Small Mammal associations with habitat structure
in riparian zones of a managed ICH Forest; Revelstoke, B.C.

by

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to the required standard

THE UNIVERSITY OF BRITISH COLUMBIA
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ABSTRACT

I investigated small mammal communities and habitat associations within riparian and upland areas of a class S2 stream in Revelstoke, B.C. Sampling sites were distributed among three types of habitat: old-growth ICH forests, 5-10-year-old clearcut, and clearcuts with 60 to 90m riparian buffers. I assessed small mammal populations and habitat associations along a transriparian gradient starting flush with the stream and going upland perpendicular to the stream (300m).

Six small mammal species or genera were captured. Deer mice (*Peromyscus maniculatus*), western jumping mice (*Zapus princeps*), voles (*Microtus* spp.), shrews (*Sorex* spp), red-backed voles (*Clethrionomys gapperi*), and short tailed weasels (*Mustela erminea*) all occupied clearcut sites. *M. erminea* was not captured within the riparian buffer strips areas, nor within the old-growth habitat. Small mammal species richness varied with sampling-site but was generally higher within the clearcut and buffered habitats where higher percent cover of shrubs and volume of downed wood were found. The relative abundance of small mammals differed among sampling-sites. Small mammal density and abundance were higher within the heterogeneous buffered habitat (composed of both clearcut and riparian buffer zones) followed by the clearcut and old-growth habitats.

Herbs (including ferns), species richness and vegetative percent cover differed among sampling-sites. There was no distance effect on vegetation species richness. Percent cover of shrubs differed significantly with distance from stream; Percent cover of herbs was greater
within old-growth and riparian buffer strip areas than in clearcut zones. Sampling-sites contained a wide range of microhabitats, so it was not possible to discern a continuous gradient or trend in habitat structure.

There was no distance effect on the pooled small mammal populations. *P. maniculatus* dominated all habitats. *Sorex* were most abundant within clearcut areas and were positively correlated with distance from the stream in the buffered habitat. *Microtus* spp. and *Z. princeps* were most abundant within old-growth and riparian buffer strips. *Z. princeps* capture rates were negatively correlated with distance from stream in clearcuts and old-growth habitats. *C. gapperi* was found only in riparian buffer strip zones when these were present within a clearcut.

My results suggest that heterogeneous habitat (clearcut with riparian buffer) increases the overall small mammal abundance and diversity. Presence of riparian buffer strips allow the density of old-growth obligate species to remain high. From my results it was not possible to suggest an ideal riparian buffer width to contain quality habitats for small mammal communities. Buffers of 60-90m wide appeared adequate to retain species diversity. Because small mammal communities seemed related to the microhabitat rather than the habitat at a larger scale, an investigation of the microhabitat associations would provide better understanding of small mammal population parameters.
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1. GENERAL INTRODUCTION

Riparian areas, as defined by the B.C. Ministry of Forest and B.C. Environment (1995b) on page 1 of the Riparian Management Area Guidebook, are “the areas that occur next to the banks of streams, lake and wetlands and include both the area dominated by continuous high moisture content and the adjacent upland vegetation that exert an influence on it.” Riparian areas promote patchiness and structural complexity creating high diversity and good quality habitat (McComb and Hagar, 1993). Furthermore Bunnell and Dupuis (1995) reported that almost 75% of the vertebrate species found in British Columbia use riparian habitat. Riparian zones are in the productive portions of forest in British Columbia where 75% of the watersheds have been partially developed. Some biogeoclimatic zones have no undeveloped watersheds larger than 50 km² left (Bunnell and Dupuis, 1995).

Because riparian areas are important to both the forest industry and wildlife communities, we require a good understanding of riparian ecosystem structure and function. Riparian zones are believed to serve different purposes, including habitat connectivity and patchiness. Their long and narrow features may provide natural routes for wildlife movements and serve as transition zones between the aquatic habitat and the adjacent uplands. They also increase the amount of edge habitat available (McComb and Hagar, 1993) contributing to biodiversity. Bunnell and Dupuis (1995) suggested that riparian zones could be important reservoirs of biodiversity because many species are more abundant and reproductively successful in these areas than in adjacent
uplands. We do not presently know how riparian areas should be managed to maintain all their valued habitat features.

To maintain habitat characteristics associated with riparian zones, different widths of buffers strips have been left in managed landscapes. In this study the small mammal communities associated with riparian areas and the adjacent uplands in a managed forest were investigated for a class S2 stream as defined by the Fish-Stream Identification Guidebook (B.C. Ministry of Forests and B.C. Environment, 1995a). The upland communities were considered because some upland species may depend on riparian habitats for part of their life cycle (Kauffman 1988, Gomez 1992, Gyug and Vaartnou 1996). It has been suggested that the integrity of the riparian ecosystem may also depend on and be influenced by the adjacent upland area. (B.C. Ministry of Forests and B.C. Environment, 1995b).

My objectives were: 1) to assess the associations between small mammal communities and selected habitat structures within ICH forest in both riparian and uplands 2) to test for effect of riparian buffer widths on small mammal species richness and abundance and 3) to determine the impact and the role of the transriparian gradient on small mammal population abundance and richness in managed ICH forest.

Chapter 1 describes the study area and sampling design. Chapter 2 discusses associations found between the small mammal community and the different types of habitats studied. Chapter 3 discusses relationships and correlations between small mammal populations and habitat structure as a function of the distance from the edge of the stream.
1.1 STUDY SITE

The study site is situated approximately 75 km north of Revelstoke in southeastern British Columbia. The riparian zones of Downie Creek drainage are included in the Revelstoke TSA (Timber Supply Area). Headwaters of Downie Creek originate in the Selkirk Mountain glaciers and flow into the Revelstoke reservoir. The bottomland area runs for a length of 20 km and is on average 400 m wide. Downie creek is classified as an S2 stream according to the Fish-Stream Identification guidebook (B.C. Ministry of Forests and B.C. Environment, 1995a). An S2 steam is defined as a fish bearing stream from 5 to 20m wide with an average gradient less than 20%.

The study area is classified as Wet Interior Cedar-Hemlock (ICHwk1 and ICHvk1). All of the sampling sites were selected from the ICHwk1 portion of the drainage, in the Wells Grey wet cool interior Cedar-Hemlock variant (B.C. Ministry of Forest, 1992). Within the ICH forest the most common habitat types are riparian forest, upslope forest, avalanche chutes and clearcuts. Among the forested biogeoclimatic zones in the province, vertebrates in the ICH zones show strong association with riparian areas, second only to the CWH zones (Bunnell et al., 1991).

Elevation varies from 400 to 1400 m with a mean annual precipitation of 1214 mm and 121 frost-free days. The riparian bottomlands are made up of a mosaic of habitat types providing a great edge effect. The area contains a rich diversity of flora and fauna supporting an old-growth dependent wildlife community (B.C. Ministry of Forest, 1992). Wolverine have been sighted in the valley as well as many other smaller carnivores and rodents including marten and beaver (Corbett, 1989).
The forest is dominated by red cedar (*Thuja plicata*) and western hemlock (*Tsuga heterophylla*) >250 year old. Most of the timber removal in the area happened between 1987 and 1991, early seral stands both with and without riparian buffers were left. The remaining riparian buffer strips vary from 30 m to 90 m wide. Following these logging operations, burning and tree planting was prescribed. No other silvicultural treatments were applied within the sample plots.

