to those reported for other tree species (e.g. Yeh and O'Malley, 1980; Guries and Ledig, 1981; Hamrick *et al*., 1981), and compared to those reported by Liu (1988) for tamarack. However, the levels of variation observed were very similar to those observed for western larch. Fins and Seeb (1986) reported that 19 western larch populations evaluated at 23 isozyme loci had an average of 1.5 alleles per locus, mean $\underline{H}_e$ of 0.061, mean $\underline{H}_o$ of 0.082, and an average of 40 percent of the loci polymorphic ($p < 1.0$). This was very close to the 1.95 alleles per locus, mean $\underline{H}_e$ of 0.066, mean $\underline{H}_o$ of 0.067 and average of 37.5 percent of loci polymorphic found in this tamarack study; closer than Liu's (1988) 1.5 alleles per locus, mean $\underline{H}_e$ of 0.091, mean $\underline{H}_o$ of 0.087 and 28.6 percent loci polymorphic (8 loci, 44 populations of tamarack).

In the present study, the upland population (Field) exhibited slightly but consistently lower $\underline{H}_o$ values than the three lowland populations (Balmoral, Bog and Twin

City). The upland population (Field) also had the greatest number of polymorphic loci,which may have been due to the larger numbers analyzed. In contrast, O'Reilly et al. (1985) observed both greater $\underline{H}_O$ and greater percentages of polymorphic isozyme loci in lowland versus upland Picea mariana populations in northern Ontario.

Significant Hardy-Weinberg deviations and relatively large $\underline{F}_{IS}$ statistics were the exceptions in this study. Seventeen (of 19) Chi-square tests showed no deviation from equilibrium genotype proportions, and the majority of $\underline{F}_{IS}$ statistics showed only very slight heterozygote excesses. These F_{IS} statistics were smaller than those reported in the Knowles et al. (1987) study of mating systems, and the Liu (1988) study of geographic variation in northern Ontario tamarack populations. It is most likely that the small deviations observed in the present study resulted from sampling error.

Given the close proximity of these four populations, their similarity is not surprising. Nei's genetic distances were very small, with only those for Pgi2 being larger than 0.0001. The largest genetic distances were pairings between the Field (upland) and each of the other (lowland) populations. These results were similar to those of O'Reilly et al. (1985) who observed less isozyme differentiation between lowland/lowland Picea mariana population pairings than between lowland /upland or upland/upland pairings.

The results of the allelic heterogeneity tests also reflected the presence of a unique allele for Idh in the Field, and highlighted some differences in frequencies of Pgi2 among the populations. The allelic heterogeneity in Fum appeared to reflect different proportions of alleles between the pair of younger and the pair of older populations (Balmoral and the Field, versus the Bog and Twin City, respectively).

SPATIAL GENETIC STRUCTURE WITHIN POPULATIONS

Summary of Analyses

The results of this investigation of spatial genetic structure within populations suggest that the alternate hypotheses of this thesis be accepted. These are: that the distribution of genotypes in local tamarack stands is not random, and that this departure from randomness can be observed in different populations. From the spatial autocorrelation analysis, 8.9 percent of the individual autocorrelation coefficients and 38.9 percent of the correlograms were significant (at 95 and 90 percent confidence levels, respectively). These significant coefficients and correlograms were distributed over all of the populations. The higher proportion of correlograms showing non-random distributions of genotypes was attributable not only to their lower confidence level, but also to the fact that the individual I values that were significant tended to be so at extreme probability levels (e.g. > 99.9 percent confidence level). In addition, weak spatial genetic structure was detected visually in 22.2 percent of the genotype maps.

Main Trends

The strongest trend observed was that of positive autocorrelation at close distance classes, or clumping of similar genotypes. Trees separated by relatively short distances (e.g. 0-5, 5-10 m) tended to be more similar than would have been expected if the distribution of genotypes was random.

Several factors could have contributed to the development of this structure or pattern. One factor might have been limited propagule dispersal. Most tamarack seeds are not likely to travel more than two tree lengths from their source (Duncan, 1954). At even one tree length from the source, Duncan reported that seedfall was less than 10 percent of that found at the base of the source. Tigerstedt et al. (1982) found, in their study of spatial genetic structure in Scots pine, that open pollinated seed families tend to disperse and land together, forming related clumps. This type of propagule dispersal could have contributed to the structure observed in the tamarack stands.

In addition, limited pollen dispersal is a factor that could have contributed to the degree of relatedness among seeds from a cohort, or from neighboring trees. Larix pollen is wingless, and therefore the majority is dispersed less than 50 m from the parent tree (Hall, 1986). However, the overall genetic similarity of the four populations must be noted, because of the role that occasional long distance pollen dispersal might have played in maintaining this similarity.

Knowles et al. (1987) observed low outcrossing rates in tamarack populations, suggesting that pollen and/or seed dispersal in tamarack may be limited. They also observed that their highest density stand (1006 trees per hectare, multi-locus outcrossing rate (t_m) = 0.908) had substantially higher outcrossing rates than the other four populations examined (t_m range: 0.537 - 0.768). The density of three of the four populations studied for this project was high: Bog, 3206 trees per hectare; Field, 2604 trees per hectare; and Twin City, 980 trees per hectare. In contrast, the density of the Balmoral population was only 230 trees per hectare. This population also showed a fairly strong autocorrelation trend.

The observed trend of positive autocorrelation at close distance classes also could have been caused by genetic differences among the seed that colonized the sites over space and time. As suggested by the work of Linhart et al. (1981), O'Reilly et al. (1982), King et al. (1984) and Schoen et al. (1985), it is possible that the contribution of individual tamarack to the gamete pool of a population is consistent neither from tree to tree, or year to year. Therefore, as noted by Roberds and Conkle (1984) in their study of genetic structure in Pinus taeda L. stands, some spatial genetic pattern may be the 'product of genetic sampling' that has important spatial and temporal components.

Patchiness in genetic constituency, or the tendency for near neighbors to be similar, also might have developed due to irregular availability of microsites for colonization. This does not appear to have been an important factor in the Field and Twin City populations, since these sites both were relatively homogeneous. However, in the Bog population, there were microsites that obviously were periodically unsuitable for establishment (e.g. the hollows of the flooded area). Indeed, the whole central portion of this stand had site and demographic characteristics that were considerably different from those on the perimeter. The Balmoral population did not have such obvious heterogeneity in site characteristics and establishment opportunities, but there was variation in water relations, and possibly fire history, across this stand.

Overall, the most striking environmental heterogeneity in the three organic sites was between the hummocks and hollows. This variation seemed likely to have been a factor influencing the distribution of established trees (e.g. there was no survival in the hollows), but not necessarily the distribution of successful genotypes. If the ages of the 1715 individuals and the ecological parameters associated with each tree had been evaluated, then the roles that microsite availability, chance effects and selection might have played in the development of spatial genetic structure could have been more clearly defined.

Results of other studies have suggested that electrophoretically detected variation either may be acted upon directly by selective forces, or may mark gene complexes that are acted upon by selection. For instance, Knowles et al. (1987), Shaw and Allard (1981), using results of electrophoretic analysis, discovered that embryo populations of tamarack and Douglas fir, respectively, showed substantially higher levels of inbreeding than did adult populations from the same stands. Shaw and Allard (1981), and Plessas and Strauss (1986) also found evidence that selection may act against inbred conifer seed or seedlings. In a series of reports, variation in allelic frequencies of electrophoretically detected loci in Avena barbata (wild oats) was correlated with variation in environmental conditions (Clegg and Allard, 1972; Hamrick and Allard, 1972; Hamrick and Holden, 1979). Linhart and others (1981) observed that spatial genetic structure in allozyme loci of Pinus ponderosa tended to be associated with particular biotic factors (e.g. aphid distribution, deer browsing). Schaal (1975) found significant correlation of edaphic factors with allozyme frequencies at 2 of 15 loci in Liatris cylindracea.

However, as was noted by Koehn (1978), even information showing correlation between variation in the environment and allozyme frequencies is inferential. The studies reported to date for plant species have fallen short of showing directly that selection operates on allozyme loci, or even on gene complexes that they may mark. Clearly, more investigation is needed to elucidate the relationships, if any, between electrophoretically detected variation and selective forces.

In addition to the tendency for neighboring trees to have similar genotypes, other trends were observed in this investigation. Some positive autocorrelation was observed at middle and large distance classes. This tended to occur in autocorrelations with rare alleles, and therefore reflected the relatively large distances between the few genotypes having the rare alleles. Negative autocorrelations at distant intervals, and fluctuations in the autocorrelation coefficients from distance class to distance class within a single correlogram also were observed. Both of these results may be explained by the lack of independence among the different autocorrelation coefficients in a single correlogram (Sokal and Wartenberg, 1983). If positive autocorrelation occurs in one distance class, then the probability that negative autocorrelation will occur in the others increases.

Comparison Among Populations

The difference in results among the four populations was intriguing. The Balmoral and Twin City populations showed the strongest tendency towards positive autocorrelation at close distance classes. The Balmoral population, which was still quite young, also covered the largest area. More than any of the others, this stand appeared to be composed of definite clumps of trees. These clumps were very widely spaced and seemed to be gradually colonizing the intervening areas. Because of the wide spacing between these clumps of trees, the closest distance class (i.e. 0-5 m) mostly contained tree pairs from within clumps. It is possible that trees within these clumps were relatively similar genetically because: they comprised a family grouping (e.g. a parent tree and offspring); they originated from a single, genetically distinct cohort; they originated from a limited number of cohorts; and/or they were established and growing under similar environmental conditions.

The Twin City population was mature and very densely spaced. Because of its high density, true clumps of trees were not readily discernable. However, often pairs or patches of trees were extremely close together (e.g. mature trees growing less than one meter apart). Positive autocorrelation in the closest distance classes again was observed, and attributable to factors similar to those suggested for the Balmoral population.

The results of spatial autocorrelation analysis of the Bog population showed some positive autocorrelation in the closest distance class, and then another peak in genetic similarity in the middle distance classes (e.g. 15-20, 25-30 m). This second peak probably reflected the distance across the central, flooded area of the stand. The perimeter trees appeared to be from a common establishment period. The central area contained a few stagnant individuals that were the same age as the perimeter trees, and then a cohort of trees from a very recent establishment period.

The results of the analysis of the Field population did not show any trend for positive autocorrelation at close distances. Instead, the only trend was a weak one of positive autocorrelation at middle distance classes. This old hay field appeared to have been colonized in successive waves, from one edge towards the center of the field. In portions, the stand was extremely dense (less than one meter between trees) and the trees were very vigorous. Overall, conditions appeared to have been nearly optimal for initial establishment (e.g. full sunlight, loamy soil), and for the distribution and mixing of pollen and of seed on the advancing edge of the stand.

The positive autocorrelation at intermediate distance classes in the Field was, as mentioned, attributable to the distance between the occurrences of a couple of alleles with low frequencies (Idh-2 and Pgi2-5). No visual pattern was detectable in the occurrence of these alleles, other than that when they were present they were distributed fairly evenly across the stand (e.g. Figure 16).

Methodology

Previously, spatial autocorrelation analysis mainly was used to examine macrogeographic rather than microgeographic patterns of variation (e.g. Bird et al., 1981; Sokal and Menozzi, 1982; Jensen, 1986; Sokal et al., 1986b). However, the results of this study show that spatial autocorrelation analysis using individual tree genotypes is a useful tool in the investigation of spatial genetic structure in plant populations. This microgeographic application can be added to those reported

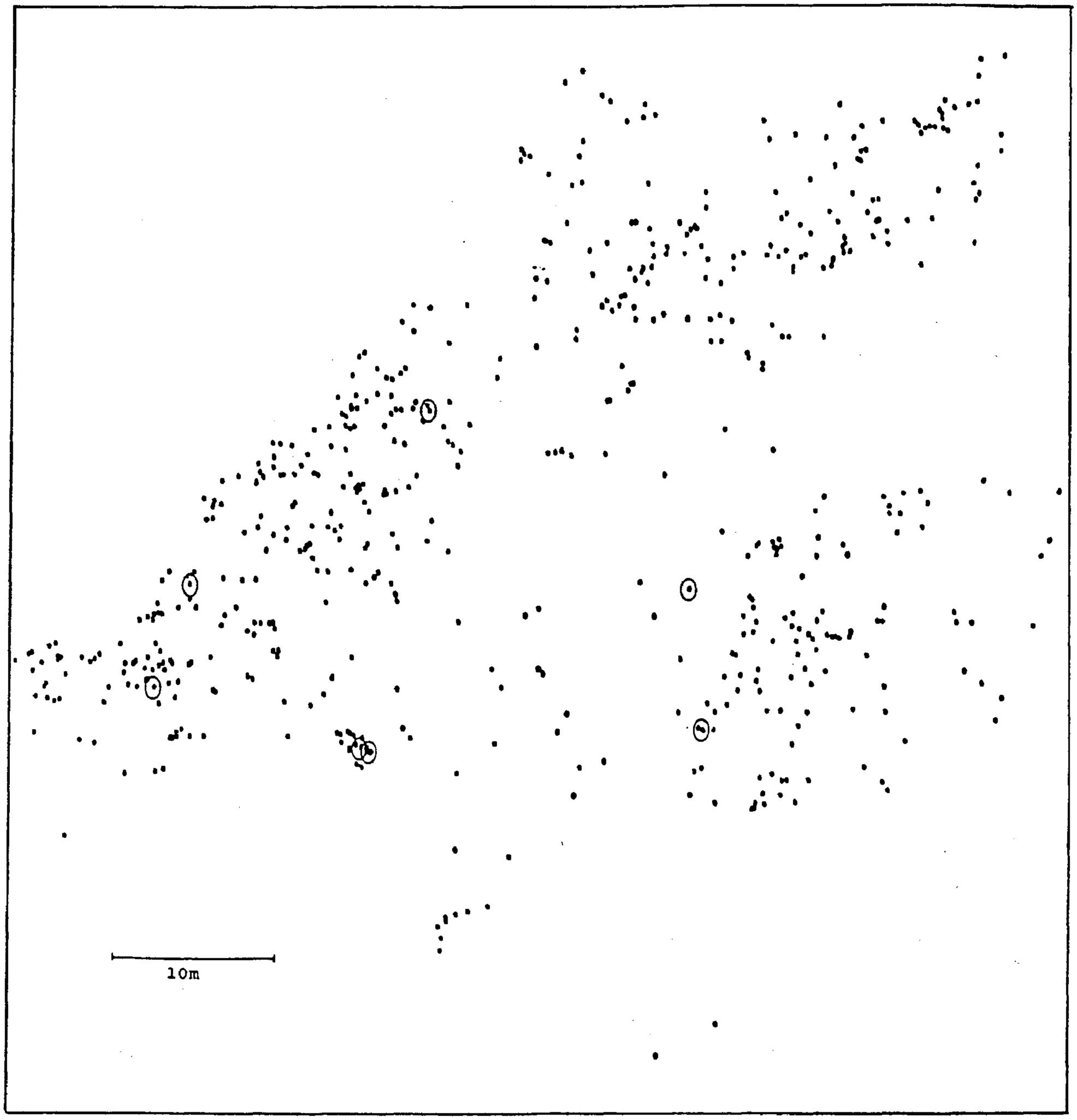

Figure 16. Spatial distribution of Idh-2 allele in Field population. (individual with: no Idh-2 allele - '•' ; one Idh-2 allele - '⊙')

by Sakai and Oden (1983), Reed and Burkhart (1985), Epperson and Clegg (1986), Waser (1987), Dewey and Heywood (1988), and Epperson and Allard (1989).

For other spatial autocorrelation analyses using genetic data, and for other studies of spatial genetic structure in populations, gene frequencies generally have been used as raw data (e.g. Waser, 1987; Sokal et al., 1986b). The present study of spatial genetic structure within populations was one of a select group that used individual plant genotypes (Epperson and Clegg, 1986; Dewey and Heywood, 1988; Epperson and Allard, 1989). In addition, this study analyzed the allozyme data from a very large number of individuals (1715).

As noted by Slatkin (1985), spatial autocorrelation analysis primarily is a descriptive tool, allowing the detection of patterns. However, its use does not result in the positive identification of the mechanisms that may have caused the development of these patterns (e.g. selection, gene flow). Instead, this application of spatial autocorrelation analysis has provided a reasonable starting point in the examination of spatial genetic structure in tamarack populations. Now, with these descriptive results showing evidence of pattern, investigation of the underlying contributory forces may be undertaken.

Finally, the results of this study suggest that visual examination of the distribution of genotypes in space can be of utility in the detection of spatial genetic structure. Pattern (usually clumping of similar genotypes) was detected visually in 22.0 percent of the plots examined. A striking 87.5 percent of these visually identified, non-random distributions of alleles were corroborated by significant autocorrelation statistics. This consistency between the visual detection of pattern (done first, without bias) and the statistical detection of pattern is notable. The spatial autocorrelation analysis did pick up additional spatial structure that was not discernable visually. However, the visual examination of genotype maps offered insight into the nature of the spatial pattern that was not obtainable from the spatial autocorrelation analysis (e.g. the tendency for trees with similar genotypes/allozyme scores to be near neighbors).

Implications for Tamarack Management

The modest amount of spatial genetic structure that was observed in these tamarack populations has some implications for the management of this species, in particular for management of its genetic resource. The implications which come to mind first are: material collected for breeding and artificial regeneration programs, material collected for genetic conservation programs, and material collected for further investigation of the species' genetic structure all should come from tamarack sampled both across space and, most likely, time. In addition, the results of the identification of a number of clones in this study suggest that vegetative reproduction by layering or sprouting may be a more important means of natural reproduction than previously reported.

CONCLUSIONS

Overall, the results of this study suggest that there is some pattern in the distribution of genotypes in tamarack stands, and that the characteristics of this deviation from randomness vary somewhat from population to population. The null hypothesis (that of random distribution of genotypes) was not supported by analysis of 8.9 percent of the autocorrelation coefficients, 38.9 percent of the correlograms and 22.2 percent of the genotype maps. The most prevalent, but not the only pattern detected was the tendency for near neighbors to be genetically similar. This pattern could be attributed to limited seed dispersal, limited pollen dispersal, colonization of areas by genetically different cohorts, and/or microhabitat heterogeneity and related selection pressures. More information is needed on the action of these forces in order to definitively assess their roles in the development of spatial genetic structure. However, given the paucity of evidence showing causal relationships between selection pressures and allozyme frequencies in plants, the spatial genetic structure detected in this study most likely is the result of family structure and/or genetic differences among colonizing cohorts. That is, the structure likely results from factors such as limited pollen flow, limited seed dispersal, consanguineous mating and/or temporal mating system variation.

By examining microgeographic patterns in the distribution of individual genotypes, this study used a fairly new application of spatial autocorrelation analysis. The results of this study support those of a number of investigators (including Linhart et al., 1981; Tigerstedt, 1982; Park and Fowler, 1982; Shea, 1985; and Sproule, 1988) who detected spatial genetic structure in other forest species.

In conclusion, spatial genetic structure appears to be a small but fairly consistent characteristic of tamarack populations. This structure should be considered in the management of tamarack, and further investigation into its development and manifestation would contribute to our understanding of the genecology of this species.

