Summary

Retention of genetic variation in populations of endangered species is a prerequisite for their future survival. This means that conservation efforts should include (among other things) genetic management of such populations. Genetic management is subject to risks that the actual genetic variation in populations is lower than estimated. It is obvious that such risks should be minimized. This thesis involves studies on two major categories of risks. The first category refers to (sampling) errors in estimating genetic variation. These errors are due to the stochastic nature of Mendelian segregation and to assumptions regarding genome structure and genetic composition. The effects of these assumptions on the probability that actual genetic variation is lower than estimated are studied. The second category of risks refers to assumptions of parentage of individuals in populations which are managed in social groups. The effects of social (mating) structure on retention of genetic variation are studied.

The genetic simulation model CHROMOFLOW has been developed to study the effects of assumptions regarding genome structure and genetic composition. This model is described in chapter 2. It allows a wide range of assumptions varying from single locus models to genome models involving multiple chromosomes and genetic crossing over. The genetic composition of populations can vary in this model from 'two alleles - equal frequency' to more complex compositions as derived from, for example, molecular studies. CHROMOFLOW estimates the expected values for different measures of genetic variation (gene diversity, observed heterozygosity, polymorphism and numbers of allelic variants) that have been retained in pedigree populations. Variances and frequency distributions of values among simulation runs, as produced by the CHROMOFLOW program, are used to determine probabilities that measures of genetic variation in any actual population are lower than expected.

Chapter 3 presents the results of a study on errors in estimating retention of genetic variation in small populations due to assumptions of genome structure and genetic composition. CHROMOFLOW experiments show that variances will decrease for increasing levels of initial gene diversity and increasing numbers of loci. Variances are especially high in models involving rare alleles. Results of simulations show that observed heterozygosity is more sensitive to sampling errors - resulting in higher variances - than gene diversity. Linkage results in larger variances compared to models that assume independent loci. Effects of linkage can be described as effectively studying lower numbers of loci than included in the model.

An increase of total genetic map length, either resulting from an increase of chromosome number or resulting from an increase of map length of individual chromosomes, will reduce the variance of genetic diversity. Frequency distributions of values of gene diversity and observed heterozygosity in individual
simulation runs have been used to determine probabilities that these values are less than 95 percent of the expected (average) value. The results of this risk analysis show that genome models can be ignored in simulation experiments and that errors are pre-dominantly determined by assumptions regarding (1) initial gene diversity at the studied loci and (2) the number of (polymorphic) loci included in the model.

The CHROMOFLOW model can handle any pedigree regardless of its complexity. Therefore, this model can be used to evaluate historical trends in retention of genetic variation in real populations. Chapter 4 presents studies on the international studbook (zoo) populations of Przewalski’s horses, Equus przewalskii, and Nepalese red pandas, Ailurus fulgens fulgens. Studies on real populations will generally be accompanied by (practical) problems such as unknown parentage. The use of demographic and species-specific biological data in making assumptions regarding unknown parentages is discussed. This chapter also presents the use of CHROMOFLOW to evaluate results of biochemical and molecular studies in (non-random) samples of individuals for which pedigree data are available. The results of protein electrophoresis in red pandas [Gentz, 1989], which showed low levels of genetic variation, have been evaluated in this study.

Pedigree analysis shows that expected gene diversity in the living red panda zoo population is 95.3% of the wild gene diversity, as of 31 December 1993. However, CHROMOFLOW experiments assuming low levels of wild gene diversity show a probability of 0.3 that actual gene diversity in the population has already decreased till 90%.

Evaluation of historical trends in both zoo populations show that retention of gene diversity and observed heterozygosity greatly benefit from implementation of cooperative breeding programs that are based on population genetic theory.

Chapter 5 describes the use of Maximal Avoidance of Inbreeding (MAI) schemes [Wright, 1921] in the genetic management of harem groups, multi-male/female colonies and in metapopulation management without having detailed pedigree data. MAI can be applied in management of such populations by considering a single paternal and maternal line for each group, regardless of the actual number of breeding males and females. General formulae to determine the exchange of offspring between groups in each generation are, in addition to the basic characteristics of MAI described by Wright[1921], presented in this chapter.

The effect of social organization (and mating structure in particular) on retention of genetic variation is discussed in Chapter 6. The simulation program GENEFLOW - an earlier version of CHROMOFLOW (see Chapter 2) - has been used to study genetic loss in small populations that are managed in social groups. Size and composition of groups - within a fixed population size of 32 individuals - and mating structure within these groups are varied in series of GENEFLOW experiments. Genetic drift is especially large in populations that are composed of large harem groups or large colonies in which reproductive success is limited to a single breeding pair. Reproductive success among group members will often - without the use of DNA fingerprinting - remain a ‘black-box’. A general recommendation for the reduction of group size and equally distributed reproduction composition needs to be based on the natural habitat.
recommendation for the population management of social species involves reduction of group size and extension of the number of groups to create a more equally distributed reproductive success, and thus, lower genetic drift. The group composition needs to be based on field data on smallest breeding demes observed in the natural habitat.