1.2 METHODS

1.2.1 Sampling sites

Trapping grids of similar size were installed at all of the sampling sites immediately adjacent to the edge of the stream extending upland. The grids had the same width (parallel to the stream) but varied in length depending on the pattern of forest cover. The sampling sites were distributed among 3 types of habitat: undisturbed old-growth, 5 to 10-year-old clearcut, and clearcut with old-growth riparian buffer (60m-90m wide). Each habitat was sampled with 2 grids for a total of 6 sampling sites. Every clearcut area, with or without a riparian buffer, was bordered by patches of old-growth forest on either side. As shown in Figure 1 the grids were positioned to minimise potential edge effects. A distance of at least 75m was always left between the grid and adjacent habitat. Grids were always set apart by a distance of at least 400 m.

I sampled during the spring and summer season of 1994 and 1995. The number of transects per grid and their average length was different between the sampling periods of 1994 and 1995. In 1994 the sampling grids were composed of 5 transriparian transects going from the
immediate edge of the stream to 150m upslope. These transects were 15m apart. In the second year of data collection, an increase in resources allowed me to extend the transects from 150m up to 300m. Although the transects were longer (Fig. 2), their number was reduced to only 3 transects per grids separated by a distance of 30m. These changes were made to attain a better assessment of the small mammal population and habitat structure in the adjacent upland zones of the riparian habitat.

1.2.2 Small mammal live trapping

I estimated small mammal relative abundance and species composition with Longworth live traps. The traps were set 15m apart along the transriparian transects with the first trapping station flush with the edge of the stream. Sites were trappe
Figure 1. Position of sampling grids in relation to the edges of the adjacent habitat (not to scale). Grids were at least 400 m apart.

Figure 2. Transect layout in each grid for the sampling years 1994 and 1995.
1.2.3 Vegetation and habitat sampling

I evaluated species composition and percent cover of herbs and shrubs by plot sampling every 30m along the transriparian transects. Ferns were included with the herbs. I recorded vegetation on transects #1, #3, and #5 of the grids in 1994. Vegetation sampling in 1995 was done on the upland part of these same transects. Shrubs and herbs (including ferns) were sampled within circular plots of 0.1ha and 1m$^2$ quadrats, respectively. Tree species, canopy cover and snags were recorded in circular plots of 0.4ha every 60m along the same transriparian transects (Fig.3).

I used line-intercept sampling to evaluate the volume of downed wood, employing the reverse triangle method, with 3 lines of 11.2m each, (Fig.4). I recorded the diameter and the decay class of each piece of wood encountered, and calculated the total DW in each sampling plot following Van Wagner (1968):

$$V(\text{m}^3/\text{ha}) = \left(\pi^2 \times \Sigma(D^2)\right) / 8 \times L$$

where: $D =$ diameter of the piece of wood

$L =$ length of the transect

Downed wood was classified following within five decay classes:

*class 1* Twigs present, bark intact, hard texture and round

*class 2* Twigs absent, bark intact or partly missing, hard and decaying texture and round

*class 3* Twigs absent, traces of bark, partly decayed and round

*class 4* Twigs absent, bark absent, blocky texture and round to oval

*class 5* Twigs absent, bark absent, soft texture and oval.
I used abiotic factors (slope gradient and position, surface substrate, soil drainage) of each site to classify them according to the guidelines of "A Field Guide for Site Identification and Interpretation for the Nelson Forest Region" (BC Ministry of Forest, 1992).
Figure 3. Vegetation sampling plot design.
Figure 4. Downed wood line-intercept sampling on 3 lines of 11.2 m long.
2. SPECIES COMPOSITION, ABUNDANCE, AND HABITAT ASSOCIATIONS

2.1 INTRODUCTION

Within a managed forest a mosaic of altered habitat is created throughout the riparian zones and uplands. Wildlife populations associated with riparian habitat are then influenced by both the remaining riparian zones and the altered stands. Changes in habitat caused by logging practices have shown a variety of impacts on small mammal community structure. Geier and Best (1980) suggested that when habitat is altered, populations of some species may benefit while others are adversely affected. Studies assessing small mammal abundance and species richness in managed landscapes have shown different impacts on community structure following harvest. Martell (1983) and Gyug and Vaartnou (1996) found that red back voles (Clethrionomys gapperi), which were prevalent in uncut stands, were replaced by deer mice (Peromyscus maniculatus) following harvest. Despite the changes in the species dominance, the total small mammal abundance seemed to remain the same in stands of different ages. Carey and Johnson (1995) found no difference of the community composition among different aged stands in Oregon forests, but reported that old-growth stands were supporting 1.5 times more individuals and biomass than managed forests. Van Horne (1981), however, found a higher small mammal density in successional stands of coastal coniferous forest in southeast Alaska.
Within unmanaged forests, among the studies conducted to assess small mammal population in riparian zones and adjacent uplands, Galindo-Leal et al. (1995) reported that the majority of these indicated a significantly higher number of small mammal species in streamside forests than in associated upland forests. Doyle (1990) and Cross (1985) found that the total population abundance and the species richness was significantly higher in riparian habitats of southwestern forests. Zuleta and Galindo -Leal (1993) found a greater species richness within riparian habitats of coastal B.C. forest but the population abundance was not significantly different. McComb et al. (1993) found no difference of the abundance and small mammal species richness between riparian and upland habitats in the Oregon Douglas fir forests but reported strong species association with each habitat. Anthony et al. (1987) noticed a higher small mammal species richness in riparian habitat compared to zones 20-30m away from the stream in old-growth forests of Western Cascades.

Within managed forests, some authors investigated small mammal populations of riparian and upland habitats. Guyg and Vaartnou (1996) observed a greater species richness and total abundance within riparian areas than upland areas of unharvested forests and clearcuts of south central B.C. Among the species captured, *Sorex bendirii* were limited to riparian habitat, while *Microtus pennsylvanicus, M. longicaudus* and *S. vagrans* showed greater abundance within the riparian zones; deer mice were more abundant in upland areas. Within clearcut stands the meadow vole (*M. pennsylvanicus*) population was dominant in riparian zones. Anthony et al. (1987) found no difference in small mammal abundance between habitats, though species richness was greater near stream zones of young, mature, and old-growth forests in the Cascade Mountain of Oregon. Gomez (1992), on the other
hand, found no difference in the species richness between stream and upslope habitats. His study was done within 5 forest types of Oregon. For seven of the nine species recorded (Neurotrichus gibbsii, Sorex bendirii, Sorex pacificus, Microtus longicaudus, Microtus townsendii, Phenacomys albipes, and Zapus trinotatus) abundance was greater within the riparian zones than upslope (Gomez, 1992). The water shrew (Sorex bendirii) was found to be an obligate of riparian areas while Clethirionomys californicus showed a strong association with the upslope habitat.

Clearly there is no consistent pattern in small mammal population abundance relative to riparian and upland habitats of unharvested and managed forests. This chapter focuses on the general habitat associations of the small mammal communities within riparian and upland areas of ICH managed forest.
2.2 METHODS

I analyzed data at the habitat level (old-growth, buffered, and clearcut habitats) and at the sampling site level. There were 6 sampling sites or 2 per habitat, namely: old-growth site #1 and #2, buffered site #1 and #2, and clearcut site #1 and #2. Results from the buffered sampling sites are often separated and presented in two categories: the riparian buffer strip area and the adjacent clearcut. This finer subdivision of the broad habitat reflects marked changes in transects through riparian buffers.

2.2.1 Vegetation and downed wood

I recorded vascular vegetation to species with the exemption of the willow family (Salix spp.). To facilitate data analysis both shrubs and herbs were grouped by soil moisture and nutrient requirements. Ferns are included within the herb data. The number of variables was reduced from 95 vegetation species to 39 vegetation groups. Tables 1 and 2 summarize the resulting classification. The soil requirements of each species were derived from “Indicator Plants of Coastal British Columbia” (Klinka and Scagel, 1989). Because the main focus of the study is the relationship between the habitat structure and the small mammal populations rather than with the specific floral species found, the grouping of the plant species does not affect the analysis and interpretation of the results. Techniques such as clustering and principle components were not employed to group the vegetation species because in my
study, location or distance from the stream is important. Grouping the vegetation species according to the variable variances would not account for locations.