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APPENDICES

APPENDIX I

ALLOZYME SCORES AND TREE LOCATIONS FOR TAMARACK IN BALMORAL POPULATION

APPENDIX I. (Balmoral population)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
1	11	11	11	11	11	11	11	11	13	11	48.0	-2.1
2	11	11	11	11	11	11	11	11	13	11	53.6	7.3
3	11	11	11	11	11	11	11	11	11	11	56.1	6.2
4	11	11	11	11	11	11	11	11	13	11	55.4	3.3
5	11	11	11	11	11	11	11	11	12	11	66.5	2.4
6	11	11	11	11	11	11	11	11	12	11	76.3	3.7
8	11	11	11	11	11	11	11	11	14	11	74.7	10.3
9	11	11	11	11	11	11	11	11	33	11	77.0	11.2
10	11	11	11	11	11	11	11	11	12	11	85.7	5.1
11	11	11	11	11	11	11	11	11	13	11	90.9	6.6
12	11	11	11	11	11	11	11	11	23	11	91.3	4.8
13	11	11	11	11	11	11	11	11	12	11	88.1	-4.2
14	11	11	11	11	11	11	11	11	12	11	73.3	-10.1
15	11	11	11	11	11	11	11	11	33	11	78.8	-19.6
16	11	11	11	11	11	11	11	11	12	11	74.4	-22.3
17	11	11	11	11	11	11	11	11	23	11	71.6	-22.4
18	11	11	11	11	11	11	11	11	12	11	68.4	-21.5
19	11	11	11	11	12	11	11	11	23	11	65.5	-20.0
20	11	11	11	11	11	11	11	11	11	11	56.8	-24.4
21	11	11	11	11	11	11	11	11	14	11	56.5	-25.0
23	11	11	11	11	11	11	11	11	11	11	57.0	-32.8
24	11	11	11	22	11	11	11	11	23	11	55.5	-33.7
25	11	11	11	11	11	11	11	11	11	11	57.1	-34.9
26	11	11	11	11	11	11	11	11	11	11	59.6	-35.3
27	11	11	11	11	11	11	11	11	14	11	59.1	-38.9
28	11	11	11	11	11	11	11	11	34	11	56.3	-40.5
29	11	11	11	11	11	11	11	11	24	11	57.2	-42.7
30	11	11	11	11	11	11	11	11	11	11	62.0	-37.8
31	11	11	11	11	11	11	11	11	13	11	63.2	-38.2
32	11	11	11	11	11	11	11	11	44	11	63.9	-35.3
34	11	11	11	11	11	11	11	11	12	11	65.1	-33.9
35	11	11	11	11	11	11	11	11	13	11	62.3	-32.6
36	11	11	11	11	11	11	11	11	11	11	64.2	-31.8
38	11	11	11	11	11	11	11	11	11	11	64.8	-31.3
39	11	11	11	12	11	11	11	11	13	11	67.3	-33.8
40	11	11	11	11	12	11	11	11	11	11	71.9	-33.2
41	11	11	11	11	11	11	11	11	22	11	71.3	-35.0
43	11	11	11	11	11	11	11	11	13	11	77.3	-35.1
47	11	11	11	11	11	11	11	11	13	11	75.8	-28.7
48	11	11	11	11	11	11	11	11	33	11	81.0	-28.5
49	11	11	11	11	11	11	11	11	13	11	78.6	-30.4
50	11	11	11	11	11	11	11	11	11	11	87.1	-27.6
52	11	11	11	11	11	11	11	11	13	11	89.3	-41.4

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
53	11	11	11	11	11	11	11	11	12	11	87.9	-41.7
54	11	11	11	11	11	11	11	11	12	11	89.8	-54.3
55	11	11	11	11	11	11	11	11	12	11	83.4	-64.1
56	11	11	11	11	11	11	11	11	33	11	83.6	-65.2
58	11	11	11	11	11	11	11	11	12	11	79.0	-67.3
59	11	11	11	11	11	11	11	11	12	11	72.9	-65.5
60	11	11	11	11	11	11	11	11	12	11	71.1	-63.2
61	11	11	11	11	11	11	11	11	12	11	69.2	-64.1
62	11	11	11	11	11	11	11	11	22	12	67.1	-64.0
63	11	11	11	11	11	11	11	11	23	11	66.8	-59.8
64	11	11	11	11	11	11	11	11	13	11	67.3	-54.1
66	11	11	11	11	12	11	11	11	11	11	68.8	-51.7
67	11	11	11	11	11	11	11	11	13	11	65.1	-49.4
68	11	11	11	11	11	11	11	11	33	11	67.5	-46.7
69	11	11	11	11	11	11	11	11	11	12	52.5	-54.3
70	11	11	11	11	11	11	11	11	12	11	51.9	-57.0
71	11	11	11	11	11	11	11	11	14	11	47.2	-56.1
72	11	11	11	11	11	11	11	11	13	11	58.2	-60.0
73	11	11	11	11	11	11	11	11	11	11	58.6	-63.4
74	11	11	11	11	11	11	11	11	11	11	60.3	-63.3
75	11	11	11	11	11	11	11	11	11	11	46.9	-71.7
76	11	11	11	11	11	11	11	11	13	11	43.4	-59.9
77	11	11	11	11	11	11	11	11	23	11	42.5	-59.6
78	11	11	11	11	11	11	11	11	13	11	42.0	-57.8
79	11	11	11	11	11	11	11	11	12	11	38.4	-57.3
80	11	11	11	11	11	11	11	11	11	11	38.3	-52.5
81	11	11	11	11	11	11	11	11	11	11	30.7	-56.1
82	11	11	11	11	11	11	11	11	13	11	31.3	-55.5
83	11	11	11	11	12	11	11	11	11	11	30.2	-57.0
84	11	11	11	11	11	11	11	11	13	11	29.7	-58.7
85	11	11	11	11	11	11	11	11	11	11	26.7	-47.9
97	11	11	11	11	11	11	11	11	13	11	21.0	-50.8
98	11	11	11	11	11	11	11	11	11	11	20.1	-49.4
99	11	11	11	11	11	11	11	11	14	11	46.8	-30.4
100	11	11	11	11	11	11	11	11	13	11	47.5	-30.6
101	11	11	11	11	11	11	11	11	11	11	50.7	-14.6
102	11	11	11	11	11	11	11	11	34	11	52.0	-4.6
103	11	11	11	11	11	11	11	11	11	11	30.6	-34.7
105	11	11	11	11	11	11	11	11	11	11	30.1	-35.0
106	11	11	11	11	11	11	11	11	11	11	29.8	-34.6
108	11	11	11	11	11	11	11	11	11	11	29.9	-34.7
109	11	11	11	11	11	11	11	11	11	11	29.9	-35.2
110	11	11	11	11	11	11	11	11	11	11	29.5	-35.1
113	11	11	11	11	11	11	11	11	33	11	29.3	-27.7

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
114	11	11	11	11	11	11	11	11	13	11	25.3	-5.9
115	11	11	11	11	11	11	11	11	13	11	24.5	-2.9
116	11	11	11	11	11	11	11	11	11	11	13.6	-2.7
117	11	11	11	11	11	11	11	11	12	11	-15.6	1.0
118	11	11	11	11	11	11	11	11	14	11	0.0	-2.2
119	11	11	11	11	11	11	11	11	14	11	-0.7	-1.7
120	11	11	11	11	11	11	11	11	11	11	4.5	-13.1
122	11	11	11	11	11	11	11	11	22	11	28.0	-69.8
123	11	11	11	11	11	11	11	11	23	11	28.4	-70.7
124	11	11	11	11	11	11	11	11	12	12	29.4	-70.8
125	11	11	11	11	11	11	11	11	13	11	37.4	-70.4
126	11	11	11	11	11	11	11	11	11	11	37.4	-75.1
127	11	11	11	12	11	11	11	11	23	11	26.4	-76.3
132	11	11	11	12	11	11	11	11	12	11	37.5	-82.2
133	11	11	11	12	11	11	11	11	11	11	34.7	-88.9
134	11	11	11	12	11	11	11	11	11	11	34.9	-89.0
135	11	11	11	12	11	11	11	11	12	11	36.0	-89.2
136	11	11	11	11	11	11	11	11	13	11	34.1	-89.5
137	11	11	11	11	11	11	11	11	12	11	35.4	-90.3
138	11	11	11	11	11	11	11	11	23	11	36.6	-87.8
139	11	11	11	11	11	11	11	11	11	11	30.3	-92.3
140	11	11	11	11	11	11	11	11	11	11	37.0	-93.4
141	11	11	11	12	11	11	11	11	12	11	43.7	-94.8
142	11	11	11	12	11	11	11	11	12	11	44.1	-94.2
143	11	11	11	11	11	11	11	11	12	11	39.3	-98.3
144	11	11	11	11	11	11	11	11	13	11	40.0	-100.4
145	11	11	11	11	11	11	11	11	11	11	40.9	-101.4
146	11	11	11	11	11	11	11	11	11	11	35.1	-100.0
147	11	11	11	11	11	11	11	11	14	11	33.0	-101.3
148	11	11	11	11	11	11	11	11	13	11	31.9	-101.1
149	11	11	11	11	11	11	11	11	11	11	34.7	-103.0
150	11	11	11	11	11	11	11	11	14	11	27.5	-103.0
151	11	11	11	11	11	11	11	11	11	11	26.5	-106.3
152	11	11	11	11	11	11	11	11	12	11	28.3	-108.5
153	11	11	11	11	11	11	11	11	11	11	21.9	-110.0
154	11	11	11	11	11	11	11	11	12	11	20.0	-105.6
155	11	11	11	11	11	11	11	11	33	11	17.4	-108.1
156	11	11	11	11	11	11	11	11	13	11	14.8	-107.2
157	11	11	11	11	11	11	11	11	33	11	13.0	-104.6
158	11	11	11	11	11	11	11	11	11	11	13.9	-103.3
159	11	11	11	11	11	11	11	11	11	11	17.0	-101.0
160	11	11	11	11	11	11	11	11	23	11	20.7	-103.3
161	11	11	11	11	11	11	11	11	12	11	20.9	-104.2
162	11	11	11	11	11	11	11	11	13	11	21.8	-103.1

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
163	11	11	11	11	11	11	11	11	12	11	21.0	-102.1
164	11	11	11	11	11	11	11	11	11	11	24.1	-103.4
165	11	11	11	11	11	11	11	11	12	11	23.9	-99.8
166	11	11	11	11	11	11	11	11	13	11	13.9	-98.9
167	11	11	11	11	11	11	11	11	11	11	9.3	-99.5
168	11	11	11	11	11	11	11	11	24	11	11.6	-100.8
169	11	11	11	11	12	11	11	11	14	11	7.9	-98.9
170	11	11	11	11	11	11	11	11	11	11	8.2	-92.5
171	11	11	11	11	11	11	11	11	13	11	9.8	-90.7
172	11	11	11	11	11	11	11	11	12	11	15.5	-86.3
173	11	11	11	11	11	11	11	11	12	11	13.7	-84.2
174	11	11	11	11	11	11	11	11	12	11	13.3	-81.8
175	11	11	11	11	12	11	11	11	11	11	17.7	-80.1
176	11	11	11	11	11	11	11	11	12	11	16.4	-79.7
177	11	11	11	11	11	11	11	11	13	11	20.7	-81.6
178	11	11	11	11	11	11	11	11	13	11	22.9	-75.1
179	11	11	11	11	11	11	11	11	23	11	19.2	-74.9
180	11	11	11	11	11	11	11	11	13	11	8.8	-73.7
181	11	11	11	11	11	11	11	11	33	11	6.6	-77.4
182	11	11	11	11	11	11	11	11	33	11	5.8	-76.4
183	11	11	11	11	11	11	11	11	11	15	7.5	-72.0
184	11	11	11	11	11	11	11	11	12	11	11.4	-69.4
185	11	11	11	11	11	11	11	11	12	11	13.9	-61.4
186	11	11	11	11	11	11	11	11	11	11	2.9	-66.6
187	11	11	11	11	11	11	11	11	15	11	-0.2	-68.0
188	11	11	11	11	11	11	11	11	33	11	10.5	-56.4
189	11	11	11	11	11	11	11	11	11	11	4.2	-50.1
190	11	11	11	11	11	11	11	11	11	11	-12.5	-14.9
191	11	11	11	11	11	11	11	11	11	11	-11.6	-14.6
192	11	11	11	11	11	11	11	11	11	11	-11.1	-15.1
193	11	11	11	11	11	11	11	11	13	11	-10.7	-15.5
194	11	11	11	11	11	11	11	11	13	11	-9.8	-17.4
195	11	11	11	11	11	11	11	11	11	11	-10.5	-26.0
196	11	11	11	11	11	11	11	11	13	11	-2.9	-30.6
197	11	11	11	11	11	11	11	11	44	11	-3.2	-34.7
198	11	11	11	11	11	11	11	11	13	11	-6.0	-35.5
199	11	11	11	11	11	11	11	11	34	11	-7.3	-36.1
200	11	11	11	11	11	11	11	11	13	11	-27.2	-30.8
201	11	11	11	11	11	11	11	11	22	11	-12.0	-41.5
202	11	11	11	11	11	11	11	11	15	11	-11.6	-40.1
203	11	11	11	11	11	11	11	11	11	11	-9.4	-40.4
204	11	11	11	11	11	11	11	11	14	11	-10.2	-42.1
205	11	11	11	11	11	11	11	11	15	11	-12.1	-42.8
206	11	11	11	11	11	11	11	11	11	11	-7.9	-43.1

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
207	11	11	11	11	11	11	11	11	11	11	-4.7	-39.8
208	11	11	11	11	11	11	11	11	13	11	-4.2	-41.7
209	11	11	11	11	11	11	11	11	14	11	-12.6	-44.0
210	11	11	11	11	11	11	11	11	22	11	-13.0	-49.0
211	11	11	11	11	11	11	11	11	44	11	-9.6	-47.1
212	11	11	11	11	11	11	11	11	11	11	-10.8	-42.4
213	11	11	11	11	11	11	11	11	22	11	-10.4	-52.2
214	11	11	11	11	11	11	11	11	11	11	-9.4	-53.3
215	11	11	11	11	12	11	11	11	12	11	-11.1	-53.3
216	11	11	11	11	11	11	11	11	11	11	-30.2	-53.5
217	11	11	11	11	11	11	11	11	12	11	-24.3	-56.5
218	11	11	11	11	11	11	11	11	11	11	-24.9	-58.6
219	11	11	11	11	11	11	11	11	23	11	-24.2	-58.8
220	11	11	11	11	11	11	11	11	12	11	-22.1	-59.7
221	11	11	11	11	11	11	11	11	33	11	-4.8	-65.3
222	11	11	11	11	11	11	11	11	11	11	-4.4	-59.3
223	11	11	11	11	11	11	11	11	11	11	-1.2	-55.2
224	11	11	11	11	11	11	11	11	33	11	-6.1	-64.3
225	11	11	11	11	11	11	11	11	11	11	-4.7	-68.2
226	11	11	11	11	11	11	11	11	11	11	-6.1	-69.0
227	11	11	11	11	12	11	11	11	14	11	-6.9	-67.1
228	11	11	11	11	11	11	11	11	11	11	-5.0	-71.5
229	11	11	11	11	11	11	11	11	12	11	-3.1	-74.2
230	11	11	11	11	11	11	11	11	13	11	0.5	-70.9
231	11	11	11	11	11	11	11	11	11	11	2.6	-71.3
232	11	11	11	11	11	11	11	11	33	11	-5.8	-76.3
233	11	11	11	11	11	11	11	11	11	11	-6.5	-76.7
234	11	11	11	11	11	11	11	11	16	11	-5.6	-78.0
235	11	11	11	11	11	11	11	11	11	11	-4.0	-79.2
236	11	11	11	11	11	11	11	11	12	11	-3.3	-79.2
237	11	11	11	11	11	11	11	11	11	11	-0.3	-83.0
238	11	11	11	11	11	11	11	11	11	11	0.2	-84.0
239	11	11	11	11	11	11	11	11	12	11	-4.0	-81.6
240	11	11	11	11	11	11	11	11	11	11	-2.7	-89.4
241	11	11	11	11	11	11	11	11	12	11	-3.2	-91.7
242	11	11	11	11	11	11	11	11	12	11	-5.9	-94.0
243	11	11	11	11	12	11	11	11	11	11	-4.6	-95.8
244	11	11	11	11	11	11	11	11	12	11	-1.2	-93.9
245	11	11	11	11	11	11	11	11	11	11	0.6	-100.0
246	11	11	11	11	11	11	11	11	12	11	-1.3	-100.9
247	11	11	11	11	11	11	11	11	13	11	0.4	-105.0
248	11	11	11	11	11	11	11	11	13	11	-2.2	-104.8
249	11	11	11	11	11	11	11	11	13	11	-2.7	-105.1
250	11	11	11	11	11	11	11	11	13	11	-4.6	-106.8

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
251	11	11	11	11	11	11	11	11	13	11	4.9	-106.3
252	11	11	11	11	11	11	11	11	12	11	9.0	-108.8
253	11	11	11	11	11	11	11	11	11	11	0.9	-112.0
255	11	11	11	11	11	11	11	11	11	11	11.5	-112.7
256	11	11	11	11	11	11	11	11	12	11	18.9	-111.8
257	11	11	11	11	11	11	11	11	11	11	11.3	-114.1
258	11	11	11	11	11	11	11	11	13	11	11.2	-114.6
259	11	11	11	11	11	11	11	11	14	11	12.3	-115.1
260	11	11	11	11	11	11	11	11	13	11	7.1	-118.0
261	11	11	11	11	11	11	11	11	12	11	6.1	-118.4
262	11	11	11	11	11	11	11	11	13	11	2.5	-117.8
263	11	11	11	11	11	11	11	11	11	12	2.4	-118.3
264	11	11	11	11	11	11	11	11	13	11	1.3	-118.8
265	11	11	11	11	11	11	11	11	13	11	-1.2	-120.1
266	11	11	11	11	11	11	11	11	13	11	-8.7	-117.8
267	11	11	11	11	11	11	11	11	13	11	-13.0	-114.6
268	11	11	11	11	11	11	11	11	11	11	-13.4	-112.6
269	11	11	11	11	11	11	11	11	11	11	-13.3	-112.8
270	11	11	11	11	11	11	11	11	13	11	-11.6	-112.7
271	11	11	11	11	11	11	11	11	13	11	-11.2	-113.2
272	11	11	11	11	11	11	11	11	33	11	-14.1	-112.5
273	11	11	11	11	11	11	11	11	14	11	-14.4	-112.2
274	11	11	11	11	11	11	11	11	11	11	-14.7	-108.9
275	11	11	11	11	11	11	11	11	12	11	-18.9	-107.5
276	11	11	11	11	11	11	11	11	33	11	-23.5	-105.1
277	11	11	11	11	11	11	11	11	11	11	-14.9	-107.0
278	11	11	11	11	11	11	11	11	11	11	-20.6	-102.1
279	11	11	11	11	11	11	11	11	11	11	-20.5	-100.1
280	11	11	11	11	11	11	11	11	13	11	-15.0	-100.1
282	11	11	11	11	11	11	11	11	12	11	-9.1	-105.8
283	11	11	11	11	11	11	11	11	11	11	-9.4	-105.8
284	11	11	11	11	11	11	11	11	11	11	-8.9	-104.5
285	11	11	11	11	11	11	11	11	12	11	-7.9	-100.7
286	11	11	11	11	11	11	11	11	33	11	-6.2	-99.3
287	11	11	11	11	11	11	11	11	14	11	-8.2	-98.0
288	11	11	11	11	11	11	11	11	11	14	-9.4	-97.3
289	11	11	11	11	11	11	11	11	11	11	-11.0	-83.8
290	11	11	11	11	11	11	11	11	11	11	-10.1	-80.0
291	11	11	11	11	11	11	11	11	11	11	-9.7	-80.3
292	11	11	11	11	11	11	11	11	13	11	-7.2	-79.8
293	11	11	11	11	11	11	11	11	23	11	-12.5	-80.7
294	11	11	11	11	11	11	11	11	12	11	-14.0	-77.5
295	11	11	11	11	11	11	11	11	11	11	-9.4	-71.8
296	11	11	11	11	11	11	11	11	14	11	-6.6	-71.0

