POPULATION SIZE, GENETIC VARIATION, AND RELATED PARAMETERS IN SMALL, ISOLATED PLANT POPULATIONS: A CASE STUDY

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1. Introduction

Theoretically, many population biological processes change when plant populations become isolated and population size declines as a result of habitat fragmentation. In one of the review chapters of this book (Oostermeijer et al.: 93-101) the most important of these theories are described, and several references were given to empirical studies demonstrating that these theories are actually valid in the field. In this chapter, a case study is presented of a single rare plant species, *Gentiana pneumonanthe* Linnaeus, 1758 which is threatened by severe habitat fragmentation in The Netherlands. As a product of a broad research project on the population viability of this species (Oostermeijer 1996), much knowledge has become available about patterns and processes concerning its genetic variation, mating system, pollination ecology, and demography. A summary of the main results of this project is presented in this paper to show how habitat fragmentation may affect the viability of a formerly common plant species.

2. Description of the study species

*Gentiana pneumonanthe* (the marsh gentian) is a long-lived perennial plant that is characteristic for wet heathlands, unfertilized hay meadows, and the margins of peat bogs in a large part of Europe. Its range extends from Great-Britain to the Ukraine and from Southern Sweden and Finland to Northern Spain. Nowadays, however, the species is declining in a large part of its distribution, mainly in countries that suffer most from habitat destruction and fragmentation, such as The Netherlands, Germany, Sweden, and Great-Britain.

The adult plant has 1 - 10 stems, which each can bear 0 - 5 flowers. Entirely vegetative adults are frequently found, however. Flowers exhibit herkogamy and protandry to avoid self-pollination. They are normally pollinated by bumble-bees (Petanidou et al. 1995). Each flower produces 400-1000 ovules, developing into small, light seeds dis-
3. Population size and genetic variation

Allozyme studies on field samples from 25 populations demonstrated a loss of genetic variation in small populations, and showed that there is very little to no gene exchange between populations in the Netherlands (Raijmann et al. 1994). The reduced genetic variation was reflected in the proportion of polymorphic loci, but not in the effective number of alleles per locus and heterozygosity (Figure 1).

However, it was found that small populations show much higher rates of self-fertilisation than larger populations, which means that the offspring may experience considerable inbreeding depression and reduction of heterozygosity. This discrepancy between maternal plants in the field and their offspring was explained from the long generation time of this perennial species, suggesting that populations have not been small long enough to have experienced several generations of inbreeding to reduce heterozygosity of the maternal plants.

In a further study, it was shown that offspring of small populations indeed had a lower performance for several life-history (fitness-related) parameters (Oostermeijer et al. 1994a). This low fitness was attributed partly to environmental stress on the maternal plants, and partly to reduced heterozygosity as a consequence of the high selfing rates mentioned above. The relationship between allozyme heterozygosity and fitness was also studied on the individual plant level (Oostermeijer et al. 1995a). The relationship appeared to be very strong, which makes it likely that there is selection against homozygotes in natural situations. It was hypothesised that this could cause a relatively high proportion of heterozygotes among the reproductive adults that persist in small populations, explaining why the relationship between population size and heterozygos-