To express the vegetation species richness I used the original species rather than the vegetation groups. The overall vegetation species richness per sampling-site was recorded for shrubs and herbs (including ferns). I tested for differences in species richness between sampling sites with Analysis of Variance (\( \alpha = 0.05 \)). The ANOVA was run separately for shrubs and herbs. When the means were found to be significantly different, I tested the difference between means with the Bonferroni’s comparison of means test (\( \alpha = 0.05 \)).

Vegetation composition was in terms of the vegetation groups (Table 1 and 2). I retained all of the vegetation groups that represented more than 1% cover per plot per site and gave their relative frequency in each habitat: old-growth, buffer strip and adjacent clearcuts areas, and clearcut. Frequency distributions are illustrated as dominance: diversity values by scaling the most frequent group as 1.0 for each habitat. I calculated the average percent vegetative cover per sampling plot and present the results for herbs (including ferns) and shrubs within each sampling site.

I performed Multivariate Analysis of Variance on vegetative cover data using SAS package with PROC GLM (\( \alpha = 0.05 \)). Shrubs and herbs were tested for sampling site effects (OG 1, OG 2, BUF 1, BUF 2, CC 1, CC 2) nested within habitat effect (old-growth, buffered, clearcut). MANOVA tests the equality of vectors of means over several treatments analyzing all of the dependent variables simultaneously, using the assumptions of multivariate normality.
and equal covariance matrices. Prior to MANOVA, the equality of the means both between habitat and between sites were tested for each dependent variable with Univariate Analysis of Variances (α= 0.05). MANOVA runs under the assumptions of normality and equality of variances. Multivariate normality was tested by a Goodness of fit test (α=0.05) on all of the variables. The variance homogeneity was tested using a Chi-Squared test (α=0.05). Because the data did not meet the assumptions, they were submitted to the angular transformation: arcsin√X. Arcsin transformation is known to create normal distribution from original percentages or proportions which usually form binomial distributions (Zar, 1984). The assumptions of normality and homogeneity of variances were tested again. Manova was run with transformed data.

Data on downed wood were treated similarly to the vegetation where the average volume per sampling plot was given for each habitat. I calculated how much of the wood volume was represented per diameter class and decay class. The average number of logs per plot recorded for each diameter class was compared among the habitats studied.

2.2.2 Small mammal populations

Small mammal species richness and composition were calculated for each sampling site. Differentiation among some species can be very difficult with live specimens. Individuals from the genera Sorex and Microtus were not identified to species with the exception of the southern red-backed vole (Clethrionomys gapperi).
Table 1. Grouping of the shrub species recorded according to the soil moisture, nitrogen level, and family. Groups are the variables used in analysis. The soil moisture and nitrogen level are indicated within the column "soil" where: N=nitrogen rich, n=nitrogen poor, m=nitrogen medium, 1=water shedding site, 2=flood plain and water receiving site, 3=very moist to wet, 4=fresh to very moist 5=fresh to moist, 6=dry to moist, 7=very dry to moderately dry, 8=disturbed site.

<table>
<thead>
<tr>
<th>Var.</th>
<th>Common name</th>
<th>Latin name</th>
<th>Soil</th>
</tr>
</thead>
<tbody>
<tr>
<td>RASB</td>
<td>Red raspberry</td>
<td>Rubus idaeus</td>
<td>N4</td>
</tr>
<tr>
<td>WMA</td>
<td>Western mountain ash</td>
<td>Sorbus scopulina</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Silka mountain ash</td>
<td>Sorbus sitchensis</td>
<td></td>
</tr>
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<td>ELDER</td>
<td>Red elderberry</td>
<td>Sambucus racemosa</td>
<td>N4</td>
</tr>
<tr>
<td>GOOS</td>
<td>Black gooseberry</td>
<td>Ribes lacustre</td>
<td>N5</td>
</tr>
<tr>
<td>MAPL</td>
<td>Douglas maple</td>
<td>Acer glabrum</td>
<td>N1,2</td>
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<td>CRAN</td>
<td>Highbush cranberry</td>
<td>Viburnum edule</td>
<td>N4</td>
</tr>
<tr>
<td>THIM</td>
<td>Thimbleberry</td>
<td>Rubus-parviflorus</td>
<td>N8</td>
</tr>
<tr>
<td>DCLB</td>
<td>Devil's club</td>
<td>Oplopanax horridus</td>
<td>N3</td>
</tr>
<tr>
<td>ALDR</td>
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Table 2: Grouping of the herb species recorded according to the soil moisture, nitrogen level and family. Groups are the variables used for the data analysis. See explanation on column "Soil" in description of Table 1.
Total numbers of individuals captured per sampling site were calculated. Results are presented as the number of captures per trap over the total number of trapping-nights. Recaptured individuals are excluded from these values in 1995. The results therefore document the average number of individuals captured once per trap. This approach allowed appropriate per unit comparison of the small mammal relative abundance in each of the habitat types. I compared the relative small mammal abundance between sampling sites with Analysis of Variance ($\alpha=0.05$) for both trapping years (1994 and 1995) separately. When the means were found to be significantly different I tested the difference between means with the Bonferroni's comparison of means test ($\alpha=0.05$).

2.2.3 Population density estimates

Mark/recapture data were collected from an open population which changed in size and composition over time. Animals were marked during the trapping season of 1995 and density estimates are calculated for that year only; no animals were marked in 1994. Relative abundance of the population was calculated weekly by the Jolly-Seber model applied within each of the sampling sites. Each week represented a trapping period. Analysis was performed with the small mammal programs for mark/recapture data analysis written by C.J.Krebs (1991). This model was developed for open populations and allows estimation of the population size at each sampling time as well as the survival rates and birth numbers between sampling times (Pollock et al. 1990). It can be run with samples that are not at regular time intervals and can be run on data extending over many years. The Jolly-Seber method works
on the assumptions that: 1) every individual has the same probability of capture at the time of the ith sample \((i = 1, 2, \ldots, k)\); 2) every marked individual has the same probability of surviving from the ith sample to the \((i + 1)\) sample; 3) individuals do not lose their marks, and marks are not overlooked at capture; and 4) sampling time is negligible in relation to intervals between samples (Krebs, 1989).

Prior to density estimation, assumption 1 was evaluated with the Leslie and Chitty test of equal catchability, which is the preferred test when dealing with more than three samples from an open population (e.g., Krebs, 1989). Leslie and Chitty test works under the principle that it is possible to have unequal catchability between marked and unmarked animals but still have equal catchability within the marked segment of the population (Krebs, 1989). Therefore it uses only the marked individuals who were caught twice or more. The null hypothesis of equal catchability was tested using a Chi square distribution \((\alpha=0.05)\).

The Jolly trappability estimates were calculated for the small mammal population found within each of the sampling sites. This estimate was chosen over the maximum and minimum trappability estimates following of Krebs and Boonstra (1984) who found that it was the best method after comparing them all. Jolly trappability is defined:

\[
\text{Jolly trappability} = \frac{\Sigma \text{(Total no. of marked individuals caught at time i)}}{\text{Estimated marked population size at time i}} (100)
\]
where S is the number of sampling times. If the assumption of equal catchability does not
hold, trappability is usually overestimated because estimates are weighted by individuals that
are caught more often (Krebs and Boonstra, 1984). Trappability was estimated because it
gives an index of the accuracy of the relative population density calculated. Accuracy
increases with the portion of the population captured.

Reported relative densities include all species except *Sorex* spp. and *Mustela erminea.*
The relative density was not calculated for the species individually because the sample sizes
were too small. Density estimates are given for each of the sampling sites separately, as well
as for the buffer strip areas and the adjacent clearcut zones, when sample sizes are large
enough to use the Jolly-Seber model. The density estimates were calculated weekly or for
time periods covering one trapping session.

