

Demographic Genetics of Brown Trout (*Salmo trutta*) and Estimation of Effective Population Size From Temporal Change of Allele Frequencies

Per Erik Jorde and Nils Ryman

Division of Population Genetics, Stockholm University, S-106 91 Stockholm, Sweden

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ABSTRACT

We studied temporal allele frequency shifts over 15 years and estimated the genetically effective size of four natural populations of brown trout (*Salmo trutta* L.) on the basis of the variation at 14 polymorphic allozyme loci. The allele frequency differences between consecutive cohorts were significant in all four populations. There were no indications of natural selection, and we conclude that random genetic drift is the most likely cause of temporal allele frequency shifts as they have measured. Effective population sizes were estimated from observed allele frequency shifts among cohorts, taking into consideration the demographic characteristics of each population. The estimated effective sizes of the four populations range from 52 to 490 individuals, and we conclude that the effective size of natural brown trout populations may differ considerably among lakes due to variation in size and other apparent characteristics. In spite of their different effective sizes all four populations have similar levels of genetic variation (average heterozygosity) indicating that extensive loss of genetic variability has been recorded, most likely because of gene flow among neighboring populations.

THE effective population size (N_e) is an essential concept when linking the theory of population genetics to the real world of natural populations (Wright 1969, p. 211). This central position stems from the wide range of demographic factors encompassed by N_e , thereby allowing a unified theoretical treatment of random genetic changes of populations. It has been notoriously difficult to obtain reliable estimates of N_e in natural populations, however, because the direct assessment of N_e requires measurements of the entire array of demographic parameters on which it depends. Such measurements are difficult to carry out in natural populations. Moreover, the precise relationship between certain demographic factors, such as various forms of nonrandom mating, and N_e remain uncertain and subject to continued theoretical refinements (Crow and Kimura 1970; Crow and Dennings 1988; Ryman and Lukac 1991; Caswell and Hill 1992; Crow 1993; Caswell 1994; Siler and Caswell 1994; Ryman et al. 1995; Wang 1995). Our knowledge of the effective size of natural populations is therefore very limited.

Indirect methods have been considered in circumventing the problems of directly evaluating N_e in natural populations (Wright et al. 1942; Kimura and Tanabe 1971; Hill 1981; Wang 1991; Barnard et al. 1992). The most promising approach is based on measurements of the amount of random genetic drift between generations that is directly proportional to the effective population

size (Nei and Tajima 1981; Nei 1982; Tajima and Nei 1984; Wang 1989). This so-called temporal method has been used to estimate N_e in natural populations from observed shifts of allozyme frequencies in various species characterized by either quite simple (i.e., discrete generations; Kimura and Tanabe 1971; Bawa et al. 1980; Hickey et al. 1990; see also Frankham 1995 and references therein) or rather peculiar (i.e., semelparity; Wang 1990; Wang and Tang 1990) life history patterns.

Although the above applications of the temporal method have been successful, it has been unclear how to apply it to the large group of organisms characterized by overlapping generations and thus have the potential for repeated breeding during a lifetime (iteroparity). For this group of organisms we have recently evaluated the dynamics of random allele frequency change within a population and derived a method for estimating N_e from observed temporal shifts of allele frequencies (Jorde and Ryman 1995). Here, we apply this method to allow the data from brown trout (*Salmo trutta*) and estimate the effective size of four natural populations in Sweden.

MATERIALS AND METHODS

The estimation procedure (Jorde and Ryman 1995) is based on observations of allele frequency differences among consecutive cohorts; this procedure requires genotype data from individuals that have been classified with respect to age as well as information on the age-specific survival and reproduction rates for the population to which they belong. The results of the present study are based on a rather extensive set of data, and we have primarily focused on aspects that relate directly to the estimation of effective size.

Corresponding author: Nils Ryman, Division of Population Genetics, Stockholm University, S-106 91 Stockholm, Sweden.
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