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
297	11	11	11	11	11	11	11	11	12	11	-10.2	-70.0
298	11	11	11	11	11	11	11	11	13	11	-13.2	-67.3
299	11	11	11	11	11	11	11	11	22	11	-10.5	-67.6
300	11	11	11	11	11	11	11	11	11	11	-9.5	-66.0
301	11	11	11	11	11	11	11	11	12	11	-27.5	-66.7
303	11	11	11	11	11	11	11	11	11	11	-27.2	-60.2
304	11	11	11	11	11	11	11	11	44	11	-40.6	-55.0
305	11	11	11	11	11	11	11	11	12	11	-39.6	-52.7
306	11	11	11	11	11	11	11	11	14	11	-32.8	-41.6
307	11	11	11	11	11	11	11	11	11	11	-40.1	-43.8
308	11	11	11	11	11	11	11	11	13	11	-40.6	-37.5
309	11	11	11	11	11	11	11	11	12	11	-37.7	-38.0
310	11	11	11	11	11	11	11	11	11	11	-38.3	-36.0
311	11	11	11	11	11	11	11	11	12	11	-34.9	-36.9
312	11	11	11	11	11	11	11	11	13	11	-34.2	-37.0
313	11	11	11	11	11	11	11	11	11	11	-30.7	-35.7
314	11	11	11	11	11	11	11	11	14	11	-36.9	-34.0
315	11	11	11	11	11	11	11	11	13	11	-36.1	-29.0
316	11	11	11	11	11	11	11	11	12	11	-36.1	-28.5
317	11	11	11	11	11	11	11	11	11	11	-35.4	-23.8
318	11	11	11	11	11	11	11	11	11	11	-34.0	-14.5
319	11	11	11	11	11	11	11	11	34	11	-37.5	-12.0
320	11	11	11	11	11	11	11	11	13	11	-44.7	-7.5
321	11	11	11	11	11	11	11	11	11	11	-44.7	-9.0
322	11	11	11	11	11	11	11	11	11	11	-49.2	-8.9
323	11	11	11	11	11	11	11	11	11	11	-45.8	-13.6
324	11	11	11	11	11	11	11	11	13	11	-51.9	-19.0
325	11	11	11	11	11	11	11	11	23	11	-57.0	-20.0
326	11	11	11	11	11	11	11	11	11	11	-57.5	-20.1
327	11	11	11	11	11	11	11	11	12	11	-56.0	-21.4
328	11	11	11	11	11	11	11	11	12	11	-52.7	-25.4
329	11	11	11	11	11	11	11	11	14	11	-51.0	-27.4
330	11	11	11	11	11	11	11	11	12	11	-54.0	-31.6
331	11	11	11	11	11	11	11	11	11	11	-48.8	-36.6
332	11	11	11	11	11	11	11	11	33	11	-53.5	-38.3
333	11	11	11	11	11	11	11	11	23	12	-49.7	-44.7
334	11	11	11	11	11	11	11	11	11	11	-44.8	-59.2
335	11	11	11	11	11	11	11	11	22	11	-40.0	-60.8
336	11	11	11	11	11	11	11	11	11	11	-49.9	-55.0
337	11	11	11	11	11	11	11	11	12	11	-45.8	-62.5
338	11	11	11	11	11	11	11	11	24	11	-38.7	-68.0
339	11	11	11	11	11	11	11	11	11	11	-39.7	-68.9
340	11	11	11	11	11	11	11	11	11	11	-41.5	-72.9
341	11	11	11	11	11	11	11	11	14	11	-43.2	-72.6

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
342	11	11	11	11	12	11	11	11	12	11	-26.2	-73.1
343	11	11	11	11	11	11	11	11	12	11	-40.2	-74.3
344	11	11	11	11	11	11	11	11	13	11	-40.5	-76.4
345	11	11	11	11	11	11	11	11	12	11	-40.3	-77.8
346	11	11	11	11	11	11	11	11	24	11	-50.5	-78.0
347	11	11	11	11	11	11	11	11	13	11	-50.2	-80.7
348	11	11	11	11	11	11	11	11	33	11	-43.8	-83.7
349	11	11	11	11	11	11	11	11	22	11	-43.7	-84.3
350	11	11	11	11	11	11	11	11	34	11	-36.7	-87.7
351	11	11	11	11	11	11	11	11	13	11	-27.5	-90.3
352	11	11	11	11	11	11	11	11	12	11	-20.4	-89.9
353	11	11	11	11	11	11	11	11	13	11	-20.9	-92.5
355	11	11	11	11	11	11	11	11	13	11	-18.4	-93.4
356	11	11	11	11	11	11	11	11	11	11	-21.9	-94.6
357	11	11	11	11	11	11	11	11	12	11	-34.5	-94.3
358	11	11	11	11	11	11	11	11	11	11	-34.2	-95.8
359	11	11	11	11	11	11	11	11	25	11	-35.2	-96.1
360	11	11	11	11	11	11	11	11	12	11	-30.6	-96.2
361	11	11	11	11	11	11	11	11	11	11	-28.7	-103.7
362	11	11	11	11	11	11	11	11	13	11	-29.3	-104.3
363	11	11	11	11	11	11	11	11	13	11	-36.3	-105.6
364	11	11	11	11	11	11	11	11	13	11	-37.1	-107.5
365	11	11	11	11	11	11	11	11	11	11	-37.3	-109.9
366	11	11	11	11	11	11	11	11	12	11	-35.0	-110.6
367	11	11	11	11	11	11	11	11	11	11	-33.7	-115.1
368	11	11	11	11	11	11	11	11	13	11	-36.7	-117.7
369	11	11	11	11	11	11	11	11	12	11	-36.1	-118.4
370	11	11	11	11	11	11	11	11	34	11	-25.1	-117.0
371	11	11	11	11	11	11	11	11	11	11	-26.5	-118.2
372	11	11	11	11	11	11	11	11	12	11	-26.3	-122.7
373	11	11	11	11	11	11	11	11	24	11	-24.9	-122.2
374	11	11	11	11	11	11	11	11	11	11	-19.2	-120.4
375	11	11	11	11	11	11	11	11	13	11	-13.3	-120.6
376	11	11	11	11	11	11	11	11	34	11	-8.0	-122.0
377	11	11	11	11	11	11	11	11	11	11	-8.8	-125.5
378	11	11	11	11	11	11	11	11	11	11	-7.1	-122.4
379	11	11	11	11	11	11	11	11	23	11	-5.1	-124.3
380	11	11	11	11	11	11	11	11	12	11	-13.3	-131.0
381	11	11	11	11	11	11	11	11	11	11	-14.8	-128.4
382	11	11	11	11	11	11	11	11	11	11	-22.8	-129.1
383	11	11	11	12	11	11	11	11	11	11	-26.9	-127.2
384	11	11	11	11	11	11	11	11	24	11	-28.6	-125.5
385	11	11	11	11	11	11	11	11	22	11	-29.3	-132.3
386	11	11	11	11	11	11	11	11	12	11	-29.1	-133.4

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
388	11	11	11	11	11	11	11	11	23	11	-28.9	-134.5
389	11	11	11	11	11	11	11	11	12	11	-28.8	-135.2
390	11	11	11	11	11	11	11	11	11	11	-25.6	-134.3
391	11	11	11	11	11	11	11	11	13	11	-25.8	-135.2
392	11	11	11	11	11	11	11	11	13	11	-31.2	-138.2
393	11	11	11	11	11	11	11	11	11	11	-31.3	-138.1
394	11	11	11	11	11	11	11	11	24	11	-33.2	-138.8
395	11	11	11	11	11	11	11	11	14	11	-36.7	-138.8
396	11	11	11	11	11	11	11	11	11	11	-39.6	-140.6
397	11	11	11	12	11	11	11	11	13	11	-44.1	-138.2
398	11	11	11	11	11	11	11	11	13	11	-45.2	-133.6
399	11	11	11	11	11	11	11	11	11	11	-39.3	-137.0
400	11	11	11	11	11	11	11	11	23	11	-39.0	-136.0
401	11	11	11	11	11	11	11	11	13	11	-40.2	-134.6
402	11	11	11	11	11	11	11	11	13	11	-36.3	-133.8
403	11	11	11	11	11	11	11	11	11	11	-35.0	-132.4
404	11	11	11	11	11	11	11	11	14	11	-33.9	-129.7
405	11	11	11	11	11	11	11	11	13	11	-34.3	-128.2
406	11	11	11	11	11	11	11	11	11	11	-36.1	-129.3
407	11	11	11	11	11	11	11	11	11	11	-36.8	-128.8
408	11	11	11	11	11	11	11	11	11	11	-41.5	-130.0
409	11	11	11	11	11	11	11	11	13	11	-42.6	-132.1
410	11	11	11	11	11	11	11	11	13	11	-40.5	-130.4
411	11	11	11	11	11	11	11	11	12	11	-47.2	-129.7
412	11	11	11	11	11	11	11	11	33	11	-47.5	-127.5
413	11	11	11	11	11	11	11	11	13	11	-47.9	-131.2
414	11	11	11	11	12	11	11	11	33	11	-47.4	-126.8
415	11	11	11	11	12	11	11	11	13	13	-47.1	-126.3
416	11	11	11	11	11	11	11	11	13	11	-44.1	-123.8
417	11	11	11	11	11	11	11	11	11	11	-40.2	-113.3
418	11	11	11	11	11	11	11	11	11	11	-56.8	-119.6
419	11	11	11	11	12	11	11	11	12	11	-58.9	-118.8
420	11	11	11	11	11	11	11	11	14	11	-57.4	-117.4
421	11	11	11	11	11	11	11	11	11	11	-58.0	-111.5
422	11	11	11	11	11	11	11	11	12	11	-54.6	-110.1
423	11	11	11	11	11	11	11	11	11	11	-54.1	-109.1
424	11	11	11	11	11	11	11	11	12	11	-53.9	-109.2
425	11	11	11	11	11	11	11	11	12	11	-50.9	-108.5
426	11	11	11	11	11	11	11	11	13	11	-50.4	-110.8
427	11	11	11	11	11	11	11	11	13	11	-49.6	-107.1
428	11	11	11	11	11	11	11	11	13	11	-47.4	-109.2
429	11	11	11	11	11	11	11	11	12	11	-46.3	-109.4
430	11	11	11	11	11	11	11	11	24	11	-45.6	-100.3
431	11	11	11	11	11	11	11	11	11	11	-45.1	-99.0

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
432	11	11	11	11	11	11	11	11	13	11	-40.2	-100.0
433	11	11	11	11	11	11	11	11	14	11	-52.5	-104.7
434	11	11	11	11	11	11	11	11	12	11	-53.4	-105.0
435	11	11	11	11	11	11	11	11	14	11	-41.8	-105.2
436	11	11	11	11	11	11	11	11	12	11	-54.7	-93.8
437	11	11	11	11	11	11	11	11	23	11	-59.4	-89.1
438	11	11	11	11	11	11	11	11	12	11	-57.7	-85.2
439	11	11	11	11	11	11	11	11	13	11	-54.7	-80.4
440	11	11	11	11	11	11	11	11	11	11	-56.4	-77.8
441	11	11	11	11	11	11	11	11	11	11	-65.0	-81.0
442	11	11	11	11	11	11	11	11	13	11	-65.8	-79.7
443	11	11	11	11	11	11	11	11	11	11	-69.5	-83.4
444	11	11	11	11	11	11	11	11	13	11	-70.0	-80.6
445	11	11	11	11	11	11	11	11	13	11	-67.9	-78.3
446	11	11	11	11	11	11	11	11	12	11	-63.9	-76.8
447	11	11	11	11	11	11	11	11	13	11	-60.9	-73.0
448	11	11	11	11	11	11	11	11	13	11	-60.9	-72.9
449	11	11	11	11	11	11	11	11	13	11	-60.3	-73.8
450	11	11	11	11	11	11	11	11	22	11	-59.7	-73.0
451	11	11	11	11	11	11	11	11	13	11	-57.1	-70.2
452	11	11	11	11	11	11	11	11	33	11	-55.1	-71.2
453	11	11	11	11	11	11	11	11	33	11	-55.7	-69.8
454	11	11	11	11	11	11	11	11	12	11	-55.3	-69.7
455	11	11	11	11	11	11	11	11	12	11	-57.1	-69.8
456	11	11	11	11	11	11	11	11	22	11	-56.2	-68.3
457	11	11	11	11	11	11	11	11	13	11	-56.4	-67.4
458	11	11	11	11	11	11	11	11	13	11	-56.7	-67.2
459	11	11	11	11	11	11	11	11	11	11	-50.3	-70.2
460	11	11	11	11	11	11	11	11	33	11	-53.5	-61.6
461	11	11	11	11	11	11	11	11	12	11	-53.8	-61.8
462	11	11	11	11	11	11	11	11	13	11	-64.6	-70.4
463	11	11	11	11	11	11	11	11	11	11	-66.5	-70.2
464	11	11	11	11	11	11	11	11	13	11	-71.9	-71.7
465	11	11	11	11	11	11	11	11	12	11	-71.7	-70.0
467	11	11	11	11	11	11	11	11	33	11	-73.1	-69.8
468	11	11	11	11	12	11	11	11	12	11	-68.2	-66.9
469	11	11	11	11	11	11	11	11	13	11	-69.0	-60.4
470	11	11	11	11	11	11	11	11	23	11	-68.2	-60.6
471	11	11	11	11	11	11	11	11	11	11	-68.7	-57.7
472	11	11	11	11	11	11	11	11	33	11	-64.0	-56.8
473	11	11	11	11	11	11	11	11	12	11	-64.1	-56.3
474	11	11	11	11	11	11	11	11	12	11	-65.1	-54.7
475	11	11	11	11	11	11	11	11	33	11	-60.4	-58.7
476	11	11	11	11	11	11	11	11	11	11	-60.0	-55.1

APPENDIX I. (Cont.) (Balmoral)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
477	11	11	11	11	11	11	11	11	11	11	-60.0	-42.2
478	11	11	11	11	11	11	11	11	11	11	-69.2	-45.9
480	11	11	11	11	11	11	11	11	13	11	-71.0	-41.7
481	11	11	11	11	11	11	11	11	11	11	-69.7	-40.5
482	11	11	11	11	12	11	11	11	13	11	-73.7	-39.3
483	11	11	11	11	11	11	11	11	13	11	-68.6	-38.4
484	11	11	11	11	11	11	11	11	13	11	-71.9	-33.0
485	11	11	11	11	11	11	11	11	12	11	-77.1	-31.9
487	11	11	11	11	11	11	11	11	12	11	-58.8	-28.6
489	11	11	11	11	11	11	11	11	13	11	-57.1	-26.8
490	11	11	11	11	11	11	11	11	11	11	-63.3	-14.8
491	11	11	11	11	11	11	11	11	23	11	-67.8	-14.0
492	11	11	11	11	11	11	11	11	11	11	-68.3	-14.5
493	11	11	11	11	11	11	11	11	12	11	-67.7	-17.3
494	11	11	11	11	11	11	11	11	12	11	-67.7	-20.6
495	11	11	11	11	11	11	11	11	12	11	-70.2	-18.3
496	11	11	11	11	11	11	11	11	13	11	-82.1	-22.0
497	11	11	11	11	11	11	11	11	11	12	-85.2	-29.3
498	11	11	11	11	11	11	11	11	14	11	-84.8	-35.1
499	11	11	11	11	11	11	11	11	13	11	-81.4	-36.4
500	11	11	11	11	11	11	11	11	13	11	-72.8	-53.6
501	11	11	11	11	12	11	11	11	11	11	-75.9	-50.4
502	11	11	11	11	11	11	11	11	33	11	-37.1	-36.1
503	11	11	11	11	11	11	11	11	11	11	-25.0	-30.9
504	11	11	11	11	11	11	11	11	13	11	-33.5	-62.3
505	11	11	11	11	11	11	11	11	11	11	-45.6	-39.3

APPENDIX II

ALLOZYME SCORES AND TREE LOCATIONS FOR TAMARACK IN BOG POPULATION

APPENDIX II. (Bog population)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1014	11	11	11	11	11	11	11	11	11	11	-47.2	10.9
1015	11	11	11	11	11	11	11	11	11	12	-47.2	9.1
1016	11	11	11	11	11	11	11	11	11	13	-47.3	7.9
1017	11	11	11	11	11	11	11	11	11	11	-46.4	9.0
1018	11	11	11	11	12	11	11	11	11	33	-46.3	8.8
1019	11	11	11	11	11	11	11	11	11	11	-44.6	8.7
1020	11	11	11	11	11	11	11	11	11	13	-44.6	9.0
1021	11	11	11	11	12	11	11	11	11	34	-44.5	9.1
1022	11	11	11	11	11	11	11	11	11	13	-44.1	9.5
1023	11	11	11	11	11	11	11	11	14	11	-44.1	8.8
1024	11	11	11	11	11	11	11	11	11	13	-44.4	8.8
1025	11	11	11	11	11	11	11	11	11	13	-44.5	8.5
1026	11	11	11	11	11	11	11	11	11	13	-44.5	8.3
1027	11	11	11	11	11	11	11	11	11	13	-44.1	7.1
1028	11	11	11	11	11	11	11	11	11	12	-42.7	7.9
1029	11	11	11	11	11	11	11	11	11	12	-42.8	9.1
1030	11	11	11	11	11	11	11	11	11	11	-42.7	9.0
1031	11	11	11	11	11	11	11	11	11	13	-41.1	8.2
1032	11	11	11	11	11	11	11	11	11	11	-42.5	8.9
1033	11	11	11	11	11	11	11	11	11	11	-42.7	8.5
1034	11	11	11	11	11	11	11	11	11	12	-42.5	6.7
1035	11	11	11	11	11	11	11	11	11	13	-44.1	5.4
1036	11	11	11	11	11	11	11	11	11	33	-46.8	5.7
1037	11	11	11	11	12	11	11	11	11	14	-47.6	4.5
1038	11	11	11	11	11	11	11	11	11	11	-46.9	4.2
1039	11	11	11	11	11	11	11	11	11	23	-47.8	3.9
1040	11	11	11	11	11	11	11	11	11	11	-48.0	3.0
1041	11	11	11	11	11	11	11	11	11	11	-48.9	4.1
1042	11	11	11	11	11	11	11	11	11	13	-48.5	4.8
1043	11	11	11	11	11	11	11	11	11	13	-49.5	3.1
1044	11	11	11	11	11	11	11	11	11	33	-41.5	2.9
1045	11	11	11	11	11	11	11	11	11	13	-42.4	2.6
1046	11	11	11	11	11	11	11	11	11	11	-41.2	4.0
1047	11	11	11	11	11	11	11	11	11	34	-40.3	4.3
1048	11	11	11	11	11	11	11	11	11	34	-40.3	4.1
1050	11	11	11	11	11	11	11	11	11	12	-39.8	3.4
1051	11	11	11	11	11	11	11	11	11	12	-39.7	2.5
1052	11	11	11	11	11	11	11	11	11	12	-40.0	1.1
1053	11	11	11	11	11	11	11	11	11	11	-37.4	1.7
1054	11	11	11	11	11	11	11	11	11	11	-37.2	0.4
1055	11	11	11	11	11	11	11	11	11	12	-36.7	2.1
1056	11	11	11	11	11	11	11	11	11	22	-36.1	5.2
1057	11	11	11	11	11	11	11	11	11	11	-35.8	6.5

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1058	11	11	11	11	11	11	11	11	11	22	-36.1	6.4
1059	11	11	11	11	11	11	11	11	11	12	-36.0	7.1
1060	11	11	11	11	11	11	11	11	11	13	-36.0	8.8
1061	11	11	11	11	11	11	11	11	11	13	-36.5	8.9
1062	11	11	11	11	11	11	11	11	11	23	-36.6	8.4
1063	11	11	11	11	11	11	11	11	11	11	-33.5	7.2
1064	11	11	11	11	11	11	11	11	11	11	-33.4	6.9
1065	11	11	11	11	11	11	11	11	11	11	-33.5	7.1
1066	11	11	11	11	11	11	11	11	11	13	-32.9	5.7
1067	11	11	11	11	11	11	11	11	11	13	-33.5	5.3
1068	11	11	11	11	11	11	11	11	11	11	-33.3	5.9
1069	11	11	11	11	11	11	11	11	11	11	-33.8	5.1
1070	11	11	11	11	11	11	11	11	11	11	-34.0	5.1
1071	11	11	11	11	11	11	11	11	11	11	-32.9	5.1
1072	11	11	11	11	11	11	11	11	11	12	-34.4	4.6
1073	11	11	11	11	11	11	11	11	11	14	-35.0	5.3
1074	11	11	11	11	11	11	11	11	11	12	-34.1	3.3
1075	11	11	11	11	11	11	11	11	11	11	-32.3	3.1
1076	11	11	11	11	11	11	11	11	11	14	-32.2	4.3
1077	11	11	11	11	11	11	11	11	11	14	-32.3	4.9
1078	11	11	11	11	11	11	11	11	11	13	-32.2	2.1
1079	11	11	11	11	11	11	11	11	11	11	-32.1	1.8
1080	11	11	11	11	11	11	11	11	11	12	-30.5	1.6
1084	11	11	11	11	11	11	11	11	11	12	-30.1	1.3
1085	11	11	11	11	11	11	11	11	11	13	-30.0	1.3
1086	11	11	11	11	11	11	11	11	11	11	-29.9	-0.1
1087	11	11	11	11	11	11	11	11	11	11	-29.7	-0.1
1088	11	11	11	11	11	11	11	11	11	11	-29.3	0.5
1090	11	11	11	11	11	11	11	11	11	12	-31.8	0.4
1091	11	11	11	11	11	11	11	11	11	11	-31.0	-0.7
1092	11	11	11	11	11	11	11	11	11	11	-30.6	-0.9
1093	11	11	11	11	11	11	11	11	11	11	-30.3	-0.8
1095	11	11	11	11	11	11	11	11	11	13	-30.1	-1.1
1096	11	11	11	11	11	11	11	11	11	11	-30.1	-0.3
1097	11	11	11	11	11	11	11	11	11	13	-33.7	-1.7
1100	11	11	11	11	11	11	11	11	11	13	-34.2	-2.3
1101	11	11	11	11	11	11	11	11	11	22	-34.6	-2.2
1102	11	11	11	11	11	11	11	11	11	13	-34.3	-2.0
1103	11	11	11	11	11	11	11	11	11	11	-34.9	-1.7
1104	11	11	11	11	11	11	11	11	11	11	-34.6	-1.7
1105	11	11	11	11	11	11	11	11	11	12	-34.5	-2.3
1106	11	11	11	11	11	11	11	11	11	13	-36.4	-3.6
1107	11	11	11	11	11	11	11	11	11	11	-41.1	-0.4
1108	11	11	11	11	11	11	11	11	11	33	-44.2	-1.1