Length of the trapping transects varied among sampling sites. The Jolly-Seber
population density was then presented as the population number per ha to facilitate the
comparison of the population density among the habitats under study. Number of ha
contained within each sampling site included the surface area found between the transriparian
transects as well as a 7.5m to 15m strip surrounding the grid which represents half the
distance between trapping stations in a transriparian and parallel to the stream fashion.
2.3 RESULTS

2.3.1 Vegetation and downed wood

Species richness

No significant difference in shrub species richness (Fig. 5) was found among the sampling sites (df=5,48, F=1.132, P=0.356, α=0.05). Herb species richness was significantly different (df=5,48, F=12.376, P=0.000, α=0.05). The Bonferroni’s comparison of means showed that the buffered site #1 was significantly different from all other sampling sites. Buffered site #2 differed from old-growth site #1 (α=0.05).

Species composition

Ferns (group F3 in Table 2), preferring moist or wet nitrogen-rich soils, dominated the old-growth areas along with devil’s club (Oplopanax horridus) (Fig.6a). Alder (Alnus spp.) and thimbleberry (Rubus parviflorus) comprised 30 to 40% of the vegetation by relative frequency. All other vegetation groups comprised between 10 to 20% of the relative frequency (Cornus stolonifera, Streptopus spp., Tiarella trifoliata, Lonicera involucrata, Circaea alpina, Corylus cornuta) and are also typical of fresh or wet nitrogen rich soils.

Riparian buffer strips zone were dominated by L. involucrata (Fig.6b) but contained several species groups at high relative frequencies (50-60%). O. horridus, R. parviflorus, Cornus canadensis, ferns, and C. stolonifera found in rich nitrogen and fresh to wet soils were
among these. Among the 7 vegetation groups composing 20 to 30% of the relative frequency some species (*Vaccinium ovalifolium* and *Equisetum arvense*) are known to be associated to nitrogen poor or medium soils.

Clearcut habitats were inhabited by vegetation species typical of disturbed sites. Thimbleberry (*R. parviflorus*) and red raspberry (*R. idaeus*) represented the highest frequencies within the clearcut zones (Fig. 6c and d), including all clearcut sampling areas with and without an adjacent riparian buffer strip. Strong dominance was most clearly expressed in clearcuts and there were fewer vegetation groups within the clearcut areas with high relative frequencies than in the buffered zones. Ferns, *Salix* spp., and *C. stolonifera* accounted for 30 to 40% of the frequency. *Populus balsamifera, Epilobium angustifolium,* and *Pteridium aquilinum* all ranged between 20 to 30% of the relative frequency.

**Vegetative cover**

Average percent cover of shrubs per plot in all sampling sites varied from 58 to over 100% cover (overlapping cover). Buffered site #2 contained 20% to 43% more shrub cover than all of the other sampling sites (Fig. 7a). Herb and fern layers exhibited two general tendencies: the clearcut zones of the buffered and non-buffered habitats contained 30% less herbs than the old-growth and riparian buffer strip sites (Fig. 7b).
Vegetation species richness in all sites

**Figure 5.** Total vegetation species richness recorded in all sampling sites. 
BUF = buffered habitat (BUFSTP+BUFCC), BUFSTP = buffer strip, 
BUFCC = clearcut adjacent to riparian buffer, OG = old-growth, and CC = clearcut.
Figure 6. Relative frequency of the vegetation composition in each habitat: old-growth (Fig. 6a), buffer strip (Fig. 6b). See Table 1 and 2 for abbreviations.
Relative frequency of vegetation groups in clearcut adjacent to riparian buffer strip habitat

Figure 6c.

Relative frequency of the vegetation groups in clearcut habitat

Figure 6d.

Figure 6. Relative frequency of the vegetation composition in each habitat: clearcut adjacent to buffer strip (Fig. 6c), clearcut (Fig. 6d). See Table 1 and 2 for abbreviations.
Data transformation (arcsin√X) did not manage to meet the assumption of multivariate normality and homogeneity of variances. All variables differed significantly from a normal distribution (P=0.0001, α=0.05) and the equality of variances test was rejected (P=0.0001, α=0.05). Failure to meet assumption affects the reliability of the MANOVA results. The data set contained a lot of zero values because species were absent from a plot. There was a significant site effect for both herb cover (df=66, 398, F=3.97, P=0.0001, α=0.05) and shrub cover (df=54, 417, F=3.32, P=0.0001, α=0.05) analysis. All vegetation groups or dependent variables (Table 1 and 2) that were found to be significant between habitat and/or site from the univariate analysis of variances (α=0.05) are shown in Tables 3 and 4. Percent cover per plot in each sampling site and P values calculated for the habitat effect and nested site effect are given.

**Downed wood**

The volume of downed wood recorded was highest in the clearcut sites (53.4m³/plot) followed by the buffered (43.4m³/plot) and old-growth habitats (37.3m³/plot). Plots were 0.1ha. Most pieces encountered on clearcut sites were logs of 7.5 to 40cm diameter, while the pieces found within the riparian buffer strips and undisturbed sites were of either small diameter (7 to 30cm) or large diameter logs (50 to 100cm).

Downed wood pieces within the clearcut zones were estimated to be in decay class 3 and 4. Decay class 4 and 5 decay wood dominated for downed wood recorded within the
Figure 7a

Figure 7b.

Figure 7. Vegetative percent cover per plot within each sampling site. The average percent cover per habitat is also given: shrubs (Fig. 7a), herbs (including ferns; Fig. 7b). OG=old-growth, BUF=buffered habitat, BUFSTP=buffer strip, BUFCC=clearcut adjacent to riparian buffer, CC=clearcut.
Table 3. Shrub groups as defined in Table 1 and 2 that were significantly different from the MANOVA analysis. The average percent cover per plot in each sampling site is given as well as the P value calculated for the habitat and nested sampling site. BUF=riparian buffer strips and adjacent clearcuts.

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<th>OG 2 %/PLOT</th>
<th>BUF 1 %/PLOT</th>
<th>BUF 2 %/PLOT</th>
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h=habitat; s(h)=site nested within habitat
Table 4. Herb groups as defined in Table 1 and 2 that were significantly different from the MANOVA analysis. The average percent cover per plot in each sampling site is given as well as the P value calculated for the habitat and nested sampling site. BUF = riparian buffer strips and adjacent clearcuts.

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h=habitat; s(h)=site nested within habitat
old-growth habitat. The riparian buffer strip areas were dominated by decay class 4 followed by class 3 decay.

2.3.2 Small mammal populations

Species richness and composition

Six small mammal species or genera were captured. Deer mouse (*Peromyscus maniculatus*), Western Jumping mouse (*Zapus princeps*), vole (*Microtus spp.*), Shrew (*Sorex spp.*), Red Backed vole (*Clethrionomys gapperi*), and short tailed weasel (*Mustela erminea*) all occupied clearcut sites. *M. erminea* was not captured within the riparian buffer strips areas, nor within the undisturbed habitats.

Small mammal abundance

The pattern of small mammal abundance varied from 1994 to 1995. The number of animals captured per trap in 1994 (Fig. 8a) was greatest within the old-growth habitat (2.03 animal/trap) followed by the buffered (1.65 animal/trap) and the clearcut habitats (1.19 animal/trap). The following sampling year, 1995, the transriparian transects were extended from 150m up to 300m upslope. The small mammal abundance then showed opposite trends. The population was the highest within the buffered and clearcut areas with 2.78 to 2.98 animals per trap (Fig. 8a). The lowest abundance was found within the undisturbed habitats with 2.08 animals per trap. The riparian buffer strip zones sustained a lower small mammal
abundance (2.50 animal/trap) compared to the adjacent clearcuts (Figure 8b). The ANOVA test run on the sampling-sites showed significant differences in small mammal population abundance among sites during both trapping years (1994: df=5,60, F=11.010, P<0.001 and 1995: df=5,108, F=10.420, P<0.001, α=0.05).

Bonferroni’s comparison of means test found that the buffered site #2 differed significantly from all sites except old-growth #2, and the old-growth site #2 differed significantly from buffer site #1 and clearcut site #1 in 1994 (α=0.05). In 1995 the population abundance was significantly different between the old-growth site #2 and all other sites except the old-growth site #1 (α=0.05). It is not possible to compare these results between years because the trapping activities in 1994 were interrupted a month and a half earlier (hantavirus) and the animals were not marked that year. Population abundance was calculated from the total trapping data for each year.

2.3.3 Population density estimates

The assumption of equal catchability was evaluated for each of the sampling sites (α=0.05). Catchability was found to be equal everywhere except within the clearcut site #2, the old-growth site #2, and the buffered site #2. The Jolly trappability varied between 54.5% and 91.3% (Table 5) with large confidence intervals.
Total population densities calculated by the Jolly-Seber model as a function of the time are illustrated in Figure 9 for each of the sampling sites in 1995. Small mammal population density within buffered site #2 seemed to be negatively correlated with time. The weekly data were then aggregated and the average small mammal density for each sampling site was calculated as the average of all weeks. The old-growth habitat sustained the lowest small mammal population density followed by the clearcut and the buffered habitat (Fig.10). The weekly population densities per ha for each trapping site are summarized in Table 6. The standard error of the population densities were often unusually high for the calculated values within the riparian buffer strip areas and the adjacent clearcut zones as a result of small sample sizes.
Figure 8. Small mammal relative abundance. Number of animals captured per trap: 1994 (Fig. 8a), 1995 (Fig. 8b). The average per habitat is given. OG = old-growth, BUF = buffered habitat, BUFSTP = buffer strip, BUFCC = clearcut adjacent to riparian buffer, CC = clearcut.
Figure 9. Jolly-Seber population density estimates of small mammals over time from 1995 captures: old-growth habitat (Fig. 9a), clearcut habitat (Fig. 9b), buffered habitat (Fig. 9c and d).
Figure 10. Average population density of small mammals per ha calculated with the Jolly-Seber model from 1995 captures: average density per sampling-site (Fig.10a), average density per habitat type (Fig. 10b). OG=old-growth, BUF=buffered habitat, BUFSTP=buffer strip, BUFCC=clearcut adjacent to riparian buffer, CC=clearcut.
Table 5. Jolly trappability calculated for each sampling site.

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<th>Sampling site</th>
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<th>Confidence intervals</th>
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<td>Buffer clearcut 1</td>
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<td>29.5 to 99.0</td>
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<tr>
<td>Clearcut 2</td>
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Table 6. Weekly Jolly-Seber population densities calculated for each sampling site.

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<th>OG 2 SE</th>
<th>BUFSTP 1 SE</th>
<th>BUFCC 1 SE</th>
<th>BUF 1 SE</th>
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2.4 DISCUSSION

The general overview given here includes all of the small mammal species captured. It reports the abundance, density and species richness of the small mammal population as a whole without treating species separately.

Because habitat structure and small mammal populations differed among the sampling-sites investigated most of the analysis treated data at the sampling site level rather than the habitat level. The sampling sites were selected for their similarities in habitat structure but exhibited more differences than expected. Percent vegetative covers of sites within habitats differed significantly. The analysis may not be entirely reliable because the assumptions of MANOVA were not met before or after data transformation (arcsin√X).

Herb cover (including ferns) was more abundant within old-growth and the riparian buffer strips zones where the exposure to solar radiation was less and the moisture levels were higher. The higher moisture of the old-growth and buffer strips areas was consistent with the vegetative species composition (Fig 6). Ferns (refer to group F3 in Table 2) and devil’s club (O. horridus) dominated the old-growth areas.

Riparian buffer strips are believed to experience edge effects and their structure becomes modified from the typical old growth habitat. The edge which is defined as the junction of two different landscape elements (Yahner, 1988) creates a transition zone which in
this case is part of the buffer strip areas. Vegetation composition of buffer strips was dominated by *L. involucrata*, typically found on high nitrogen and wet sites. *R. parviflorus*, typical of disturbed and high nitrogen sites, represented 60% of the vegetation composition in buffer strips (Fig. 6b). That species also dominated the clearcuts but accounted for only 25% of the old-growth vegetation composition. The vegetation composition thus seemed to illustrate a transition stage of the buffer strip habitat structure, where species were generally found at a higher frequency than in the other habitats (Fig. 6). Vegetation species richness (Fig. 5) and cover (Fig. 7) were too variable to permit general statements. These habitat components were found to be either non-significant among sites or particular to each sampling site.

Downed wood is believed to provide an important source of refuge, resting areas, and feeding and breeding sites for wildlife (Bunnell *et al.* 1991, 1997). Downed wood may favor certain populations like species of the *Sorex* genus foraging on insects (Craig, 1995). The volumes available, the average diameter, and the level of decay differed and seemed to indicate that riparian buffer strips once again were intermediate between old-growth and clearcut zones.

The pattern of small mammal relative abundance seemed to differ between trapping years (1994 and 1995). Trapping data of 1994 and 1995 were not tested against each other because of the disparity in transect length, duration of trapping season, and marking process. Small mammal relative abundance differed significantly among sites in 1994 (ANOVA: df=5, 60, F=11.010, P<0.001, α=0.05). Relative abundance seemed the highest within the old-
growth habitat. When sampling sites were examined separately, the highest abundance was found within old-growth site #2 (Fig. 8a) and was significantly different from relative small mammal abundance in buffer site #1 and clearcut site #1 (Bonferroni's comparison of means test, $\alpha=0.05$). Small mammal relative abundance in 1994 was also high within buffered site #2 and significantly different from abundance calculated in all other sampling-sites except old-growth #2. There was no strong difference among habitats in 1994.

In 1995, when the captures included the associated upland species, the overall picture changed with the highest overall abundance within buffered habitat and the lowest in old-growth habitat (Fig. 8b). Small mammal relative abundance differed significantly among sites (ANOVA: $df=5, 108, F=10.420, P<0.001, \alpha=0.05$). In most cases clearcut areas of buffered sites showed a higher abundance than the buffer strip zones. Only the relative abundance calculated within old-growth site #2 was found significantly different from all other sampling-sites (except old-growth site #1; Bonferroni’s comparison of means test, $\alpha=0.05$). Small mammal relative abundance was found to differ significantly within only one of the six sampling-sites in 1995, and again there were no pronounced differences among habitats.

The population density calculated by the Jolly-Seber model followed the overall relative abundance pattern of 1995 captures (Fig. 8b). The density seemed slightly higher within the buffered and clearcut habitats followed by old growth habitat (Fig. 10).
3. TRANSRIPARIAN GRADIENT AND HABITAT ASSOCIATIONS

3.1 INTRODUCTION

The majority of the studies on small mammal populations and riparian habitats compare the riparian communities with separated upland communities (e.g.: Doyle 1990, Cross 1985, Zuleta and Galindo-Leal 1993, Gyug and Vaartou 1996). From the few studies investigating transriparian changes in small mammal communities, McComb et al. (1993) found that deer mice, Pacific jumping mice, shrew moles, and marsh shrew capture rates decreased with distance from the stream while Clethrionomys occidentalis increased at 200m and more from the stream. Gomez (1992) found that along 200m transriparian transects, capture rates of S. pacificus and S. bendirii were higher near streams than farther away. Clethrionomys californicus was more abundant at distances farther from the stream.