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1109	11	11	11	11	11	11	11	11	11	24	-45.6	-2.8
1110	11	11	11	11	11	11	11	11	11	11	-47.3	-2.7
1111	11	11	11	11	11	11	11	11	11	23	-43.4	-2.5
1112	11	11	11	11	11	11	11	11	11	11	-44.5	-3.9
1113	11	11	11	11	11	11	11	11	11	11	-42.6	-1.6
1114	11	11	11	11	11	11	11	11	11	11	-41.4	-2.8
1115	11	11	11	11	11	11	11	11	11	13	-39.6	-2.9
1116	11	11	11	11	11	11	11	11	11	11	-39.4	-4.5
1117	11	11	11	11	11	11	11	11	11	34	-38.6	-4.8
1119	11	11	11	11	11	11	11	11	11	11	-41.5	-4.8
1120	11	11	11	11	11	11	11	11	11	23	-42.1	-4.9
1121	11	11	11	11	11	11	11	11	11	11	-46.2	-6.2
1122	11	11	11	11	11	11	11	11	11	11	-43.6	-6.6
1123	11	11	11	11	11	11	11	11	11	14	-42.7	-6.8
1124	11	11	11	11	11	11	11	11	11	11	-42.0	-6.8
1125	11	11	11	11	11	11	11	11	11	13	-41.2	-5.8
1126	11	11	11	11	11	11	11	11	11	13	-40.4	-7.2
1127	11	11	11	11	11	11	11	11	11	12	-40.0	-6.8
1128	11	11	11	11	11	11	11	11	11	12	-39.8	-6.9
1129	11	11	11	11	11	11	11	11	11	12	-38.6	-7.2
1130	11	11	11	11	11	11	11	11	11	33	-36.7	-4.8
1131	11	11	11	11	11	11	11	11	11	11	-37.1	-5.1
1132	11	11	11	11	11	11	11	11	11	12	-37.1	-5.4
1133	11	11	11	11	11	11	11	11	11	13	-37.1	-6.1
1134	11	11	11	11	11	11	11	11	11	13	-37.6	-5.9
1135	11	11	11	11	11	11	11	11	11	34	-37.2	-6.0
1136	11	11	11	11	11	11	11	11	11	12	-37.1	-6.5
1137	11	11	11	11	11	11	11	11	11	12	-37.4	-6.4
1138	11	11	11	11	11	11	11	11	14	23	-37.3	-7.5
1139	11	11	11	11	11	11	11	11	11	13	-38.0	-7.2
1140	11	11	11	11	11	11	11	11	11	12	-37.8	-7.9
1141	11	11	11	11	11	11	11	11	11	11	-37.3	-7.9
1143	11	11	11	11	11	11	11	11	11	13	-35.8	-8.2
1144	11	11	11	11	11	11	11	11	11	13	-35.9	-8.2
1147	11	11	11	11	11	11	11	11	11	13	-36.6	-7.7
1148	11	11	11	11	11	11	11	11	11	23	-35.8	-8.9
1149	11	11	11	11	11	11	11	11	11	24	-35.4	-8.9
1150	11	11	11	11	11	11	11	11	11	13	-36.7	-8.6
1151	11	11	11	11	11	11	11	11	11	13	-37.2	-8.8
1152	11	11	11	11	11	11	11	11	11	23	-37.5	-9.4
1153	11	11	11	11	11	11	11	11	11	11	-38.5	-9.4
1154	11	11	11	11	11	11	11	11	11	11	-40.1	-10.2
1155	11	11	11	11	11	11	11	11	11	11	-39.8	-10.1
1156	11	11	11	11	11	11	11	11	11	11	-39.8	-9.7

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1157	11	11	11	11	11	11	11	11	11	11	-40.0	-9.7
1159	11	11	11	11	11	11	11	11	11	23	-39.7	-9.1
1160	11	11	11	11	11	11	11	11	11	11	-41.9	-9.9
1161	11	11	11	11	11	11	11	11	11	13	-36.6	3.3
1163	11	11	11	11	11	11	11	11	11	13	-42.6	-8.6
1164	11	11	11	11	11	11	11	11	11	23	-46.7	-7.4
1165	11	11	11	11	12	11	11	11	11	12	-46.6	-9.5
1166	11	11	11	11	11	11	11	11	11	23	-45.1	-9.6
1167	11	11	11	11	11	11	11	11	11	11	-43.7	-13.8
1168	11	11	11	11	11	11	11	11	11	13	-42.4	-15.8
1169	11	11	11	11	11	11	11	11	14	13	-41.9	-16.6
1170	11	11	11	11	11	11	11	11	11	13	-41.8	-16.7
1171	11	11	11	11	11	11	11	11	11	13	-42.7	-9.9
1172	11	11	11	11	11	11	11	11	11	15	-40.3	-12.6
1173	11	11	11	11	11	11	11	11	11	11	-40.0	-14.8
1174	11	11	11	11	11	11	11	11	11	13	-37.6	-14.2
1175	11	11	11	11	11	11	11	11	11	11	-38.4	-14.7
1176	11	11	11	11	11	11	11	11	11	33	-39.2	-15.0
1177	11	11	11	11	11	11	11	11	11	23	-38.4	-15.3
1178	11	11	11	11	11	11	11	11	11	24	-37.9	-15.6
1179	11	11	11	11	11	11	11	11	11	13	-37.5	-16.3
1180	11	11	11	11	11	11	11	11	11	13	-38.0	-16.0
1181	11	11	11	11	11	11	11	11	11	13	-37.1	-16.4
1182	11	11	11	11	11	11	11	11	11	12	-35.8	-16.0
1183	11	11	11	11	12	11	11	11	11	11	-38.6	-10.5
1184	11	11	11	11	12	11	11	11	11	11	-27.9	-10.2
1185	11	11	11	11	11	11	11	11	11	13	-37.4	-10.7
1186	11	11	11	11	11	11	11	11	11	11	-37.4	-11.1
1187	11	11	11	11	11	11	11	11	11	12	-37.0	-11.7
1188	11	11	11	11	11	11	11	11	11	12	-35.9	-12.4
1189	11	11	11	11	11	11	11	11	11	24	-35.5	-13.5
1190	11	11	11	11	11	11	11	11	11	24	-35.1	-13.6
1191	11	11	11	11	11	11	11	11	11	24	-34.7	-13.7
1192	11	11	11	11	11	11	11	11	11	24	-34.1	-13.2
1193	11	11	11	11	11	11	11	11	11	24	-34.1	-12.9
1194	11	11	11	11	11	11	11	11	11	24	-34.1	-12.8
1195	11	11	11	11	11	11	11	11	11	14	-34.3	-11.9
1196	11	11	11	11	11	11	11	11	11	14	-34.3	-11.7
1197	11	11	11	11	11	11	11	11	11	22	-33.7	-11.1
1198	11	11	11	11	11	11	11	11	11	34	-34.2	-9.2
1199	11	11	11	11	11	11	11	11	11	13	-32.8	-8.1
1200	11	11	11	11	11	11	11	11	11	13	-34.2	-3.7
1201	11	11	11	11	11	11	11	11	11	33	-31.9	-7.3
1202	11	11	11	11	11	11	11	11	11	13	-31.1	-7.3

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1203	11	11	11	11	11	11	11	11	11	13	-30.7	-7.3
1204	11	11	11	11	11	11	11	11	11	13	-30.7	-7.4
1205	11	11	11	11	11	11	11	11	11	13	-31.1	-3.4
1206	11	11	11	11	11	11	11	11	11	13	-32.1	-8.6
1207	11	11	11	11	11	11	11	11	11	11	-32.1	-9.1
1208	11	11	11	11	11	11	11	11	11	12	-28.8	-6.5
1209	11	11	11	11	11	11	11	11	11	13	-29.7	-6.9
1210	11	11	11	11	11	11	11	11	11	22	-30.1	-7.0
1211	11	11	11	11	11	11	11	11	11	13	-28.5	-6.6
1212	11	11	11	11	11	11	11	11	11	13	-28.4	-7.3
1213	11	11	11	11	11	11	11	11	11	23	-29.2	-4.3
1214	11	11	11	11	11	11	11	11	11	13	-28.6	-3.7
1215	11	11	11	11	11	11	11	11	11	13	-28.5	-3.3
1216	11	11	11	11	11	11	11	11	11	11	-29.9	-2.8
1217	11	11	11	11	11	11	11	11	11	34	-28.7	-1.0
1218	11	11	11	11	11	11	11	11	11	24	-28.2	-0.9
1219	11	11	11	11	11	11	11	11	11	11	-28.5	1.7
1220	11	11	11	11	11	11	11	11	11	12	-26.9	2.2
1221	11	11	11	11	11	11	11	11	11	12	-27.1	2.3
1222	11	11	11	11	11	11	11	11	11	13	-28.5	3.5
1223	11	11	11	11	11	11	11	11	11	14	-29.2	3.7
1224	11	11	11	11	11	11	11	11	11	14	-28.7	4.0
1225	11	11	11	11	11	11	11	11	11	33	-30.8	3.0
1226	11	11	11	11	11	11	11	11	11	13	-30.6	4.2
1227	11	11	11	11	11	11	11	11	11	11	-30.6	4.7
1228	11	11	11	11	11	11	11	11	11	11	-30.6	5.0
1230	11	11	11	11	11	11	11	11	11	11	-32.1	7.3
1231	11	11	11	11	11	11	11	11	11	11	-31.4	7.4
1232	11	11	11	11	11	11	11	11	11	13	-30.4	6.2
1233	11	11	11	11	11	11	11	11	11	12	-28.6	6.8
1234	11	11	11	11	11	11	11	11	11	12	-28.8	7.8
1235	11	11	11	11	11	11	11	11	11	12	-28.8	8.5
1236	11	11	11	11	11	11	11	11	11	12	-28.8	9.2
1237	11	11	11	11	11	11	11	11	11	11	-27.5	9.1
1238	11	11	11	11	11	11	11	11	11	12	-24.5	9.7
1239	11	11	11	11	11	11	11	11	11	13	-23.6	9.1
1240	11	11	11	11	11	11	11	11	11	12	-24.1	9.0
1241	11	11	11	11	11	11	11	11	11	12	-25.3	6.1
1242	11	11	11	11	11	11	11	11	11	44	-27.4	7.1
1243	11	11	11	11	11	11	11	11	11	23	-27.5	6.7
1244	11	11	11	11	11	11	11	11	11	13	-28.7	5.6
1245	11	11	11	11	11	11	11	11	11	12	-26.7	4.4
1246	11	11	11	12	11	11	11	11	11	13	-26.0	4.3
1247	11	11	11	11	11	11	11	11	11	11	-25.6	-0.4

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1248	11	11	11	11	11	11	11	11	11	13	-25.4	-0.9
1249	11	11	11	11	11	11	11	11	11	13	-25.4	-2.0
1250	11	11	11	11	11	11	11	11	11	33	-25.4	-2.4
1251	11	11	11	11	11	11	11	11	11	13	-24.5	-2.4
1252	11	11	11	11	11	11	11	11	11	12	-24.8	-1.5
1253	11	11	11	11	11	11	11	11	11	11	-24.5	-0.9
1254	11	11	11	11	11	11	11	11	11	12	-29.9	-0.1
1255	11	11	11	11	11	11	11	11	11	12	-22.0	2.2
1256	11	11	11	11	11	11	11	11	11	11	-21.1	1.4
1257	11	11	11	11	11	11	11	11	11	12	-21.7	1.8
1258	11	11	11	11	11	11	11	11	11	22	-20.1	1.3
1259	11	11	11	11	11	11	11	11	11	33	-19.9	1.1
1260	11	11	11	11	11	11	11	11	11	33	-20.4	0.8
1261	11	11	11	11	11	11	11	11	11	33	-20.6	0.6
1262	11	11	11	11	11	11	11	11	11	11	-20.6	-0.5
1263	11	11	11	11	11	11	11	11	11	11	-20.3	-0.8
1264	11	11	11	11	11	11	11	11	11	34	-22.0	4.2
1265	11	11	11	11	11	11	11	11	11	11	-18.4	3.3
1266	11	11	11	11	11	11	11	11	11	11	-18.0	3.2
1267	11	11	11	11	11	11	11	11	12	14	-17.0	2.4
1268	11	11	11	11	11	11	11	11	12	14	-17.2	2.4
1269	11	11	11	11	11	11	11	11	11	22	-16.3	2.2
1270	11	11	11	11	11	11	11	11	11	23	-16.6	2.8
1271	11	11	11	11	11	11	11	11	11	13	-15.9	3.5
1272	11	11	11	11	11	11	11	11	11	13	-15.8	3.7
1273	11	11	11	11	11	11	11	11	11	13	-14.5	2.4
1274	11	11	11	11	11	11	11	11	11	23	-15.6	2.3
1275	11	11	11	11	11	11	11	11	11	13	-14.3	2.7
1276	11	11	11	11	11	11	11	11	11	13	-13.0	2.5
1277	11	11	11	11	11	11	11	11	11	11	-13.0	3.2
1278	11	11	11	11	11	11	11	11	11	13	-12.1	2.4
1279	11	11	11	11	11	11	11	11	11	12	-11.8	1.9
1280	11	11	11	11	11	11	11	11	11	33	-19.0	-1.7
1281	11	11	11	11	11	11	11	11	14	11	-17.0	-1.4
1282	11	11	11	11	11	11	11	11	11	11	-15.6	-3.9
1283	11	11	11	11	11	11	11	11	11	14	-15.3	-4.5
1284	11	11	11	11	11	11	11	11	11	24	-14.7	-5.0
1285	11	11	11	11	11	11	11	11	11	13	-2.0	-3.8
1286	11	11	11	11	11	11	11	11	14	13	-16.8	-3.6
1287	11	11	11	11	11	11	11	11	11	14	-21.8	-2.4
1288	11	11	11	11	11	11	11	11	11	11	-20.7	-4.2
1289	11	11	11	11	11	11	11	11	11	11	-22.3	-4.5
1290	11	11	11	11	11	11	11	11	11	13	-22.9	-5.2
1291	11	11	11	11	11	11	11	11	11	11	-22.4	-4.2

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1292	11	11	11	11	11	11	11	11	11	11	-24.1	-3.9
1293	11	11	11	11	11	11	11	11	11	13	-23.5	-4.6
1294	11	11	11	11	11	11	11	11	11	13	-24.7	-4.7
1295	11	11	11	11	11	11	11	11	11	12	-25.1	-3.4
1296	11	11	11	11	11	11	11	11	15	11	-25.2	-3.1
1297	11	11	11	11	11	11	11	11	11	13	-27.5	-3.3
1298	11	11	11	11	11	11	11	11	11	11	-27.5	-3.7
1299	11	11	11	11	11	11	11	11	11	11	-25.1	-5.7
1300	11	11	11	11	11	11	11	11	11	13	-24.1	-5.7
1301	11	11	11	11	11	11	11	11	11	12	-20.0	-5.3
1302	11	11	11	11	11	11	11	11	11	11	-19.0	-5.4
1303	11	11	11	11	11	11	11	11	11	12	-19.0	-6.0
1304	11	11	11	11	11	11	11	11	11	11	-19.5	-6.6
1305	11	11	11	11	11	11	11	11	11	12	-19.5	-7.2
1306	11	11	11	11	11	11	11	11	11	13	-19.0	-7.4
1307	11	11	11	11	11	11	11	11	11	11	-19.0	-8.0
1308	11	11	11	11	11	11	11	11	11	11	-18.3	-8.8
1309	11	11	11	11	11	11	11	11	11	11	-18.4	-9.2
1310	11	11	11	11	11	11	11	11	11	11	-19.7	-10.3
1311	11	11	11	11	11	11	11	11	11	11	-22.8	-8.3
1312	11	11	11	11	11	11	11	11	11	23	-23.0	-8.4
1313	11	11	11	11	11	11	11	11	11	13	-24.5	-7.4
1314	11	11	11	11	11	11	11	11	11	13	-24.4	-7.7
1315	11	11	11	11	11	11	11	11	11	13	-24.4	-7.8
1316	11	11	11	11	11	11	11	11	11	12	-24.9	-7.4
1317	11	11	11	11	11	11	11	11	11	12	-25.8	-7.7
1318	11	11	11	11	11	11	11	11	11	12	-25.6	-8.0
1319	11	11	11	11	11	11	11	11	11	13	-27.1	-7.9
1320	11	11	11	11	11	11	11	11	11	11	-27.1	-7.1
1321	11	11	11	11	11	11	11	11	11	33	-26.7	-10.0
1322	11	11	11	11	11	11	11	11	11	33	-25.8	-10.1
1323	11	11	11	11	11	11	11	11	11	11	-26.0	-10.9
1324	11	11	11	11	11	11	11	11	11	11	-26.2	-10.5
1325	11	11	11	11	11	11	11	11	11	14	-25.7	-11.0
1326	11	11	11	11	11	11	11	11	11	15	-25.7	-10.4
1327	11	11	11	11	11	11	11	11	11	13	-24.3	-10.7
1328	11	11	11	11	11	11	11	11	11	11	-24.3	-11.1
1329	11	11	11	11	11	11	11	11	11	11	-23.1	-9.7
1330	11	11	11	11	11	11	11	11	11	12	-21.7	-10.6
1331	11	11	11	11	11	11	11	11	11	13	-21.4	-11.5
1333	11	11	11	11	11	11	11	11	11	13	-23.2	-11.3
1334	11	11	11	11	11	11	11	11	11	13	-19.6	-11.8
1335	11	11	11	11	11	11	11	11	11	11	-19.1	-11.4
1336	11	11	11	11	11	11	11	11	11	13	-23.2	-14.2