Studies of transriparian gradients in riparian zones should take into account the adjacent upland portions. It has been suggested that upstream and upslope influences are inseparable from the riparian zone. The integrity of a riparian ecosystem depends on and is influenced by the adjoining upland area (B.C. Ministry of Forests and Ministry of Environment, 1995b). Considering the importance of the uplands to the riparian habitat it must be recognized that narrow riparian buffer strips that do not contain upslope habitat in a managed landscape may not meet the needs of upslope associates, such as C. gapperi (McComb and Hagar, 1993). Very few studies on small mammals and riparian habitat were able to suggest proper riparian buffer width to sustain the population investigated. Gomez
(1992) and McComb et al. (1993) suggested that streamside corridors wider than 150m should be sufficient to include the optimal habitat used by *C. gapperi*.

In this chapter I examine the small mammal and vegetative communities along transriparian gradients that extend from the edge of the stream to upslope areas (300m away from stream). Johnson and Lowe (1985) suggested delimiting the inland extent of the riparian areas by functional differences rather than physical or biological definition, because of non-apparent and gradual differences in habitat that may originate farther away from the observed riparian zones. Johnson and Lowe (1985) also considered the transriparian gradient a major factor in controlling the biological biodiversity and structural complexity of riparian zones in the southwestern U.S. My objective is to evaluate the distances or gradient at which small mammal population parameters may change and to relate these to differences in habitat structure. Such data should permit better assessment of the role and effect of riparian buffers in managed landscapes on small mammal communities. The riparian buffer strip width (60-90 m) investigated here is therefore assessed for its role into sustaining the small mammal population under study.
3.2 METHODS

I analyzed data at the habitat level (old-growth, buffered, and clearcut habitats) and at the sampling site level. There were 6 sampling sites or 2 per type of habitat, namely: old growth #1 and #2, buffered #1 and #2, and clearcut #1 and #2. Results from the buffered sampling sites are often separated into two sets of data: the riparian buffer strip area, and the adjacent clearcut zone. I performed this subdivision to permit more specific evaluation of habitat associations of the small mammal populations.

I recorded vegetation species richness and percent cover as a function of the distance from the edge of the stream going upslope for each habitat and sampling site. The cover and species richness are calculated for both the shrubs and herbs (including ferns). I calculated the vegetative cover from the vegetation group variables and the species richness from the original species. Because the vegetation was sampled every 30m (Fig.3), the cover and species richness per plot is given at 30m intervals starting flush with the stream to the end of the transriparian transects.

Sampling site and distance effects on shrub and herb species richness were tested with a two-way ANOVA ($\alpha=0.05$). I analyzed the vegetative percent cover the same way with two-way ANOVA ($\alpha=0.05$). I ran a t-test ($\alpha=0.05$) on the buffered site data to evaluate if the vegetation from the buffer strips and adjacent clearcuts were drawn from the same populations.
I recorded small mammal species richness, composition and relative abundance as a function of the distance from the stream. The traps were set at 15-m intervals along the transriparian transects (Fig. 3). The small mammal population parameters were then calculated for every 15-m interval starting flush with the stream going upland. The mammal species richness and composition was plotted for all sampling sites and each trapping year (1994 and 95).

I analyzed data on population relative abundance (# animals/trap for all species pooled) for both trapping years separately. I tested the sampling site and distance effects on the population abundance with a two-way ANOVA (α = 0.05). I ran a t-test (α=0.05) on the buffered site data when the distance effect was significant to evaluate if the small mammal data from the buffer strips and adjacent clearcuts were drawn from the same populations.

I looked at the small mammal species and genera individually. I calculated the normalized abundance of each species per type of habitat (old-growth, buffer strip, adjacent clearcut, clearcut) for both trapping years. Normalized abundance was calculated using total number of animals captured (excluding recaptures) per trapping unit and trap/night within each habitat. Frequency distributions of normalized abundance are illustrated by scaling the most abundant species as 1.0 for each habitat and having the other species standardized according to that most abundant species. Deer mice were not included with the frequency distribution of 1994 small mammal normalized abundance. Deer mice dominated the small mammal population and when included, did not allow detection of differences among the other small mammal species that were captured in very low numbers.
I present plots of the small mammal species capture rates along the transriparian gradient with the exception of *P. maniculatus* and *M. erminea*. These graphs use capture data of the second trapping year only (1995) because capture data in 1994 are very low for all of the species other than *P. maniculatus*. The trapping season was short in 1994 and perhaps not representative. Deer mice were not included because they dominate the small mammal population. Analyses of the entire small mammal population are greatly influenced by this species and are a good indication of its abundance and distribution among the habitats (See Chapter 2). Short tailed weasel data were insufficient to produce representative plots. Graphs were produced for all habitats (old-growth, buffered clearcut, and clearcut). Linear distributions of the capture rates of small mammal species with distance from the stream among the habitats were developed. The significance of each slope of the capture rate over the distance from the stream was tested using a two-tailed student’s *t* test on a Simple Linear Regression drawn from the functional relationship: \( Y_i = \alpha + \beta X_i \) (\( \alpha = 0.05 \)). The coefficient of determination \( (r^2) \) or the proportion of total variation in \( Y \) accounted for by the fitted regression also designated as the strength of the straight-line relationship (Zar, 1984) was calculated for each regression.
3.3 RESULTS

3.3.1 Vegetation

Species richness

Species richness of shrubs and herbs (including ferns) are given along transriparian gradients for each sampling site (Fig.11). Herbs species richness within the old-growth site #2 was reduced by half from 150m going upland. The slope changed from level to 40% at 150m away from the stream affecting the habitat characteristics. The herb species richness within buffered site #1 increased from 90m on, where the transition from the buffer strip to the adjacent clearcut area occurred (Fig.11c). This clearcut zone contained some temporary streams that might have influenced the herb layer composition.

Site and distance effects were not significant for shrub species richness (df=5,40, F=1.222, P=0.198 and df=8,40, F=1.473, P=0.317, α=0.05) nor was a distance effect significant for herb species richness (df=8,40, F=1.438, P=0.211, α=0.05), but the site effect was found significant (df=5,40, F=13.279, P<0.001, α=0.05).

Percent vegetative cover

None of the habitats and sampling sites demonstrated a specific trend in the distribution of percent cover of shrubs and herbs with distance from the stream (Fig.12, 13,
and 14). A sharp increase (3.5 times higher) of shrub cover from 180m and greater occurred within the undisturbed site #1 (Fig. 12a). This portion of the sampling site included a depression with greater soil moisture that favoured the growth of shrubs typical of high nitrogen soil namely *O. horridus*, *Alnus* spp., and *R. parviflorus*.

There was a significant site and distance effect from the RCB design analysis (df=5, 40, F=3.46, P=0.015 and df=8, 40, F=2.224, P=0.006, α=0.05) for shrub percent cover. No significant distance effect was found for herb cover but the site effect was significant (df=5, 40, F=5.884, P<0.001, df=8, 40, F=0.991, P=0.457, α=0.05). A *t*-test run on shrub cover showed that the means from the buffer strip and adjacent clearcut populations were not significantly different and therefore drawn from the same population (df=9, *t*=2.15, and df=8, *t*=0.52, α=0.05).
Figure 11a. Vegetation species richness in old-growth site 1

Figure 11b. Vegetation species richness in old-growth site 2

Figure 11c. Vegetation species richness in buffered site 1

Figure 11. Vegetation species richness and distance from the stream: old-growth site 1 (Fig.11a), old-growth site 2 (Fig. 11b), buffered site 1 (Fig.11c).
Figure 11. Vegetation species richness and distance from the stream: buffered site 2 (Fig. 11d), clearcut site 1 (Fig. 11e), clearcut site 2 (Fig. 11f).
Figure 12a. Percent shrub cover per plot within the old growth sampling-sites as a function of the distance from the stream.

Figure 12b. Percent herb cover per plot within the old growth sampling-sites as a function of the distance from the stream.

Figure 12. Percent vegetative cover per plot within the old growth sampling-sites as a function of the distance from the stream: percent shrub cover (Fig. 12a), percent herb cover (Fig. 12b).
Figure 13. Percent vegetative cover per plot within the buffered sampling sites as a function of the distance from the stream: percent shrub cover (Fig. 13a), percent herb cover (Fig. 13b).
Figure 14. Percent vegetative cover per plot within the clearcut sampling sites as a function of the distance from the stream. a) percent shrub cover, b) percent herb cover.
3.3.2 Small mammal populations

*Species richness and species composition*

In 1994 the number of small mammal species captured along the 150-m transects within the old-growth and clearcut sampling sites varied between 2 and 3. Members of *Sorex* spp. and *M. erminea* were absent from the old-growth. All of the species and genera captured were found within the clearcut habitat (*P. maniculatus, Microtus* spp., *C. gapperi, Z. princeps, Sorex* spp., *M. erminea*; Fig. 15). Small mammal species richness was generally higher in the buffered site #2 ranging between 3 and 5 species captured. Buffered site #1 had the poorest species richness of all sites with only 1 or 2 species at most distances (Fig. 15). Only *M. erminea* was absent from the buffered habitats.

In 1995 the small mammal species richness in relation to the distance from the stream followed two different trends. In half of the sampling sites including old-growth site #2, buffered site #2, and clearcut site #1, the average number of taxa found for most distances varied between 1 and 3. Remaining sites (old growth site #1, buffered site #1, clearcut site #2) had a higher species richness ranging between 3 and 5 species and genera at all distances. *M. erminea* and *C. gapperi* were absent from the old-growth habitat. All the species and genera captured were present within the buffered and clearcut habitats (Fig. 16).
Small mammal abundance

In 1994 the site effect was found significant for small mammal abundance (Fig. 17) with a Randomized Complete Block design (df=5,50, F=11.094, P<0.001). There was no significant distance effect for small mammal abundance (df=10,50, F=1.046, P=0.421, α=0.05). In 1995 (Fig. 18) there was no significant effect of the distance on the small mammal abundance (df=18,90, F=0.825, P=0.667, α=0.05). The site effect was found significant (df=5,90, F=10.116, P<0.001, α=0.05).

Gradient and species

Normalized small mammal abundance frequency was calculated for all of the species and genera captured. *P. maniculatus* dominated all habitats for both trapping years. *Sorex* spp. were found dominant, after the deer mice, in most of the clearcut areas (1994 and 1995). *Microtus* spp. reached its highest normalized abundance within old-growth habitat for both trapping years and within buffer strip habitat (1994). Normalized abundance frequencies for this genus were higher within the non-buffered clearcut areas than within the buffered ones. If a riparian buffer was present, the frequency was higher within the buffer strip than within the adjacent clearcut area. *Z. princeps* dominated the old-growth and buffer strip areas after *P. maniculatus* in 1995 (Fig. 20) while its highest abundance frequencies were found within all clearcut areas in 1994 (Fig. 19). The normalized abundance of the species was higher within buffered clearcuts than within the non-buffered ones for both trapping years. *C. gapperi*
Figure 15. Small mammal species distribution and composition in relation to the distance from the stream. Capture data from 1994.
Figure 16. Small mammal species distribution and composition in relation to the distance from the stream. Capture data from 1995. See legend on Fig. 15.
Figure 17. Small mammal relative abundance in 1994 and distance from the stream in each sampling site: old-growth habitat (Fig. 17a.), buffered habitat (Fig. 17b), clearcut habitat (Fig. 17c).
Figure 18. Small mammal relative abundance in 1995 and distance from the stream in each sampling site: old growth habitat (Fig. 18a.), buffered habitat (Fig 18b.), clearcut habitat (Fig 18c.)
seemed to favour riparian buffer strip and non-buffered clearcut areas in 1994 and 1995 over old-growth and buffered clearcuts (Fig. 19 and 20). In 1995, despite the fact that \textit{C. gapperi} normalized abundance frequency was high within non-buffered clearcut habitat, the species was not captured within clearcut portions of buffered habitat but was important within the adjacent riparian buffer strips zones (Fig. 20).

Capture rates of each small mammal species or genus as a function of distance from stream are presented in Figure 21. Regression slopes of \textit{Z. princeps} capture rates with distance from the stream were significantly different from 0 within clearcut and old-growth habitats (df=1, t=±2.544, P=0.024, and df=1, \( t=±4.277, P=0.0001, \alpha=0.05 \)). Both slopes were negatively correlated with gradient. Capture rates regression slope of \textit{Sorex} spp within the buffered habitat was found significantly different from 0 but positively correlated with gradient (df=1, 17, \( t=±2.305, P=0.034, \alpha=0.05 \)). All of the remaining capture rate regression slopes shown in figure 21 were found non significant (\( \alpha=0.05 \); Table 7).

Coefficients of determination (\( r^2 \)) calculated for each regression line were low, ranging from 0 to 0.585 (Table 7). It indicates that the portion of the variation explained by the regression (\( r^2 \)) were low. Seven of the ten regression slopes tested were non significant or equal to zero explaining the low coefficients of determination.
Figure 19. Normalized abundance of small mammal species among habitat with 1994 captures: Old-growth (Fig.19a), Riparian buffer strip (Fig.19b), buffered clearcut (Fig. 19c), clearcut (Fig. 19d). *P. maniculatus* was excluded because its abundance was too high in comparison with the other species therefore hiding the patterns of abundance frequencies.
Figure 20. Normalized abundance of small mammal species among habitat with 1995 captures: Old-growth (Fig. 20a), Riparian buffer strip (Fig. 20b), buffered clearcut (Fig. 20c), clearcut (Fig. 20d).
Figure 21. Scatter plot of the capture rates within each habitat: *Z. princeps* (Fig. 21a), *Microtus* spp. (Fig. 21b), *Sorex* spp. (Fig. 21c), *C. gapperi* (Fig. 21d).
Table 7. Results from t-tests on the significance of each linear regression slope for small mammal capture rates and distance from stream. Coefficients of determination are given.

<table>
<thead>
<tr>
<th>Species or gender</th>
<th>Habitat</th>
<th>df</th>
<th>t (two-tailed)</th>
<th>P</th>
<th>( r^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Z. princeps</strong></td>
<td>Old-growth</td>
<td>1,13</td>
<td>± 4.277</td>
<td>0.0001</td>
<td>0.585</td>
</tr>
<tr>
<td></td>
<td>Buffered</td>
<td>1,13</td>
<td>± 0.882</td>
<td>0.394</td>
<td>0.056</td>
</tr>
<tr>
<td></td>
<td>Clearcut</td>
<td>1,13</td>
<td>± 2.544</td>
<td>0.024</td>
<td>0.332</td>
</tr>
<tr>
<td><strong>Microtus spp.</strong></td>
<td>Old-growth</td>
<td>1,13</td>
<td>± 1.202</td>
<td>0.251</td>
<td>0.100</td>
</tr>
<tr>
<td></td>
<td>Buffered</td>
<td>1,13</td>
<td>± 1.916</td>
<td>0.078</td>
<td>0.220</td>
</tr>
<tr>
<td></td>
<td>Clearcut</td>
<td>1,13</td>
<td>0</td>
<td>1.000</td>
<td>0.0</td>
</tr>
<tr>
<td><strong>Sorex spp.</strong></td>
<td>Old-growth</td>
<td>1,15</td>
<td>± 0.424</td>
<td>0.677</td>
<td>0.012</td>
</tr>
<tr>
<td></td>
<td>Buffered</td>
<td>1,17</td>
<td>± 2.305</td>
<td>0.034</td>
<td>0.238</td>
</tr>
<tr>
<td></td>
<td>Clearcut</td>
<td>1,13</td>
<td>± 0.684</td>
<td>0.506</td>
<td>0.035</td>
</tr>
<tr>
<td><strong>C. gapperi</strong></td>
<td>Old-growth</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Buffered</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Clearcut</td>
<td>1,13</td>
<td>± 0.604</td>
<td>0.556</td>
<td>0.027</td>
</tr>
</tbody>
</table>

Species found only within riparian buffer strip area of buffered habitat.
3.4 DISCUSSION

Vegetative cover and species richness did not display regular or specific trends with distance from the stream among the habitats. Only percent cover of shrubs was affected by distance from the stream but showed no significant differences between the riparian buffer strip areas and adjacent clearcuts. Herbs showed no generalized trends with distance from stream. The sites contained differences that are expressed as various microhabitats. It was therefore not possible to discern a continuous gradient or trend in habitat structure.