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1337	11	11	11	11	11	11	11	11	11	11	-23.0	-13.1
1338	11	11	11	11	11	11	11	11	11	12	-23.8	-13.6
1339	11	11	11	11	11	11	11	11	11	23	-27.1	-14.0
1340	11	11	11	11	11	11	11	11	11	11	-29.6	-12.5
1341	11	11	11	11	11	11	11	11	11	11	-29.7	-12.1
1342	11	11	11	11	11	11	11	11	11	13	-29.8	-11.4
1343	11	11	11	11	11	11	11	11	11	13	-30.5	-11.3
1344	11	11	11	11	11	11	11	11	11	13	-29.4	-11.8
1345	11	11	11	11	11	11	11	11	11	12	-29.8	-12.2
1346	11	11	11	11	11	11	11	11	11	13	-29.9	-13.8
1347	11	11	11	11	11	11	11	11	11	11	-29.9	-14.1
1348	11	11	11	11	11	11	11	11	11	11	-30.2	-14.2
1349	11	11	11	11	11	11	11	11	11	11	-31.0	-14.4
1350	11	11	11	11	11	11	11	11	11	13	-31.0	-15.2
1351	11	11	11	11	11	11	11	11	11	13	-31.0	-15.8
1352	11	11	11	11	11	11	11	11	11	13	-31.4	-15.8
1353	11	11	11	11	11	11	11	11	11	13	-32.3	-15.0
1354	11	11	11	11	11	11	11	11	11	11	-33.0	-14.1
1355	11	11	11	11	11	11	11	11	11	12	-33.0	-14.0
1356	11	11	11	12	11	11	11	11	11	12	-32.7	-13.4
1357	11	11	11	11	11	11	11	11	11	14	-33.4	-11.9
1358	11	11	11	11	11	11	11	11	11	11	-33.4	-17.0
1359	11	11	11	11	11	11	11	11	11	14	-33.0	-17.0
1360	11	11	11	11	11	11	11	11	11	13	-33.1	-17.5
1361	11	11	11	11	11	11	11	11	11	11	-31.2	-17.0
1362	11	11	11	11	11	11	11	11	11	11	-31.2	-16.9
1363	11	11	11	11	11	11	11	11	11	11	-34.9	-17.8
1364	11	11	11	11	11	11	11	11	11	23	-35.8	-18.8
1365	11	11	11	11	11	11	11	11	11	24	-35.7	-18.8
1366	11	11	11	11	11	11	11	11	11	23	-35.8	-19.2
1367	11	11	11	11	11	11	11	11	11	22	-36.0	-19.4
1368	11	11	11	11	11	11	11	11	11	13	-33.3	-19.8
1369	11	11	11	11	11	11	11	11	11	13	-36.1	-20.9
1370	11	11	11	11	11	11	11	11	11	11	-38.9	-21.1
1371	11	11	11	11	11	11	11	11	11	13	-33.5	-22.3
1372	11	11	11	11	11	11	11	11	11	23	-33.2	-22.0
1373	11	11	11	11	11	11	11	11	11	11	-33.2	-22.5
1374	11	11	11	11	11	11	11	11	11	11	-31.2	-20.1
1375	11	11	11	11	11	11	11	11	11	12	-31.4	-19.6
1376	11	11	11	11	11	11	11	11	11	12	-30.9	-19.7
1377	11	11	11	11	11	11	11	11	11	11	-30.8	-19.8
1378	11	11	11	11	11	11	11	11	11	14	-30.8	-20.5
1379	11	11	11	11	11	11	11	11	11	11	-30.4	-21.3
1380	11	11	11	11	11	11	11	11	11	11	-31.3	-20.9

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1381	11	11	11	11	11	11	11	11	11	13	-31.1	-21.7
1382	11	11	11	11	11	11	11	11	11	12	-30.6	-31.6
1383	11	11	11	11	11	11	11	11	11	14	-30.6	-21.7
1384	11	11	11	11	11	11	11	11	11	11	-30.4	-23.1
1385	11	11	11	11	11	11	11	11	11	11	-30.6	-22.8
1386	11	11	11	11	11	11	11	11	11	12	-32.6	-24.0
1387	11	11	11	11	11	11	11	11	11	11	-33.4	-23.9
1388	11	11	11	11	11	11	11	11	11	11	-33.2	-25.2
1389	11	11	11	11	11	11	11	11	11	14	-30.5	-25.9
1391	11	11	11	11	11	11	11	11	11	14	-33.3	-26.1
1392	11	11	11	11	11	11	11	11	11	25	-33.3	-27.5
1393	11	11	11	11	11	11	11	11	11	33	-34.3	-27.8
1394	11	11	11	11	11	11	11	11	11	23	-34.3	-28.6
1395	11	11	11	11	11	11	11	11	11	12	-34.4	-28.9
1396	11	11	11	11	11	11	11	11	11	11	-35.8	-28.8
1397	11	11	11	11	11	11	11	11	11	13	-36.2	-27.5
1398	11	11	11	11	11	11	11	11	11	23	-36.0	-27.0
1399	11	11	11	11	11	11	11	11	11	23	-34.9	-23.3
1400	11	11	11	11	11	11	11	11	11	23	-35.5	-23.2
1401	11	11	11	11	11	11	11	11	11	23	-36.0	-23.7
1402	11	11	11	11	11	11	11	11	11	12	-42.5	-26.3
1403	11	11	11	11	11	11	11	11	11	15	-34.5	-30.3
1404	11	11	11	11	11	11	11	11	11	23	-36.3	-30.0
1405	11	11	11	11	11	11	11	11	11	13	-32.7	-31.1
1406	11	11	11	11	11	11	11	11	11	13	-31.1	-28.3
1407	11	11	11	11	11	11	11	11	11	33	-30.6	-31.0
1408	11	11	11	11	11	11	11	11	11	23	-30.6	-28.5
1409	11	11	11	11	11	11	11	11	11	24	-30.6	-28.3
1410	11	11	11	11	11	11	11	11	11	11	-29.7	-27.9
1411	11	11	11	11	11	11	11	11	11	12	-28.1	-28.2
1412	11	11	11	11	11	11	11	11	11	12	-27.6	-24.9
1413	11	11	11	11	11	11	11	11	11	11	-28.9	-24.5
1414	11	11	11	11	11	11	11	11	11	14	-29.0	-24.5
1415	11	11	11	11	11	11	11	11	11	12	-29.0	-23.8
1416	11	11	11	11	11	11	11	11	11	11	-28.0	-22.5
1417	11	11	11	11	11	11	11	11	11	13	-28.0	-22.1
1418	11	11	11	11	11	11	11	11	11	11	-28.8	-19.6
1419	11	11	11	11	11	11	11	11	11	11	-28.9	-19.4
1420	11	11	11	11	11	11	11	11	11	12	-28.0	-19.7
1421	11	11	11	11	11	11	11	11	11	22	-26.7	-8.1
1422	11	11	11	11	11	11	11	11	11	11	-25.4	-15.8
1423	11	11	11	11	11	11	11	11	11	11	-25.4	-15.7
1424	11	11	11	11	11	11	11	11	11	11	-25.4	-15.8
1425	11	11	11	11	11	11	11	11	11	12	-23.8	-17.3

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1426	11	11	11	11	11	11	11	11	11	33	-22.9	-17.2
1427	11	11	11	11	11	11	11	11	11	12	-22.0	-18.0
1428	11	11	11	11	11	11	11	11	12	11	-23.8	-19.8
1429	11	11	11	11	11	11	11	11	11	14	-24.2	-19.4
1430	11	11	11	11	11	11	11	11	11	14	-24.2	-19.6
1431	11	11	11	11	11	11	11	11	11	11	-27.9	-20.7
1432	11	11	11	11	11	11	11	11	11	14	-27.6	-21.8
1433	11	11	11	11	11	11	11	11	11	22	-27.5	-21.9
1434	11	11	11	12	11	11	11	11	11	24	-24.2	-23.9
1435	11	11	11	11	12	11	11	11	11	11	-23.7	-26.5
1436	11	11	11	11	11	11	11	11	11	12	-23.7	-23.2
1437	11	11	11	11	11	11	11	11	11	11	-23.7	-22.9
1438	11	11	11	11	11	11	11	11	11	12	-22.2	-22.9
1439	11	11	11	11	11	11	11	11	11	13	-20.8	-23.4
1440	11	11	11	11	11	11	11	11	11	13	-19.0	-22.2
1441	11	11	11	11	11	11	11	11	11	14	-19.4	-24.6
1442	11	11	11	11	11	11	11	11	11	12	-22.1	-18.8
1443	11	11	11	11	11	11	11	11	11	12	-21.9	-19.1
1444	11	11	11	11	11	11	11	11	11	12	-21.9	-19.2
1445	11	11	11	11	11	11	11	11	11	12	-22.3	-16.8
1446	11	11	11	11	11	11	11	11	11	13	-22.2	-16.8
1447	11	11	11	11	11	11	11	11	11	13	-21.2	-16.6
1448	11	11	11	11	11	11	11	11	11	14	-16.2	-17.6
1449	11	11	11	11	11	11	11	11	11	13	-14.7	-15.2
1450	11	11	11	11	11	11	11	11	11	11	-15.9	-16.5
1451	11	11	11	11	11	11	11	11	11	13	-12.4	-17.8
1452	11	11	11	11	11	11	11	11	11	12	-12.5	-15.7
1453	11	11	11	11	11	11	11	11	11	44	-15.8	-12.7
1454	11	11	11	11	11	11	11	11	11	11	-14.4	-11.4
1455	11	11	11	11	11	11	11	11	11	12	-15.4	-9.8
1456	11	11	11	11	11	11	11	11	11	13	-15.4	-8.1
1457	11	11	11	11	11	11	11	11	11	11	-16.0	-7.0
1458	11	11	11	11	11	11	11	11	11	14	-15.3	-4.7
1459	11	11	11	11	11	11	11	11	11	23	-11.8	-7.4
1460	11	11	11	11	11	11	11	11	11	11	-11.8	-9.1
1461	11	11	11	11	11	11	11	11	11	13	-11.0	-9.0
1462	11	11	11	11	11	11	11	11	11	11	-10.5	-10.3
1463	11	11	11	11	11	11	11	11	11	13	-7.8	-11.1
1464	11	11	11	11	11	11	11	11	12	13	-9.0	-10.3
1465	11	11	11	11	11	11	11	11	11	22	-6.8	-6.3
1466	11	11	11	11	11	11	11	11	11	11	-10.1	-4.2
1467	11	11	11	11	11	11	11	11	11	12	-17.1	5.3
1468	11	11	11	11	11	11	11	11	11	22	-18.4	7.3
1469	11	11	11	11	11	11	11	11	11	12	-18.2	7.2

APPENDIX II. (Cont.) (Bog)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgm	Pgi 2	South	East
1470	11	11	11	11	11	11	11	11	11	11	-17.2	6.8
1471	11	11	11	11	11	11	11	11	11	13	-16.8	6.6
1472	11	11	11	11	11	11	11	11	11	12	-15.7	7.9
1473	11	11	11	11	11	11	11	11	11	11	-15.7	6.7
1474	11	11	11	11	11	11	11	11	11	11	-14.8	6.6
1475	11	11	11	11	11	11	11	11	11	11	-15.3	6.2
1476	11	11	11	11	11	11	11	11	11	12	-18.6	8.8
1477	11	11	11	11	11	11	11	11	11	12	-19.6	9.1
1478	11	11	11	11	11	11	11	11	11	22	-13.9	8.0
1479	11	11	11	11	11	11	11	11	11	12	-13.9	9.6
1481	11	11	11	11	11	11	11	11	11	13	-14.7	9.1
1482	11	11	11	11	11	11	11	11	11	13	-14.8	8.7
1483	11	11	11	11	11	11	11	11	11	13	-12.8	7.6
1484	11	11	11	11	11	11	11	11	11	33	-10.1	8.0
1485	11	11	11	11	11	11	11	11	11	33	-10.5	7.6
1486	11	11	11	11	11	11	11	11	11	12	-10.9	8.4
1487	11	11	11	11	11	11	11	11	11	33	-11.0	9.1
1488	11	11	11	11	11	11	11	11	11	13	-11.2	9.1
1489	11	11	11	11	11	11	11	11	11	12	-10.5	6.7
1490	11	11	11	11	11	11	11	11	11	23	-9.0	4.9
1491	11	11	11	11	11	11	11	11	11	13	-9.1	2.8
1492	11	11	11	11	11	11	11	11	11	12	-7.0	2.0
1493	11	11	11	11	11	11	11	11	11	12	-8.0	2.7
1494	11	11	11	11	11	11	11	11	11	11	-6.2	3.5
1495	11	11	11	11	11	11	11	11	11	11	-4.9	2.4
1496	11	11	11	11	11	11	11	11	11	23	-6.6	4.2
1497	11	11	11	11	11	11	11	11	11	12	-5.5	4.5
1498	11	11	11	11	11	11	11	11	11	11	-5.9	4.1
1499	11	11	11	11	11	11	11	11	11	23	-5.5	6.5
1500	11	11	11	11	11	11	11	11	11	23	-5.7	6.9
6000	11	11	11	11	11	11	11	11	11	33	-34.8	-5.7
6001	11	11	11	11	11	11	11	11	11	33	-35.1	-4.3
6002	11	11	11	12	11	11	11	11	11	12	-32.1	-4.3
6003	11	11	11	11	11	11	11	11	11	12	-33.3	-2.7
6004	11	11	11	11	11	11	11	11	11	12	-35.1	-3.8
6006	11	11	11	11	11	11	11	11	11	13	-34.8	-7.8
6007	11	11	11	11	11	11	11	11	11	13	-33.3	-7.4
6008	11	11	11	11	11	11	11	11	11	13	-34.1	-7.9
6009	11	11	11	11	11	11	11	11	11	11	-35.9	-0.6
6010	11	11	11	11	11	11	11	11	11	34	-33.9	1.5
6011	11	11	11	11	11	11	11	11	11	33	-27.7	-1.9
6012	11	11	11	11	11	11	11	11	11	13	-32.3	-6.3

APPENDIX III

ALLOZYME SCORES AND TREE LOCATIONS FOR TAMARACK IN FIELD POPULATION

APPENDIX III. (Field population)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2000	11	11	11	11	11	11	11	11	13	11	-18.8	17.8
2001	11	11	11	11	11	11	11	11	13	11	-19.1	18.5
2002	11	11	11	11	11	11	12	11	12	12	-19.2	17.9
2003	11	11	11	11	11	11	11	11	13	11	-19.2	15.4
2004	11	11	11	11	11	11	11	11	11	11	-19.8	18.4
2005	11	11	11	11	12	11	11	11	11	11	-19.7	13.9
2006	11	11	11	11	11	11	11	11	11	11	-19.7	6.6
2007	11	11	11	11	11	11	11	11	44	11	-21.5	7.0
2008	11	11	11	11	11	11	11	11	11	11	-23.8	5.6
2009	11	11	11	11	11	11	11	11	12	11	-24.9	6.2
2010	11	11	11	11	11	11	11	11	13	11	-27.8	4.4
2011	11	11	11	11	11	11	11	11	11	11	-27.5	4.6
2012	11	11	11	11	11	11	11	11	22	11	-31.7	4.4
2013	11	11	11	11	11	11	11	11	13	11	-31.3	3.5
2014	11	11	11	11	11	11	11	11	11	11	-30.9	-0.7
2015	11	11	11	11	11	11	11	11	12	11	-27.8	1.4
2016	11	11	11	11	11	11	11	11	11	11	-26.6	2.0
2017	11	11	11	11	11	11	11	11	13	11	-23.0	1.6
2018	11	11	11	11	11	11	11	11	13	11	-16.2	-0.9
2019	11	11	11	11	11	11	11	11	13	11	-15.7	2.5
2020	11	11	11	11	11	11	11	11	13	11	-12.5	1.2
2021	11	11	11	11	11	11	11	11	11	11	-12.2	-0.1
2022	11	11	11	11	11	11	11	11	11	11	-11.6	-1.5
2023	11	11	11	11	11	11	11	11	12	11	-10.5	-1.8
2024	11	11	11	11	12	11	11	11	11	11	-12.0	-0.8
2025	11	11	11	11	11	11	11	11	11	11	-9.7	-1.9
2026	11	11	11	11	11	11	11	11	12	11	-11.2	-2.0
2028	11	11	11	11	11	11	11	11	11	11	-11.8	-1.5
2029	11	11	11	11	11	11	11	11	11	11	-23.4	-3.8
2030	11	11	11	11	11	11	11	11	14	11	-24.0	-4.2
2031	11	11	11	11	11	11	11	11	11	11	-26.5	-4.6
2032	11	11	11	11	11	11	11	11	13	11	-28.6	-7.5
2033	11	11	11	11	11	11	11	11	11	11	-27.4	-8.7
2034	11	11	11	11	11	11	11	11	11	11	-27.2	-8.7
2035	11	11	11	11	12	11	11	11	12	11	-23.8	-7.7
2036	11	11	11	11	11	11	11	11	12	11	-23.7	-7.6
2037	11	11	11	11	11	11	11	11	11	11	-23.4	-6.8
2038	11	11	11	11	11	11	11	11	12	11	-23.3	-6.8
2039	11	11	11	11	11	11	11	11	11	11	-23.0	-7.2
2040	11	11	11	11	11	11	11	12	23	11	-22.7	-6.6
2041	11	11	11	12	11	11	11	11	13	11	-22.8	-6.8
2042	11	11	11	11	11	11	11	11	11	11	-22.5	-6.3
2043	11	11	11	11	11	11	11	12	23	11	-22.5	-6.4

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2044	11	11	11	11	11	11	11	11	33	11	-21.5	-6.8
2045	11	11	11	11	12	11	11	11	11	11	-21.7	-7.1
2046	11	11	11	11	11	11	11	11	11	11	-21.1	-0.8
2047	11	11	11	11	11	11	11	11	34	11	-23.1	-8.1
2048	11	11	11	11	11	11	11	11	13	11	-22.7	-7.6
2049	11	11	11	11	11	11	11	11	12	11	-23.6	-7.4
2052	11	11	11	11	11	11	11	11	23	11	-23.6	-8.2
2053	11	11	11	11	11	11	11	11	11	11	-23.7	-8.4
2054	11	11	11	11	11	11	11	11	13	11	-25.5	-10.0
2055	11	11	11	11	11	11	11	11	12	11	-23.5	-11.4
2056	11	11	11	11	11	11	11	11	11	11	-25.7	-11.6
2057	11	11	11	11	12	11	11	11	11	11	-26.2	-9.2
2058	11	11	11	11	11	11	11	11	11	11	-28.6	-12.1
2059	11	11	11	11	11	11	11	11	13	11	-29.0	-12.0
2060	11	11	11	11	11	11	11	11	11	15	-30.4	-12.2
2061	11	11	11	11	11	11	11	11	12	11	-30.5	-12.2
2062	11	11	11	11	11	11	11	11	13	11	-30.8	-12.3
2064	11	11	11	11	11	11	11	11	12	11	-30.8	-12.5
2065	11	11	11	11	11	11	11	11	13	11	-30.8	-13.1
2066	11	11	11	11	11	11	11	11	13	11	-30.9	-13.5
2067	11	11	11	11	11	11	11	11	12	11	-30.3	-13.9
2068	11	11	11	11	11	11	11	11	13	11	-30.1	-13.5
2070	11	11	11	11	11	11	11	11	11	11	-27.4	-13.9
2072	11	11	11	11	11	11	11	11	12	11	-27.2	-13.6
2073	11	11	11	11	11	11	11	11	11	11	-29.0	-12.3
2074	11	11	11	11	11	11	11	11	11	11	-26.5	-16.0
2075	11	11	11	11	11	11	11	11	11	11	-26.4	-15.9
2076	11	11	11	11	11	11	11	11	11	11	-17.1	-25.2
2077	11	11	11	11	11	11	11	11	14	11	-23.5	-16.6
2078	11	11	11	11	11	11	11	11	11	11	-23.5	-17.5
2079	11	11	11	11	11	11	11	11	11	11	-24.0	-18.0
2080	11	11	11	11	11	11	11	11	13	11	-23.4	-18.7
2081	11	11	11	11	11	11	11	11	12	11	-23.8	-18.3
2082	11	11	11	11	11	11	11	11	11	11	-23.5	-18.3
2083	11	11	11	11	11	11	11	11	13	11	-23.4	-18.6
2084	11	11	11	11	11	11	11	11	12	11	-21.1	-21.5
2085	11	11	11	12	11	11	11	11	14	11	-25.6	-19.4
2086	11	11	11	11	11	11	11	11	33	11	-26.0	-18.4
2087	11	11	11	11	11	11	11	11	13	11	-27.0	-18.2
2088	11	11	11	11	11	11	11	11	13	11	-28.1	-17.5
2089	11	11	11	11	11	11	11	11	13	11	-28.2	-17.4
2090	11	11	11	11	11	11	11	11	23	11	-28.6	-16.2
2091	11	11	11	11	11	11	11	11	13	11	-30.7	-15.5
2092	11	11	11	11	11	11	11	11	23	11	-28.2	-18.6

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2093	11	11	11	11	11	11	11	11	13	11	-28.4	-18.7
2094	11	11	11	11	11	11	11	11	13	11	-28.2	-19.2
2095	11	11	11	11	11	11	11	11	11	11	-27.8	-19.1
2096	11	11	11	11	11	11	11	11	12	11	-28.1	-19.4
2097	11	11	11	11	11	11	11	11	13	11	-28.6	-20.1
2098	11	11	11	11	11	11	11	11	11	11	-27.9	-20.3
2099	11	11	11	11	11	11	11	11	11	11	-27.8	-19.8
2100	11	11	11	11	11	11	11	12	12	11	-26.7	-19.7
2101	11	11	11	12	11	11	11	11	33	11	-27.1	-20.2
2102	11	11	11	11	11	11	11	11	11	11	-26.9	-18.8
2103	11	11	11	11	11	11	11	11	12	11	-27.0	-18.8
2104	11	11	11	11	11	11	11	11	13	11	-26.7	-20.8
2105	11	11	11	11	11	11	11	11	11	11	-26.9	-21.3
2106	11	11	11	11	11	11	11	11	11	11	-26.7	-22.5
2108	11	11	11	11	11	11	11	11	11	11	-25.7	-22.8
2109	11	11	11	11	11	11	11	11	11	11	-23.1	-23.4
2110	11	11	11	11	11	11	11	11	33	11	-23.3	-24.3
2111	11	11	11	12	11	11	11	11	23	11	-25.9	-25.6
2112	11	11	11	11	12	11	11	11	12	11	-25.8	-25.9
2113	11	11	11	11	11	11	11	11	11	11	-23.8	-27.1
2114	11	11	11	12	11	11	11	11	23	11	-26.0	-26.3
2115	11	11	11	11	11	11	11	11	13	11	-26.1	-27.0
2116	11	11	11	11	11	11	11	11	13	11	-26.7	-26.5
2117	11	11	11	11	11	11	11	11	11	11	-26.9	-26.4
2118	11	11	11	11	11	11	11	11	11	11	-28.3	-26.7
2119	11	11	11	11	11	11	11	11	33	11	-29.5	-25.8
2120	11	11	11	11	11	11	11	11	13	11	-28.4	-28.3
2121	11	11	11	11	11	11	11	11	11	11	-28.8	-27.5
2122	11	11	11	11	11	11	11	11	13	11	-28.9	-27.3
2123	11	11	11	11	11	11	11	11	13	11	-27.8	-27.2
2124	11	11	11	11	11	11	11	11	23	11	-29.3	-26.2
2125	11	11	11	11	11	11	11	11	23	11	-28.5	-25.7
2126	11	11	11	11	11	11	11	11	11	11	-28.7	-25.7
2127	11	11	11	11	11	11	11	11	11	11	-28.6	-25.5
2128	11	11	11	11	11	11	11	11	11	11	-28.6	-24.2
2129	11	11	11	11	11	11	11	11	13	11	-28.3	-23.7
2130	11	11	11	11	11	11	11	11	22	11	-28.5	-23.4
2131	11	11	11	11	11	11	11	11	13	11	-28.8	-23.1
2132	11	11	11	11	11	11	11	11	12	11	-27.5	-25.2
2133	11	11	11	11	11	11	11	11	13	11	-28.2	-21.5
2134	11	11	11	11	11	11	11	11	11	11	-27.6	-21.6
2135	11	11	11	11	11	11	11	11	11	11	-29.5	-21.8
2136	11	11	11	11	11	11	11	11	11	11	-28.3	-20.9
2137	11	11	11	11	11	11	11	11	11	11	-28.2	-21.0

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2138	11	11	11	11	11	11	11	11	11	11	-29.0	-19.3
2139	11	11	11	11	11	11	11	11	13	11	-29.5	-19.6
2140	11	11	11	11	11	11	11	11	13	11	-21.4	-19.1
2141	11	11	11	11	11	11	11	11	11	11	-21.2	-19.6
2142	11	11	11	11	11	11	11	11	11	11	-31.0	-19.8
2143	11	11	11	11	11	11	11	11	12	11	-31.0	-20.6
2144	11	11	11	11	11	11	11	11	23	11	-31.2	-20.1
2146	11	11	11	11	11	11	11	11	13	11	-31.4	-19.7
2147	11	11	11	11	11	11	11	11	22	11	-31.5	-19.4
2148	11	11	11	11	11	11	11	11	12	11	-31.4	-19.2
2149	11	11	11	11	11	11	11	11	11	11	-32.1	-19.5
2150	11	11	11	11	11	11	11	11	12	11	-31.8	-18.2
2151	11	11	11	11	11	11	11	11	12	11	-33.6	-19.2
2152	11	11	11	11	12	11	11	11	11	11	-32.4	-17.5
2153	11	11	11	11	11	11	11	11	11	11	-31.8	-17.1
2154	11	11	11	11	11	11	11	12	12	11	-33.3	-17.5
2155	11	11	11	11	11	11	11	11	11	11	-34.1	-17.2
2156	11	11	11	11	11	11	11	11	11	11	-47.6	-18.2
2157	11	11	11	11	11	11	11	11	11	11	-34.2	-18.8
2160	11	11	11	11	11	11	11	11	13	11	-31.3	-15.3
2161	11	11	11	11	11	11	11	11	11	11	-33.7	-15.4
2162	11	11	11	11	11	11	11	11	13	11	-31.8	-14.6
2163	11	11	11	11	11	11	11	11	11	11	-33.6	-14.2
2164	11	11	11	11	11	11	11	11	22	11	-33.6	-13.4
2165	11	11	11	11	11	11	11	11	13	11	-37.0	-13.3
2166	11	11	11	11	11	11	11	11	12	11	-37.7	-13.1
2167	11	11	11	11	11	11	11	11	13	11	-36.5	-12.3
2168	11	11	11	11	11	11	11	11	11	11	-37.0	-11.5
2169	11	11	11	11	11	11	11	11	23	11	-35.5	-12.8
2170	11	11	11	11	11	11	11	11	12	11	-36.2	-11.5
2171	11	11	11	11	11	11	11	11	34	11	-35.5	-10.7
2172	11	11	11	11	11	11	11	11	11	11	-35.9	-10.1
2173	11	11	11	11	11	11	11	11	12	11	-35.8	-10.3
2175	11	11	11	11	11	11	11	11	13	11	-35.6	-10.4
2176	11	11	11	11	11	11	11	11	11	11	-35.0	-9.9
2177	11	11	11	11	11	11	11	11	23	11	-37.1	-10.0
2179	11	11	11	11	11	11	11	11	11	11	-37.0	-9.0
2180	11	11	11	11	11	11	11	11	14	11	-38.0	-8.8
2181	11	11	11	11	11	11	11	11	13	11	-36.8	-8.6
2182	11	11	11	11	11	11	11	11	11	11	-37.1	-8.2
2184	11	11	11	11	11	11	11	11	12	11	-36.2	-8.3
2185	11	11	11	11	11	11	11	11	11	11	-34.1	-9.0
2186	11	11	11	11	11	11	11	11	13	11	-34.1	-5.8
2187	11	11	11	11	11	11	11	11	13	11	-35.7	-6.6

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2188	11	11	11	11	11	11	11	11	14	11	-35.9	-6.5
2189	11	11	11	11	11	11	11	11	12	11	-36.6	-4.9
2190	11	11	11	11	12	11	11	11	11	11	-35.4	-1.4
2191	11	11	11	11	11	11	11	11	13	11	-37.4	-2.5
2192	11	11	11	11	11	11	11	11	14	11	-36.1	-2.7
2193	11	11	11	11	11	11	11	11	13	11	-35.7	-4.6
2194	11	11	11	11	11	11	11	11	23	11	-38.6	-6.7
2195	11	11	11	11	11	11	11	11	12	11	-39.3	-7.2
2196	11	11	11	11	11	11	11	11	13	11	-38.0	-6.4
2197	11	11	11	11	11	11	11	11	23	11	-39.6	-7.2
2198	11	11	11	11	11	11	11	11	11	11	-39.5	-7.0
2199	11	11	11	11	11	11	11	11	11	11	-39.7	-7.1
2200	11	11	11	11	11	11	11	11	14	11	-39.8	-6.8
2201	11	11	11	11	11	11	11	11	13	11	-40.4	-7.6
2202	11	11	11	11	11	11	11	11	13	11	-42.2	-8.8
2203	11	11	11	11	11	11	11	11	14	11	-39.6	-8.0
2204	11	11	11	11	11	11	11	11	12	11	-39.4	-5.4
2205	11	11	11	11	11	11	11	11	33	11	-39.2	-5.3
2206	11	11	11	11	11	11	11	11	11	11	-39.1	-5.5
2207	11	11	11	11	11	11	11	11	11	11	-39.3	-4.7
2208	11	11	11	11	11	11	11	11	11	11	-39.6	-3.9
2210	11	11	11	11	11	11	11	11	11	11	-32.2	-4.6
2211	11	11	11	11	11	11	11	11	11	11	-32.6	-4.7
2212	11	11	11	11	11	11	11	11	11	11	-34.2	-7.5
2213	11	11	11	11	11	11	11	11	13	11	-33.4	-6.6
2214	11	11	11	11	11	11	11	11	11	11	-33.8	-6.0
2215	11	11	11	11	11	11	11	11	22	11	-33.8	-6.0
2216	11	11	11	11	11	11	11	11	33	11	-33.4	-5.0
2217	11	11	11	11	11	11	11	11	11	11	-32.1	-9.1
2218	11	11	11	11	11	11	11	11	11	11	-34.2	-9.6
2219	11	11	11	11	11	11	11	11	11	11	-36.7	-14.1
2220	11	11	11	11	11	11	11	11	11	11	-37.6	-16.1
2221	11	11	11	11	11	11	11	11	12	11	-38.4	-16.1
2222	11	11	11	11	11	11	11	11	13	11	-38.7	-16.0
2223	11	11	11	11	11	11	11	11	11	11	-38.9	-16.6
2224	11	11	11	11	11	11	11	11	11	11	-38.5	-15.6
2225	11	11	11	11	11	11	11	11	13	11	-37.5	-16.5
2226	11	11	11	11	11	11	11	11	23	11	-33.4	10.8
2227	11	11	11	11	11	11	11	11	13	11	-31.2	11.7
2228	11	11	11	11	11	11	11	11	12	11	-28.4	13.3
2229	11	11	11	11	11	11	11	11	23	11	-25.0	13.2
2230	11	11	11	11	11	11	11	12	12	11	-23.9	14.6
2231	11	11	11	11	11	11	11	11	12	11	-25.0	15.4
2232	11	11	11	11	11	11	11	11	33	11	-25.6	15.0

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2233	11	11	11	11	11	11	11	11	11	11	-23.9	15.3
2234	11	11	11	11	11	11	11	11	11	11	-23.9	13.8
2235	11	11	11	11	11	11	11	11	23	11	-21.2	14.2
2236	11	11	11	11	11	11	11	11	23	11	-21.4	14.6
2237	11	11	11	11	11	11	11	11	11	11	-24.0	14.4
2238	11	11	11	11	11	11	11	11	33	11	-21.8	8.5
2239	11	11	11	11	11	11	11	11	11	11	-21.0	19.0
2240	11	11	11	11	11	11	11	11	11	11	-20.8	18.2
2241	11	11	11	11	11	11	11	11	11	11	-18.8	17.7
2242	11	11	11	11	11	11	11	11	11	11	-19.2	20.4
2243	11	11	11	11	11	11	11	11	11	11	-19.7	19.5
2244	11	11	11	11	11	11	11	11	13	11	-20.6	19.9
2245	11	11	11	11	12	11	11	11	13	11	-20.6	19.6
2246	11	11	11	11	11	11	11	11	13	11	-20.6	21.3
2247	11	11	11	11	11	11	11	11	13	11	-21.5	24.7
2248	11	11	11	11	11	11	11	11	23	11	-25.2	24.0
2249	11	11	11	11	11	11	11	11	12	11	-23.0	20.2
2250	11	11	11	11	11	11	11	11	13	11	-24.1	20.6
2251	11	11	11	11	11	11	11	11	11	11	-25.1	19.5
2252	11	11	11	11	11	11	11	11	12	11	-25.0	21.2
2253	11	11	11	11	11	11	11	11	12	11	-26.8	21.4
2254	11	11	11	11	11	11	11	11	11	11	-27.3	20.2
2255	11	11	11	11	11	11	11	11	12	11	-25.1	18.7
2256	11	11	11	11	11	11	11	11	12	11	-26.4	18.2
2257	11	11	11	11	12	11	11	11	23	11	-26.5	16.8
2258	11	11	11	11	11	11	11	11	13	11	-25.5	16.2
2259	11	11	11	11	11	11	11	11	11	11	-27.3	16.0
2260	11	11	11	11	11	11	11	11	13	11	-27.4	17.0
2261	11	11	11	12	11	11	11	11	13	11	-28.7	16.7
2262	11	11	11	11	11	11	11	11	24	11	-28.8	16.5
2263	11	11	11	11	11	11	11	11	23	11	-27.7	18.1
2264	11	11	11	11	11	11	11	11	12	11	-27.0	18.0
2265	11	11	11	11	11	11	11	11	11	11	-29.6	19.0
2266	11	11	11	11	11	11	11	11	11	11	-30.2	17.8
2267	11	11	11	12	11	11	11	11	23	11	-30.0	17.2
2268	11	11	11	11	11	11	11	11	11	11	-31.2	17.2
2269	11	11	11	11	11	11	11	12	11	11	-33.0	13.8
2270	11	11	11	12	11	11	11	11	12	11	-36.7	15.9
2271	11	11	11	11	11	11	11	11	11	11	-35.1	17.5
2272	11	11	11	12	11	11	11	11	11	11	-35.8	18.0
2273	11	11	11	11	11	11	11	11	13	11	-36.0	19.0
2274	11	11	11	11	11	11	11	11	11	11	-36.2	19.4
2275	11	11	11	11	11	11	11	11	13	11	-35.7	19.1
2276	11	11	11	11	11	11	11	11	33	11	-35.6	19.2

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2277	11	11	11	11	11	11	11	11	13	11	-35.7	19.5
2278	11	11	11	11	11	11	11	11	11	11	-35.2	19.2
2279	11	11	11	11	11	11	11	11	12	11	-33.8	20.9
2280	11	11	11	11	11	11	11	11	11	11	-31.1	19.8
2281	11	11	11	11	11	11	11	11	13	11	-30.8	18.0
2282	11	11	11	11	11	11	11	11	11	11	-32.3	17.7
2283	11	11	11	11	11	11	11	11	13	11	-31.8	17.8
2284	11	11	11	11	11	11	11	11	12	11	-32.4	17.6
2285	11	11	11	11	11	11	11	11	12	11	-35.9	18.1
2286	11	11	11	11	11	11	11	11	12	11	-31.4	20.3
2287	11	11	11	11	11	11	11	11	23	11	-31.5	22.1
2288	11	11	11	11	11	11	11	11	13	11	-30.9	21.8
2290	11	11	11	11	11	11	11	11	11	11	-30.4	20.7
2291	11	11	11	11	11	11	11	11	11	11	-30.6	20.2
2292	11	11	11	11	11	11	11	11	33	11	-29.6	20.5
2293	11	11	11	11	11	11	11	11	13	11	-27.6	22.3
2294	11	11	11	11	11	11	11	11	12	11	-20.0	26.1
2295	11	11	11	11	11	11	11	11	11	11	-20.5	25.8
2296	11	11	11	11	11	11	11	11	11	11	-23.1	27.2
2297	11	11	11	11	11	11	11	11	12	11	-25.0	26.0
2298	11	11	11	11	11	11	11	11	11	11	-26.7	25.9
2299	11	11	11	11	11	11	11	11	12	11	-28.7	24.8
2300	11	11	11	11	11	11	11	11	14	11	-29.9	23.8
2301	11	11	11	11	11	11	11	11	22	11	-30.9	25.8
2302	11	11	11	11	11	11	11	11	11	11	-30.9	25.5
2303	11	11	11	11	11	11	11	11	11	11	-31.8	25.9
2304	11	11	11	11	11	11	11	11	11	11	-31.4	30.3
2305	11	11	11	11	11	11	11	11	11	11	-30.8	30.4
2306	11	11	11	11	11	11	11	11	12	11	-27.6	30.9
2307	11	11	11	11	11	11	11	11	12	11	-26.8	32.0
2308	11	11	11	11	11	11	11	11	11	11	-25.9	33.2
2309	11	11	11	11	11	11	11	11	11	11	-24.5	32.8
2310	11	11	11	11	11	11	11	11	13	11	-30.6	35.2
2312	11	11	11	11	11	11	11	11	11	11	-36.1	36.2
2313	11	11	11	11	11	11	11	11	33	11	-35.1	35.7
2314	11	11	11	11	11	11	11	11	23	11	-30.8	31.4
2315	11	11	11	11	11	11	11	11	13	11	-36.9	28.3
2316	11	11	11	11	11	11	11	11	11	11	-36.7	26.7
2317	11	11	11	11	11	11	11	11	13	11	-37.8	26.9
2318	11	11	11	11	11	11	11	11	12	11	-38.5	28.6
2319	11	11	11	11	11	11	11	11	11	11	-39.3	28.2
2320	11	11	11	11	11	11	11	11	11	11	-37.9	26.2
2321	11	11	11	11	11	11	11	11	13	11	-38.3	26.2

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2322	11	11	11	11	11	11	11	11	13	11	-39.2	27.1
2323	11	11	11	11	11	11	11	11	11	11	-38.9	22.2
2324	11	11	11	11	11	11	11	11	11	12	-38.9	25.9
2325	11	11	11	11	11	11	11	11	11	11	-38.0	21.7
2326	11	11	11	11	11	11	11	11	11	11	-35.1	21.8
2327	11	11	11	11	11	11	11	11	13	11	-36.3	21.9
2328	11	11	11	11	11	11	11	11	33	11	-35.8	23.4
2329	11	11	11	11	11	11	11	11	12	11	-35.2	23.6
2330	11	11	11	11	11	11	11	11	12	11	-30.1	21.3
2331	11	11	11	11	11	11	11	11	13	11	-29.8	21.5
2332	11	11	11	11	11	11	11	11	15	11	-28.7	20.6
2333	11	11	11	11	11	11	11	11	11	11	-27.8	21.0
2334	11	11	11	11	11	11	11	11	12	11	-29.0	21.7
2335	11	11	11	11	11	11	11	11	12	11	-30.0	22.4
2336	11	11	11	11	11	11	11	11	11	11	-29.9	22.9
2339	11	11	11	11	11	11	11	11	12	11	-29.8	23.1
2340	11	11	11	11	11	11	11	11	13	11	-30.2	23.9
2341	11	11	11	11	11	11	11	11	11	11	-39.2	36.8
2342	11	11	11	11	11	11	11	11	22	11	-39.2	33.7
2343	11	11	11	11	12	11	11	11	12	11	-39.9	32.1
2344	11	11	11	11	11	11	11	11	11	11	-43.3	16.1
2346	11	11	11	11	11	11	11	11	12	11	-46.2	10.2
2347	11	11	11	11	11	11	11	11	11	11	-45.8	10.0
2348	11	11	11	11	11	11	11	11	22	11	-46.2	10.3
2349	11	11	11	11	12	11	11	11	12	11	-47.4	9.7
2351	11	11	11	11	11	11	11	11	13	11	-45.1	8.8
2352	11	11	11	11	11	11	11	11	23	11	-45.1	8.7
2353	11	11	11	11	11	11	11	11	11	11	-41.7	8.6
2354	11	11	11	11	11	11	11	11	11	11	-41.6	6.4
2355	11	11	11	11	11	11	11	11	12	11	-41.8	5.0
2356	11	11	11	11	11	11	11	11	12	11	-41.9	5.8
2357	11	11	11	11	11	11	11	11	12	11	-41.8	5.4
2358	11	11	11	11	11	11	11	11	11	11	-41.0	-0.8
2359	11	11	11	11	11	11	11	11	13	12	-40.3	-3.4
2360	11	11	11	11	11	11	11	11	12	11	-42.4	-4.2
2361	11	11	11	11	11	11	11	11	13	11	-42.6	-4.8
2362	11	11	11	11	11	11	11	11	11	11	-43.6	-5.4
2363	11	11	11	11	11	11	11	11	12	11	-43.5	-7.4
2364	11	11	11	11	11	11	11	11	11	11	-42.0	-7.9
2365	11	11	11	11	11	11	11	11	13	11	-43.4	-7.6
2366	11	11	11	11	11	11	11	11	13	12	-43.5	-8.9
2367	11	11	11	11	11	11	11	11	13	11	-44.3	-8.1
2368	11	11	11	11	11	11	11	11	13	11	-44.2	-7.9
2369	11	11	11	11	11	11	11	11	23	11	-44.7	-7.5