Small mammal relative abundance showed no significant distance effect for both trapping years. Two-way ANOVA were run on all of the small mammal species pooled. *P. maniculatus* dominated the populations studied and is described as an abundant generalist by Duessier and Shugart (1979). The results of the analysis on distance effect may reflect primarily abundance patterns of *P. maniculatus*. Small mammal species richness was generally higher within the buffered and clearcut habitats for both trapping years where shrub cover seemed higher. Gomez (1992) found that the small mammal species richness was higher within shrub habitats than old-growth. Many studies (Cross 1985, McComb et al. 1993, Doyle 1990), comparing riparian zones with mature and old-growth uplands found that the species richness was higher within the riparian zones.

Alder (1988) found that most small mammals demonstrated affinities for specific microhabitat types on either control or experimental grids and suggested that microhabitat
structure is a potentially important force in organizing small mammal populations. Carey and Johnson (1995) could not show cause and effect relationships between habitat structure and small mammal populations. They found that coarse woody debris and shrub percent cover play primary roles into determining the small mammal species abundance and suggested that variations that exist in forest stands, even in stands of similar age structure, is sufficient to account for marked variation in small mammal species abundance. Such relations were not strongly evident in my data, though some affinities were apparent. Deer mice dominated in all habitats. *Z. princeps* normalized abundance showed its highest values within old-growth and buffer strip areas in 1995 (Fig. 6). Regression lines on capture rates were significantly and negatively correlated with distance from water within buffered and clearcut habitats (Table 7). *Z. princeps* capture rates in other studies were found to be higher within streamside zones (Gomez 1992, McComb et al. 1993). The species is associated with moist, grassy areas of forested regions and negatively associated with conifer tree cover. Results of my study suggest an association of *Z. princeps* with riparian habitat structure although there was no significant correlation of the capture rates within the buffered habitat. In the clearcut area of buffered site #1 of the present study there were temporary streams that appear to have favoured the herb layer (Fig. 11), providing suitable microhabitats for *Z. princeps* and accounting partially for the zero slope of the capture rate regression line with distance from stream within buffered habitats.

After deer mice *Sorex* spp. were most abundant in clearcut areas (Fig. 19 and 20), where volumes of downed wood were highest. Geir and Best (1980) found that removal of woody debris from the forest floor could reduce the abundance of two shrew species
(S. tridecemlineatus, S. cinereus) that were captured. Craig (1995) did not directly associate the shrew populations to the amount of downed wood but rather with abundant, moderately-sized pieces of wood, and increased vegetative and litter cover. Gomez (1992) found that S. orarius was positively correlated with the number of large logs while S. townsendii and S. vagrans were positively correlated with percent cover of thimbleberry, forbs and grasses and negatively correlated with amount of large logs.

*Microtus* spp. showed a greater relative frequency within old-growth and riparian buffer strip habitat than within clearcut zones. The genus was found to be more abundant within streamsides than upland but was also predominant in riparian clearcut areas (Gyug and Vaartnou, 1996). In my study sites without riparian buffer strips there was a higher relative frequency of *Microtus* spp. than those adjacent to riparian buffer strips (Fig. 19 and 20).

Red-backed vole was found dominant within unharvested forest (Gyug and Vaartnou 1996, Martell 1983) and became rare within 3 years following logging while *P. maniculatus* became the dominant species of clearcut blocks (Martell, 1983). Healy and Brooks (1988) found that red-backed voles were more abundant in younger than older stands of west Virginia. In 1994 *C. gapperi* was present in all habitats studied (old-growth, riparian buffer strip, buffered clearcut, and clearcut) but capture data were very low, making any conclusion on the population abundance and distribution patterns difficult. In 1995 populations were relatively abundant within clearcut and riparian buffer strip habitat while no individuals were captured within non-buffered clearcut and old-growth habitats. Results suggest that *C. gapperi* favoured riparian buffer strip habitat, when available, over adjacent
clearcuts. There was no strong evidence of riparian associated species in my data. Doyle (1990) and Gomez (1992) suggested that riparian habitats act as a source habitat for riparian associated species and early seral upland areas act as a dispersal sink. Adjacent clearcut areas are possibly habitat sinks. Sinks are refuge areas to which surplus individuals can disperse, and where survivorship and reproduction may be poor relative to that in high-quality habitats (Fretwell and Lucas, 1969). The adjacent clearcut areas could also be source habitats because of some of their characteristic features such as high volumes of downed wood and high shrub cover. To identify possible source habitat, the analysis must assess the small mammal fitness with variables like reproduction and survival rates. Data collection in this study did not allow this type of analysis.
4. CONCLUSIONS AND RECOMMENDATIONS

Sampling site components differed considerably within habitats. Similar sampling sites, especially when dealing with riparian habitat, will more than likely always differ structurally. To assess habitat structure associations with small mammals a sufficient number of replicates should be sampled. Gallindo et al. (1995) suggested that at least three sampling areas would allow some degree of statistical confidence and avoid the acceptance of an exceptional occurrence as the norm. Carey and Johnson (1995) found that their sampling sizes (50 trapping stations per grid) in managed and old-growth stands were small relative to complexity and variability encountered thus producing statistical tests with low power. More extensive study designs should include sampling of different watersheds and stream classes to account for the structural differences.

Because small mammal population seemed related to the microhabitat rather than to the habitat at a larger scale, an investigation at a smaller scale of the microhabitat associations would provide better understanding of the small mammal population parameters. Geier and Best (1980) suggested that responses of small mammal species to microhabitat variables differed considerably. Microhabitat features most frequently related to species abundances were plant-species richness and percent cover.

Results suggest that the small mammal population abundance and density were higher within heterogeneous habitat composed of both clearcut and riparian buffer strips. Some
species, such as *C. gapperi*, were sometimes found confined to the riparian buffer strip areas of buffered clearcut sites and others, such as *Z. princeps*, seemed closely associated with streamsides. Other species, such as members of *Sorex* seemed associated with clearcuts. Cross (1985) suggested that cut-over forest habitats with riparian leave-strips supported several species known to be riparian or forest obligates. Doyle (1990) suggested that riparian habitat may be superior based on greater availability of water and forage. Riparian buffers should be sufficiently wide to contain a variety of habitats. From my results it is not possible to suggest an ideal width although the 60-90m riparian buffer investigated here seemed a minimal width to sustain certain habitat sensitive species such as *C. gapperi*.

Long term studies are preferable because small mammal populations have been found to fluctuate considerably. To effectively manage riparian habitats for small mammal species, it is extremely important to document seasonal and year to year variability in community patterns (Galindo *et al.*, 1995).
LITERATURE CITED