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2370	11	11	11	11	11	11	11	11	11	11	-44.7	-7.2
2371	11	11	11	11	11	11	11	11	12	11	-45.4	-8.4
2373	11	11	11	11	11	11	11	11	13	11	-43.6	-7.9
2376	11	11	11	11	11	11	11	11	11	11	-44.7	-7.6
2377	11	11	11	11	11	11	11	11	11	11	-45.1	-6.6
2379	11	11	11	11	11	11	11	11	11	11	-45.5	-7.3
2380	11	11	11	11	11	11	11	11	12	11	-44.4	-5.0
2381	11	11	11	11	11	11	11	11	12	11	-44.6	-4.7
2382	11	11	11	11	11	11	11	11	13	11	-45.6	-5.9
2383	11	11	11	11	11	11	11	11	12	11	-45.5	-5.0
2384	11	11	11	11	12	11	11	11	11	11	-46.7	-5.3
2385	11	11	11	11	11	11	11	11	11	11	-46.6	-5.0
2386	11	11	11	11	11	11	11	11	11	11	-47.3	-5.9
2387	11	11	11	11	11	11	11	11	23	11	-46.8	-7.5
2388	11	11	11	11	11	11	11	11	12	11	-44.8	-7.6
2389	11	11	11	11	11	11	11	11	11	11	-48.0	-7.1
2390	11	11	11	11	11	11	11	11	13	11	-48.3	-6.7
2391	11	11	11	11	11	11	11	11	13	11	-47.3	-4.1
2393	11	11	11	11	11	11	11	11	12	11	-47.0	-4.4
2394	11	11	11	11	11	11	11	11	13	11	-44.6	-4.4
2396	11	11	11	11	11	11	11	11	11	11	-43.9	-3.0
2399	11	11	11	11	11	11	11	11	11	12	-45.1	-1.3
2401	11	11	11	11	11	11	11	11	11	15	-43.6	0.0
2403	11	11	11	11	11	11	11	11	12	11	-41.9	-0.6
2404	11	11	11	11	11	11	11	11	12	11	-42.6	-1.4
2405	11	11	11	11	11	11	11	11	11	11	-42.3	-1.1
2406	11	11	11	11	11	11	11	11	33	11	-43.5	-1.7
2407	11	11	11	11	11	11	11	12	11	11	-44.6	-2.6
2408	11	11	11	11	11	11	11	11	14	11	-45.0	-2.8
2409	11	11	11	11	11	11	11	11	11	11	-45.1	-3.4
2410	11	11	11	11	11	11	11	11	11	11	-44.7	-3.6
2411	11	11	11	11	11	11	11	11	13	11	-40.4	-9.6
2413	11	11	11	11	11	11	11	11	12	11	-40.5	-9.8
2414	11	11	11	11	11	11	11	11	22	11	-38.6	-11.0
2415	11	11	11	11	12	11	11	11	11	11	-38.4	-11.1
2416	11	11	11	11	11	11	11	11	11	11	-39.9	-13.4
2417	11	11	11	11	11	11	11	11	11	11	-40.3	-13.0
2418	11	11	11	11	11	11	11	11	12	11	-41.1	-13.3
2419	11	11	11	11	11	11	11	11	11	11	-40.6	-13.2
2420	11	11	11	11	11	11	11	11	13	11	-41.5	-12.3
2421	11	11	11	11	11	11	11	11	11	11	-40.3	12.3
2422	11	11	11	11	11	11	11	11	11	11	-40.4	-11.9
2423	11	11	11	11	11	11	11	11	11	11	-40.4	-11.7
2424	11	11	11	12	11	11	11	11	12	11	-40.4	-11.0

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2425	11	11	11	11	12	11	11	11	12	11	-40.3	-14.5
2426	11	11	11	11	11	11	11	11	13	11	-40.0	-15.5
2427	11	11	11	11	11	11	11	11	11	11	-40.9	-12.3
2428	11	11	11	11	11	11	11	11	34	11	-42.5	-12.4
2429	11	11	11	11	11	11	11	11	33	11	-42.4	-11.9
2430	11	11	11	11	11	11	11	11	13	11	-42.3	-11.2
2431	11	11	11	11	11	11	11	11	11	11	-43.3	-9.8
2432	11	11	11	11	11	11	11	11	13	11	-41.8	-10.2
2433	11	11	11	11	11	11	11	11	12	11	-41.0	-10.6
2434	11	11	11	11	11	11	11	11	12	11	-50.3	-4.3
2435	11	11	11	11	11	11	11	11	12	11	-49.7	-3.6
2436	11	11	11	11	11	11	11	11	11	11	-48.9	-1.3
2437	11	11	11	11	11	11	11	11	12	11	-46.7	1.7
2438	11	11	11	11	11	11	11	11	11	11	-48.0	1.9
2439	11	11	11	11	11	11	11	11	12	11	-49.7	6.8
2440	11	11	11	11	11	11	11	11	11	11	-49.2	6.7
2441	11	11	11	11	11	11	11	11	23	11	-51.3	8.4
2442	11	11	11	11	11	11	11	11	11	11	-51.0	9.0
2443	11	11	11	11	11	11	11	11	12	11	-50.4	10.5
2444	11	11	11	11	11	11	11	11	11	11	-51.4	9.5
2445	11	11	11	11	11	11	11	11	13	11	-51.9	9.6
2446	11	11	11	11	11	11	11	11	13	11	-51.2	10.4
2448	11	11	11	11	11	11	11	11	13	11	-51.6	8.7
2449	11	11	11	11	11	11	11	11	11	11	-53.4	7.8
2450	11	11	11	11	11	11	11	11	12	11	-52.0	9.8
2451	11	11	11	11	11	11	11	11	12	11	-53.0	10.5
2452	11	11	11	11	11	11	11	11	11	11	-52.8	11.3
2453	11	11	11	11	11	11	11	11	16	11	-53.7	10.2
2454	11	11	11	11	11	11	11	11	11	11	-53.7	11.0
2455	11	11	11	11	12	11	11	11	12	11	-53.5	10.9
2456	11	11	11	11	11	11	11	11	11	11	-53.8	11.5
2457	11	11	11	11	11	11	11	11	11	11	-2.9	11.8
2458	11	11	11	11	11	12	11	11	14	11	-50.8	12.3
2459	11	11	11	11	11	11	11	11	12	11	-50.4	11.6
2460	11	11	11	11	11	11	11	11	12	11	-50.4	13.8
2461	11	11	11	11	11	11	11	11	13	11	-50.4	15.1
2462	11	11	11	11	11	11	11	11	15	11	-49.0	15.2
2463	11	11	11	11	11	11	11	11	11	11	-49.0	15.9
2464	11	11	11	11	11	11	11	11	11	11	-48.2	17.5
2465	11	11	11	11	11	11	11	11	22	11	-48.0	17.5
2466	11	11	11	11	11	11	11	11	11	11	-47.2	18.4
2467	11	11	11	11	11	11	11	11	11	11	-47.5	18.4
2468	11	11	11	11	11	11	11	11	11	11	-49.3	20.0
2469	11	11	11	11	11	11	11	11	23	11	-49.3	19.6

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2470	11	11	11	11	11	11	11	11	23	11	-42.0	19.0
2471	11	11	11	11	11	11	11	11	12	11	-49.3	22.2
2472	11	11	11	11	11	11	11	11	22	11	-57.0	19.6
2473	11	11	11	11	11	11	11	11	13	11	-50.0	19.0
2475	11	11	11	12	11	11	11	11	13	11	-53.8	20.3
2476	11	11	11	11	11	11	11	11	34	11	-53.5	20.3
2477	11	11	11	11	11	11	11	11	13	11	-54.2	22.8
2478	11	11	11	11	11	11	11	11	14	11	-54.6	21.1
2479	11	11	11	11	11	11	11	11	11	11	-53.7	16.6
2480	11	11	11	11	11	11	11	11	24	11	-52.8	15.8
2481	11	11	11	11	11	11	11	11	13	11	-50.6	15.8
2482	11	11	11	11	11	11	11	11	11	11	-50.3	16.5
2483	11	11	11	11	11	11	11	11	12	11	-54.3	15.0
2484	11	11	11	11	11	11	11	11	12	11	-53.1	14.9
2485	11	11	11	11	11	11	11	11	11	11	-54.7	13.6
2486	11	11	11	11	11	11	11	11	23	11	-55.1	14.6
2487	11	11	11	11	12	11	11	11	12	11	-54.7	12.4
2488	11	11	11	11	11	11	11	11	13	11	-55.3	11.6
2489	11	11	11	11	11	11	11	11	13	11	-54.5	11.6
2490	11	11	11	11	11	11	11	11	22	11	-55.1	12.5
2491	11	11	11	11	11	11	11	11	11	11	-56.3	11.4
2492	11	11	11	11	11	11	11	11	11	11	-56.7	10.5
2493	11	11	11	11	11	11	11	11	11	11	-56.7	10.3
2494	11	11	11	11	11	11	11	11	11	11	-59.3	11.3
2495	11	11	11	11	11	12	11	11	12	11	-54.9	7.6
2496	11	11	11	11	11	11	11	11	11	11	-55.4	8.7
2497	11	11	11	11	11	11	11	11	11	11	-52.9	4.9
2498	11	11	11	11	11	11	11	11	13	11	-51.8	4.1
2499	11	11	11	11	11	11	11	11	33	11	-53.1	4.2
2500	11	11	11	11	11	11	11	11	12	11	-48.7	4.2
2501	11	11	11	11	11	11	11	11	11	11	-29.9	22.7
2502	11	11	11	11	11	11	11	11	11	11	-56.7	13.3
2503	11	11	11	11	11	11	11	11	11	11	-55.9	13.7
2504	11	11	11	11	11	11	11	11	12	11	-56.3	14.0
2505	11	11	11	12	11	11	11	11	11	11	-56.3	14.3
2506	11	11	11	11	11	11	11	11	33	11	-56.4	14.2
2507	11	11	11	12	11	11	11	11	23	11	-4.9	15.5
2508	11	11	11	11	11	11	11	11	22	11	-54.5	16.6
2509	11	11	11	11	11	11	11	11	13	11	-54.7	17.2
2510	11	11	11	11	11	11	11	11	23	11	-55.2	18.9
2511	11	11	11	11	11	11	11	11	11	11	-54.6	18.7
2512	11	11	11	11	11	11	11	11	13	11	-54.5	19.4
2513	11	11	11	11	11	11	11	11	11	11	-54.9	19.9
2514	11	11	11	11	11	11	11	11	12	11	-54.5	20.8

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2515	11	11	11	11	11	11	11	11	11	11	-53.7	22.2
2516	11	11	11	11	11	11	11	11	11	11	-53.9	22.7
2517	11	11	11	11	11	11	11	11	12	11	-54.3	22.8
2518	11	11	11	11	11	11	11	11	11	11	-54.7	23.4
2519	11	11	11	11	11	11	11	11	11	11	-55.7	23.5
2520	11	11	11	11	11	11	11	11	23	11	-54.8	23.8
2521	11	11	11	11	11	11	11	11	11	11	-55.3	23.5
2522	11	11	11	11	11	11	11	11	13	11	-55.1	23.4
2523	11	11	11	11	11	11	11	11	33	11	-55.8	25.2
2524	11	11	11	11	11	11	11	11	12	11	-56.7	23.1
2525	11	11	11	11	11	11	11	11	11	11	-57.4	22.6
2526	11	11	11	11	11	11	11	11	14	11	-56.0	21.4
2527	11	11	11	11	11	11	11	11	12	11	-56.6	20.8
2528	11	11	11	11	11	11	11	11	13	11	-59.5	21.4
2530	11	11	11	11	11	11	11	11	12	11	-57.3	19.9
2531	11	11	11	11	11	11	11	11	12	11	-58.7	19.2
2532	11	11	11	11	11	11	11	11	33	11	-58.7	14.9
2533	11	11	11	11	11	11	11	11	13	11	-57.7	14.9
2534	11	11	11	11	11	11	11	11	22	11	-63.3	18.5
2535	11	11	11	11	11	11	11	11	13	12	-62.1	18.9
2536	11	11	11	11	11	11	11	11	11	11	-62.4	20.5
2537	11	11	11	11	11	11	11	11	13	11	-62.2	22.4
2538	11	11	11	11	11	11	11	11	12	11	-60.4	22.9
2539	11	11	11	11	11	11	11	11	11	11	-60.7	24.4
2540	11	11	11	11	11	11	11	11	13	12	-60.8	24.3
2541	11	11	11	11	11	11	11	11	11	11	-61.4	24.8
2542	11	11	11	11	11	11	11	11	13	11	-58.6	24.0
2544	11	11	11	11	11	11	11	11	12	11	-57.3	24.9
2545	11	11	11	11	11	11	11	11	12	11	-58.2	25.2
2546	11	11	11	11	11	11	11	11	12	11	-58.2	25.5
2547	11	11	11	11	11	11	11	11	13	11	-56.8	25.4
2548	11	11	11	11	12	11	11	11	23	11	-56.8	25.5
2549	11	11	11	11	11	11	11	11	11	11	-56.1	26.1
2550	11	11	11	11	11	11	11	11	11	11	-55.3	26.1
2551	11	11	11	11	11	11	11	11	12	11	-54.0	28.2
2552	11	11	11	11	11	11	11	11	24	11	-56.9	27.4
2553	11	11	11	11	11	11	11	11	11	11	-57.0	28.9
2554	11	11	11	12	11	11	11	11	12	11	-55.4	31.5
2555	11	11	11	11	11	11	11	11	13	11	-58.8	29.3
2556	11	11	11	11	11	11	11	11	11	11	-58.2	31.6
2557	11	11	11	11	11	11	11	11	13	11	-58.6	31.8
2558	11	11	11	11	11	11	11	11	22	11	-59.2	31.5
2559	11	11	11	11	11	11	11	11	12	11	-60.4	31.7
2560	11	11	11	11	11	11	11	11	13	11	-61.4	33.2

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2561	11	11	11	11	11	11	11	11	13	11	-62.4	33.2
2562	11	11	11	11	11	11	11	11	22	11	-62.7	29.9
2563	11	11	11	11	11	11	11	11	23	11	-62.8	29.6
2564	11	11	11	11	11	11	11	11	12	11	-63.5	29.5
2565	11	11	11	11	11	11	11	11	13	11	-63.8	29.5
2566	11	11	11	11	11	11	11	11	13	11	-64.1	30.3
2567	11	11	11	11	11	11	11	11	22	11	-64.4	31.2
2568	11	11	11	11	11	11	11	11	11	11	-64.5	31.7
2569	11	11	11	11	11	11	11	11	33	11	-66.2	31.8
2570	11	11	11	11	11	11	11	11	13	11	-67.6	33.4
2571	11	11	11	11	11	11	11	11	11	11	-67.3	31.9
2572	11	11	11	11	11	11	11	11	23	11	-64.6	29.7
2573	11	11	11	11	11	11	11	11	13	11	-64.0	29.4
2574	11	11	11	11	11	11	11	11	11	11	-62.9	29.1
2575	11	11	11	11	11	11	11	11	13	11	-62.9	28.8
2576	11	11	11	11	11	11	11	11	11	11	-62.5	28.2
2577	11	11	11	11	11	11	11	11	11	11	-62.8	28.5
2578	11	11	11	11	11	11	11	11	22	11	-63.0	28.1
2579	11	11	11	11	11	11	11	11	11	11	-63.2	27.9
2580	11	11	11	11	11	11	11	11	13	11	-61.3	24.5
2581	11	11	11	11	11	11	11	11	13	11	-62.9	24.6
2582	11	11	11	11	11	11	11	11	33	11	-62.2	24.1
2583	11	11	11	11	12	11	11	11	11	11	-63.3	25.8
2584	11	11	11	11	11	11	11	11	13	11	-64.3	23.2
2585	11	11	11	12	11	11	11	11	13	11	-55.6	4.8
2586	11	11	11	11	11	11	11	11	11	11	-55.4	5.1
2587	11	11	11	11	11	11	11	11	12	11	-56.7	6.2
2588	11	11	11	11	11	11	11	11	13	11	-59.4	7.1
2589	11	11	11	11	11	11	11	11	12	11	-59.2	6.5
2590	11	11	11	11	11	11	11	11	13	11	-59.9	5.0
2591	11	11	11	11	11	11	11	11	12	11	-60.9	3.2
2592	11	11	11	11	11	11	11	11	12	11	-61.5	3.3
2593	11	11	11	11	11	11	11	11	12	11	-61.3	3.4
2594	11	11	11	11	11	11	11	11	13	11	-61.1	3.8
2595	11	11	11	11	11	11	11	11	13	11	-61.0	7.0
2596	11	11	11	11	11	11	11	11	11	11	-62.0	7.2
2597	11	11	11	11	11	11	11	11	11	11	-63.3	10.0
2598	11	11	11	11	11	11	11	11	12	15	-63.5	11.0
2599	11	11	11	11	11	11	11	11	11	11	-63.7	11.8
2600	11	11	11	11	11	11	11	11	13	11	-64.4	11.1
2601	11	11	11	11	12	11	11	11	24	11	-64.6	8.9
2602	11	11	11	11	11	11	11	11	11	11	-65.0	8.4
2603	11	11	11	11	11	11	11	11	11	11	-66.6	7.2
2604	11	11	11	11	11	11	11	11	13	11	-65.8	6.1

APPENDIX III. (Cont.) (Field)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
2605	11	11	11	11	11	11	11	11	13	11	-51.4	-0.2
2606	11	11	11	11	11	11	11	11	12	11	-51.2	-2.5
2607	11	11	11	11	11	11	11	11	12	11	-51.4	-3.6

APPENDIX IV

ALLOZYME SCORES AND TREE LOCATIONS FOR TAMARACK IN TWIN CITY POPULATION

APPENDIX IV. (Twin City population)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
3000	11	11	11	11	11	11	11	11	24	11	-2.3	28.0
3001	11	11	11	11	11	11	11	11	11	11	-3.7	29.2
3002	11	11	11	11	11	11	11	11	11	11	-3.1	29.4
3003	11	11	11	11	11	11	11	11	14	11	-6.0	26.3
3004	11	11	11	11	11	11	11	11	14	11	-6.6	25.5
3005	11	11	11	11	11	11	11	11	23	11	-6.4	30.7
3006	11	11	11	11	11	11	11	11	13	11	-6.8	31.1
3007	11	11	11	11	11	11	11	11	11	11	-6.0	33.8
3008	11	11	11	11	11	11	11	11	13	11	-6.0	34.8
3009	11	11	11	11	11	11	11	11	24	11	-5.2	35.1
3010	11	11	11	11	11	11	11	11	13	11	-4.4	34.3
3011	11	11	11	11	11	11	11	11	13	11	-2.9	34.9
3012	11	11	11	11	11	11	11	11	13	11	-3.3	32.9
3013	11	11	11	11	11	11	11	11	13	11	-4.0	32.9
3014	11	11	11	11	11	11	11	11	11	11	-4.1	32.1
3015	11	11	11	11	11	11	11	11	13	11	-2.1	32.3
3016	11	11	11	11	11	11	11	11	33	11	-0.1	32.1
3017	11	11	11	11	11	11	11	11	12	11	0.6	31.7
3018	11	11	11	11	11	11	11	11	12	11	1.3	31.3
3019	11	11	11	11	11	11	11	11	33	11	0.2	30.1
3020	11	11	11	11	11	11	11	11	11	11	-1.0	30.5
3021	11	11	11	11	11	11	11	11	11	11	-9.3	30.0
3022	11	11	11	11	11	11	11	11	11	11	-10.8	29.9
3023	11	11	11	11	11	11	11	11	11	11	-10.6	31.4
3024	11	11	11	11	11	11	11	11	23	11	-10.7	30.4
3025	11	11	11	11	11	11	11	11	13	11	-10.5	28.0
3026	11	11	11	11	11	11	11	11	14	11	-11.5	27.8
3027	11	11	11	11	11	11	11	11	13	11	-12.5	27.5
3028	11	11	11	11	11	11	11	11	12	11	-8.1	25.5
3029	11	11	11	11	11	11	11	11	11	11	-7.2	26.3
3030	11	11	11	11	11	11	11	11	33	11	-7.9	25.0
3031	11	11	11	11	11	11	11	11	34	11	-7.7	25.1
3032	11	11	11	11	11	11	11	11	11	11	-7.5	23.8
3033	11	11	11	11	11	11	11	11	12	11	-13.6	25.9
3034	11	11	11	11	11	11	11	11	11	11	-14.7	28.1
3035	11	11	11	11	11	11	11	11	13	11	-15.6	27.3
3036	11	11	11	11	11	11	11	11	12	11	-15.5	26.5
3037	11	11	11	11	11	11	11	11	11	11	-13.1	24.3
3038	11	11	11	11	11	11	11	11	13	11	-12.5	23.4
3039	11	11	11	11	11	11	11	11	14	11	-16.4	24.5
3040	11	11	11	11	11	11	11	11	13	11	-19.2	17.9
3041	11	11	11	11	11	11	11	11	11	11	-20.4	19.3
3042	11	11	11	11	11	11	11	11	11	11	-21.2	20.4

APPENDIX IV. (Cont.) (Twin City)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
3043	11	11	11	11	11	11	11	11	13	11	-22.1	18.5
3044	11	11	11	11	11	11	11	11	33	11	-19.9	16.0
3045	11	11	11	11	11	11	11	11	23	11	-14.7	13.0
3046	11	11	11	11	11	11	11	11	13	11	-14.4	11.8
3048	11	11	11	11	11	11	11	11	13	11	-14.1	10.7
3049	11	11	11	11	11	11	11	11	11	11	-10.1	14.9
3050	11	11	11	11	11	11	11	11	11	11	-10.0	13.6
3051	11	11	11	11	11	11	11	11	11	11	-9.2	18.3
3052	11	11	11	11	11	11	11	11	14	11	-6.7	20.1
3053	11	11	11	11	11	11	11	11	23	11	-5.1	18.8
3054	11	11	11	11	11	11	11	11	13	11	-7.9	18.5
3055	11	11	11	11	11	11	11	11	34	11	-7.9	14.0
3056	11	11	11	11	11	11	11	11	11	11	-9.0	12.8
3057	11	11	11	11	11	11	11	11	13	11	-8.0	11.5
3058	11	11	11	11	11	11	11	11	12	11	-7.3	10.5
3059	11	11	11	11	11	11	11	11	13	11	-6.0	13.7
3060	11	11	11	11	11	11	11	11	23	11	-6.2	13.5
3061	11	11	11	11	11	11	11	11	24	11	-7.5	10.6
3062	11	11	11	11	11	11	11	11	14	11	-4.5	13.4
3063	11	11	11	11	11	11	11	11	23	11	-3.6	12.8
3064	11	11	11	11	11	11	11	11	12	11	-3.3	13.6
3065	11	11	11	11	11	11	11	11	13	11	-5.2	14.0
3066	11	11	11	11	11	11	11	11	12	11	-4.5	14.5
3067	11	11	11	11	11	11	11	11	11	11	-1.5	12.1
3068	11	11	11	11	11	11	11	11	13	11	-2.1	11.8
3069	11	11	11	11	11	11	11	11	11	11	-1.3	11.5
3070	11	11	11	11	11	11	11	11	23	11	-2.1	11.5
3071	11	11	11	11	11	11	11	11	13	11	-2.5	10.9
3072	11	11	11	11	11	11	11	11	11	11	-3.1	10.4
3073	11	11	11	11	11	11	11	11	11	11	1.9	13.7
3075	11	11	11	11	11	11	11	11	11	11	3.3	16.0
3077	11	11	11	11	11	11	11	11	13	11	4.1	16.9
3078	11	11	11	11	11	11	11	11	15	11	5.2	15.4
3079	11	11	11	11	11	11	11	11	12	11	6.5	15.7
3080	11	11	11	11	11	11	11	11	15	11	6.5	15.4
3081	11	11	11	11	11	11	11	11	11	11	6.3	19.4
3082	11	11	11	11	11	11	11	11	22	11	3.7	25.3
3083	11	11	11	11	11	11	11	11	11	11	5.3	25.5
3084	11	11	11	11	11	11	11	11	13	11	6.8	31.3
3085	11	11	11	11	11	11	11	11	13	11	10.2	33.8
3086	11	11	11	11	11	11	11	11	13	11	11.5	34.3
3087	11	11	11	11	11	11	11	11	12	11	15.3	27.4
3088	11	11	11	11	11	11	11	11	13	11	14.5	25.9
3089	11	11	11	11	11	11	11	11	13	11	15.8	25.6

APPENDIX IV. (Cont.) (Twin City)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
3090	11	11	11	11	11	11	11	11	12	11	15.4	24.9
3091	11	11	11	11	11	11	11	11	12	11	14.5	23.4
3092	11	11	11	11	11	11	11	11	12	11	6.6	17.5
3093	11	11	11	11	11	11	11	11	12	11	-9.3	34.8
3094	11	11	11	11	11	11	11	11	11	11	-10.3	35.0
3095	11	11	11	11	11	11	11	11	11	11	-11.3	34.2
3096	11	11	11	11	11	11	11	11	11	11	-11.8	31.7
3097	11	11	11	11	11	11	11	11	11	11	-13.0	31.2
3098	11	11	11	11	11	11	11	11	13	11	-16.4	29.9
3099	11	11	11	11	11	11	11	11	13	11	-16.7	31.3
3100	11	11	11	11	11	11	11	11	11	11	-16.7	31.7
3101	11	11	11	11	11	11	11	11	13	11	-7.8	38.7
3102	11	11	11	11	11	11	11	11	23	12	-6.6	47.4
3103	11	11	11	11	11	11	11	11	13	11	-7.4	44.0
3105	11	11	11	11	11	11	11	11	13	11	-7.4	41.6
3106	11	11	11	11	11	11	11	11	13	11	-8.8	39.8
3107	11	11	11	11	11	11	11	11	11	11	-9.1	38.9
3108	11	11	11	11	11	11	11	11	22	11	-9.4	42.7
3109	11	11	11	11	11	11	11	11	14	11	-10.2	42.3
3110	11	11	11	11	11	11	11	11	13	11	-9.2	44.9
3111	11	11	11	11	11	11	11	11	14	11	-9.4	44.7
3112	11	11	11	11	11	11	11	11	13	11	-8.9	45.9
3113	11	11	11	11	11	11	11	11	11	11	-10.2	44.1
3114	11	11	11	11	11	11	11	11	13	11	-11.5	42.9
3115	11	11	11	11	11	11	11	11	12	11	-11.9	45.4
3116	11	11	11	11	11	11	11	11	33	11	-12.6	44.9
3117	11	11	11	11	11	11	11	11	11	11	-9.7	47.4
3118	11	11	11	11	11	11	11	11	11	11	-14.0	45.6
3119	11	11	11	11	11	11	11	11	14	11	-14.3	44.6
3120	11	11	11	11	11	11	11	11	14	11	-16.2	43.3
3121	11	11	11	11	11	11	11	11	13	11	-11.8	41.8
3122	11	11	11	11	11	11	11	11	12	11	-11.5	39.6
3123	11	11	11	11	11	11	11	11	11	11	-14.4	41.1
3124	11	11	11	11	11	11	11	11	12	11	-13.1	38.8
3125	11	11	11	11	11	11	11	11	13	11	-14.5	38.5
3126	11	11	11	11	11	11	11	11	11	11	-14.8	42.6
3127	11	11	11	11	11	11	11	11	11	11	-16.8	40.1
3128	11	11	11	11	11	11	11	11	11	11	-17.5	37.6
3129	11	11	11	11	11	11	11	11	11	11	-18.2	38.0
3130	11	11	11	11	11	11	11	11	33	11	-18.4	38.6
3131	11	11	11	11	11	11	11	11	11	11	-19.0	38.1
3132	11	11	11	11	11	11	11	11	11	11	-15.4	37.3
3133	11	11	11	11	11	11	11	11	14	11	-15.4	37.9
3134	11	11	11	11	11	11	11	11	13	11	-15.5	35.5

APPENDIX IV. (Cont.) (Twin City)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
3135	11	11	11	11	11	11	11	11	14	11	-17.2	35.6
3136	11	11	11	11	11	11	11	11	12	11	-18.0	35.3
3137	11	11	11	11	11	11	11	11	13	11	-14.0	36.0
3138	11	11	11	11	11	11	11	11	11	11	-20.8	37.6
3139	11	11	11	11	11	11	11	11	12	11	-20.3	37.6
3140	11	11	11	11	11	11	11	11	13	11	-21.1	33.6
3141	11	11	11	11	11	11	11	11	14	11	-21.4	29.3
3142	11	11	11	11	11	11	11	11	11	11	-21.6	28.8
3143	11	11	11	11	11	11	11	11	13	11	-22.0	20.9
3144	11	11	11	11	11	11	11	11	13	22	-23.4	20.4
3145	11	11	11	11	11	11	11	11	13	11	-23.5	21.0
3146	11	11	11	11	11	11	11	11	11	11	-24.3	20.7
3147	11	11	11	11	11	11	11	11	12	11	-28.8	22.3
3148	11	11	11	11	11	11	11	11	11	11	-28.8	19.3
3149	11	11	11	11	11	11	11	11	13	11	-27.9	24.3
3150	11	11	11	11	11	11	11	11	13	11	-25.4	20.4
3152	11	11	11	11	11	11	11	11	12	12	-25.3	20.8
3153	11	11	11	11	11	11	11	11	11	11	-24.5	19.4
3154	11	11	11	11	11	11	11	11	12	11	-28.8	12.3
3155	11	11	11	11	11	11	11	11	13	11	-11.4	6.9
3156	11	11	11	11	11	11	11	11	11	11	-9.4	7.0
3157	11	11	11	11	11	11	11	11	13	11	-9.5	6.4
3158	11	11	11	11	11	11	11	11	12	11	-7.8	5.0
3159	11	11	11	11	11	11	11	11	13	11	-2.9	6.1
3160	11	11	11	11	11	11	11	11	13	11	-2.7	6.5
3161	11	11	11	11	11	11	11	11	12	11	-2.1	6.3
3162	11	11	11	11	11	11	11	11	23	11	-2.7	7.9
3163	11	11	11	11	11	11	11	11	13	11	-1.5	7.9
3164	11	11	11	11	11	11	11	11	14	11	1.5	10.7
3165	11	11	11	11	11	11	11	11	22	11	1.0	5.8
3166	11	11	11	11	11	11	11	11	12	11	2.0	6.3
3167	11	11	11	11	11	11	11	11	13	11	10.9	-0.8
3168	11	11	11	11	11	11	11	11	11	11	13.0	0.6
3169	11	11	11	11	11	11	11	11	12	11	13.2	4.1
3170	11	11	11	11	11	11	11	11	14	11	15.4	14.1
3171	11	11	11	11	11	11	11	11	14	11	16.2	16.7
3172	11	11	11	11	11	11	11	11	23	11	17.5	18.3
3173	11	11	11	11	11	11	11	11	13	11	19.7	19.7
3174	11	11	11	11	11	11	11	11	13	11	21.1	23.0
3175	11	11	11	11	11	11	11	11	11	11	6.9	24.8
3176	11	11	11	11	11	11	11	11	33	11	12.0	39.8
3177	11	11	11	12	11	11	11	11	33	11	12.9	40.5
3178	11	11	11	11	11	11	11	11	12	11	14.0	41.6
3179	11	11	11	11	11	11	11	11	13	11	18.0	43.8

APPENDIX IV. (Cont.) (Twin City)

Tree Number	Allozyme Score										Tree Location	
	Aat 1	Aat 2	Ald 2	Ald 3	Fum	Gdh	Hk	Idh	Pgi 2	Pgm	South	East
3180	11	11	11	12	12	11	11	11	11	11	17.2	43.9
3181	11	11	11	11	11	11	11	11	33	11	17.2	44.2
3182	11	11	11	11	11	11	11	11	14	11	14.8	44.2
3183	11	11	11	11	11	11	11	11	13	11	14.6	43.8
3184	11	11	11	11	11	11	11	11	11	11	13.5	45.4
3185	11	11	11	11	11	11	11	11	13	11	14.1	44.8
3186	11	11	11	11	12	11	11	11	12	11	14.8	46.7
3187	11	11	11	11	11	11	11	11	12	11	5.7	47.1
3188	11	11	11	11	11	11	11	11	11	11	4.8	48.5
3189	11	11	11	11	11	11	11	11	13	11	5.2	50.2
3190	11	11	11	11	11	11	11	11	14	12	6.7	51.2
3191	11	11	11	11	11	11	11	11	13	11	4.1	51.4
3192	11	11	11	11	11	11	11	11	13	11	-0.3	48.0
3193	11	11	11	11	11	11	11	11	14	11	0.2	47.3
3194	11	11	11	11	11	11	11	11	11	11	3.0	45.2
3195	11	11	11	11	11	11	11	11	14	11	4.8	44.8
3196	11	11	11	11	11	11	11	11	12	11	3.5	46.7
3197	11	11	11	11	11	11	11	11	23	11	5.9	46.7
3198	11	11	11	11	11	11	11	11	23	11	4.4	41.8
3199	11	11	11	11	11	11	11	11	11	11	5.5	44.2
3200	11	11	11	11	11	11	11	11	11	11	6.1	40.8

APPENDIX V

AUTOCORRELATION COEFFICIENTS FOR BALMORAL POPULATION

Appendix V. Autocorrelation coefficients (Moran's I values) for Balmoral population.

Locus -Allele	Distance Class (m)									
	0-5	5-10	10-15	15-20	20-25	25-30	30-35	35-65	65-110	110-200
Ald3-2	0.1620***	0.0780***	0.1140***	0.0250	-0.0040	0.0010	-0.0180	0.0050	-0.0170***	-0.0130
Fum-2	0.0110	-0.0150	0.0240	-0.0220	-0.0120	0.0000	-0.0120	-0.0020	0.0020	-0.0080
Pgi2-1	-0.0030	-0.0150	-0.0010	0.0450***	0.0030	-0.0010	0.0040	-0.0050	-0.0070	0.0040
Pgi2-2	0.0830*	-0.0090	0.0210	0.0280	-0.0190	0.0130	-0.0150	-0.0100	-0.0020	0.0050
Pgi2-3	0.0440	0.0150	0.0130	-0.0020	-0.0200	-0.0130	-0.0100	-0.0050	-0.0030	0.0020
Pgi2-4	0.0510	0.0020	0.0110	-0.0100	-0.0100	-0.0180	0.0010	-0.0080	0.0010	-0.0020
Pgi2-5	0.1370***	-0.0090	-0.0060	-0.0060	-0.0090	0.0110	0.0120	-0.0030	-0.0090	0.0050
Pgm-1	-0.0130	-0.0060	-0.0220	-0.0110	0.0140	-0.0040	-0.0100	-0.0020	-0.0020	0.0000
Pgm-2	-0.0020	-0.0020	-0.0060	0.0140	-0.0100	0.0100	-0.0090	-0.0020	-0.0050	0.0020
Mean	0.0522	0.0043	0.0164	0.0090	-0.0074	-0.0001	-0.0063	-0.0036	-0.0047	-0.0006

* Significant at 95 percent confidence level.

** Significant at 99 percent confidence level.

*** Significant at 99.9 percent confidence level.

APPENDIX VI

AUTOCORRELATION COEFFICIENTS FOR BOG POPULATION

Appendix VI. Autocorrelation coefficients (Moran's _I_ values) for Bog population.

Locus -Allele	Distance Class (m) 0-5	5-10	10-15	15-20	20-25	25-30	30-35	35-50
Ald3-2	-0.0090	-0.0070	0.0010	-0.0040	-0.0010	0.0050	-0.0040	0.0000
Fum-2	0.0110	0.0020	-0.0010	0.0000	0.0010	-0.0030	-0.0310	-0.0100
Pgi2-2	-0.0050	0.0010	0.0080	-0.0080	-0.0170*	-0.0050	0.0170	0.0010
Pgi2-3	0.0450***	-0.0050	-0.0180	-0.0080	0.0030	0.0220**	-0.0180	-0.0100
Pgi2-4	0.0250*	-0.0130	-0.0130	0.0080	-0.0070	-0.0010	-0.0200	-0.0090
Pgi2-5	0.0100	-0.0050	-0.0010	0.0080*	-0.0020	-0.0080	-0.0110	-0.0350***
Pgm-1	0.0120	0.0030	-0.0110	0.0010	-0.0050	-0.0040	-0.0040	0.0050
Pgm-2	0.0130	-0.0030	-0.0050	0.0090*	0.0020	-0.0210**	-0.0120	-0.0070
Pgm-4	0.0060	-0.0070	-0.0060	-0.0060	-0.0030	0.0240***	-0.0120	-0.0090
Mean	0.0120	-0.0038	-0.0051	0.0000	-0.0017	0.0010	-0.0106	-0.0082

* Significant at 95 percent confidence level.

** Significant at 99 percent confidence level.

*** Significant at 99.9 percent confidence level.

APPENDIX VII

AUTOCORRELATION COEFFICIENTS FOR FIELD POPULATION

Appendix VII. Autocorrelation coefficients (Moran's I values) for Field population.

Locus -Allele	Distance Class (m)									
	0-5	5-10	10-15	15-20	20-25	25-30	30-35	35-40	40-45	45-78
Ald3-2	-0.0050	0.0040	-0.0100	-0.0020	-0.0060	-0.0040	-0.0020	0.0020	0.0080	-0.0030
Fum-2	-0.0120	-0.0100	-0.0040	0.0020	0.0030	-0.0010	-0.0030	-0.0040	0.0010	0.0030
Gdh-2	-0.0040	0.0160**	-0.0030	-0.0050	-0.0080	-0.0050	-0.0040	-0.0030	-0.0030	0.0020
Idh-2	-0.0010	0.0000	-0.0080	0.0010	0.0160**	-0.0080	0.0050	-0.0110	-0.0090	-0.0050
Pgi2-1	-0.0160	0.0000	0.0020	0.0000	-0.0050	0.0000	0.0020	0.0020	0.0020	-0.0090
Pgi2-2	-0.0160	0.0040	0.0040	0.0020	0.0090	-0.0020	0.0020	-0.0070	-0.0100	-0.0120
Pgi2-3	-0.0170	0.0030	-0.0030	0.0000	-0.0030	0.0000	-0.0080	0.0030	-0.0060	0.0050
Pgi2-4	0.0050	-0.0030	-0.0110	0.0000	-0.0020	-0.0110	0.0070	0.0030	0.0020	-0.0030
Pgi2-5	-0.0040	-0.0040	-0.0020	-0.0030	0.0110**	-0.0080	-0.0050	-0.0030	-0.0020	0.0010
Pgm-2	-0.0100	0.0080	-0.0110	-0.0120	-0.0010	0.0040	0.0060	-0.0030	0.0040	-0.0080
Pgm-5	-0.0020	-0.0090	-0.0080	0.0060	0.0050	-0.0040	-0.0070	-0.0040	0.0100	-0.0020
Mean	-0.0075	0.0008	-0.0049	-0.0008	0.0022	-0.0040	-0.0008	-0.0023	-0.0003	-0.0028

* Significant at 95 percent confidence level.

** Significant at 99 percent confidence level.

*** Significant at 99.9 percent confidence level.

APPENDIX VIII

AUTOCORRELATION COEFFICIENTS FOR TWIN CITY POPULATION

Appendix VIII. Autocorrelation coefficients (Moran's *I* values) for Twin City population.

Locus -Allele	Distance Class (m) 0-5	5-10	10-15	15-20	20-25	25-30	30-35	35-40	40-57
Ald3-2	-0.0040	0.0520***	0.0010	0.0010	-0.0070	-0.0140	-0.0260	-0.0330	-0.0470
Fum-2	0.0940***	0.0060	0.0010	0.0070	-0.0080	-0.0100	-0.0260	-0.0380	-0.0700**
Pgi2-2	-0.0400	0.0130	0.0220	-0.0030	0.0050	-0.0290	-0.0160	-0.0190	-0.0130
Pgi2-3	-0.0280	0.0250	-0.0170	0.0000	-0.0100	-0.0210	-0.0060	0.0070	0.0170
Pgi2-4	-0.0150	-0.0110	-0.0180	-0.0110	0.0130	-0.0040	-0.0010	0.0150	-0.0250
Pgi2-5	0.0950***	-0.0010	-0.0120	-0.0120	-0.0060	-0.0120	-0.0380*	-0.0040	0.0100
Pgm-2	0.0450*	0.0000	0.0040	-0.0200	-0.0240	-0.0170	0.0300*	-0.0320	0.0130
Mean	0.0210	0.0120	-0.0027	-0.0054	-0.0053	-0.0153	-0.0119	-0.0149	-0.0164

* Significant at 95 percent confidence level.

** Significant at 99 percent confidence level.

*** Significant at 99.9 percent confidence level.