A role of an experimental fish in fish genetics and breeding science

MASAMICHI NAKAJIMA

Graduate School of Agricultural Science, Tohoku University, Sendai 981-8555, Japan

(mnkjm@bios.tohoku.ac.jp)

SUMMARY: A model fish is important for the experiment of fish genetics and breeding science. One of the role of model experiment in fish genetics is to perform the experiment which need long time in the commercially important fish. The guppy, *Poecilia reticulata*, has been frequently used as model experiment of fish genetics, because of its many varieties and breeds, short life cycle, ease of breed and reproductive capacity.

In this review, inbreeding depression and genetic influence for the growth were considered. In the former problem, small number of parents leads the genetic drift and homozygotes of lethal recessive genes were observed. And in latter problem, it was suggested that the small number of genes which locate on sex-chromosome are influencing the growth in the guppy.

KEY WORDS: genetic drift, guppy, heterosis, heritability, Inbreeding, Isozyme, *Poecilia reticulata*, quantitative trait,

Introduction

One of the role of model experiment in fish genetics is the perform of the experiment which need long time in the fish which is commercially important, such as an experiment of genetic drift, effect of inbreeding occurred during the maintenance of stock population and genetic control of specific trait. The conditions which required to experimental fish are follows, "generation time is short", "saving space", "maintenance is easy", "easy to regulate a hereditally conditions", etc. The guppy, *Poecilia reticulata*, has been used for model experiments in fish genetics and breeding sciences, because of its short life cycle, capacity to reproduce and ease of breeding. In mature males of the guppy, aquarists have bred a variety of color types and color patterns, which are the base of the experimental strains. In our laboratory, several strains were maintained as closed colony and these strains were used as experimental strain. In this review, model experiments used guppy were introduced, which were focused on the strain differences among experimental strain, strain management, effect of inbreeding and genetic influence for the growth.

Genetic drift and inbreeding depression

The laboratory strains maintained as closed colonies were created based on morphological characteristics. However, it is unknown how and when the original population has derived from the native distribution. The genetic differentiation among laboratory strains was examined by isozymes^{1,2)}. Macaranas and Fujio¹⁾ reported two major groups in the guppy strains, one was standard type and the other was fancy type. However, these two groups could not been observed after 10 years. Genetic relationship among 16 strains were represented at Fig.1. The data from Barinova *et al.*²⁾ using UPGMA³⁾ based on genetic distance⁴⁾ between strains.

Fig. 1 Genetic relationship among 16 laboratory strains of the guppy.

The strains which have same origin such as F and F22, D and D1, A, B and C, and S3 and S3HL indicated close relationship, except that, S and S3, and T and T1 did not indicate close relationship. In the comparison of the results between Macaranas & Fujio¹⁾ and Barinova *et al.*²⁾, remarked increase of genetic distance was found between S and S3 strain and T and T1 strains. Barinova *et al.* (1997) suggested the significant positive correlation ($P < 0.05$) between genetic distance among strains and the time after subdivision in the subdivided strains (Fig. 2). They concluded that the bottlenecking and founder effects that accompanied selection in producing and maintaining these populations caused the loss of identification of two major groups.

Fig.2 Correlation between genetic distance and the time after subdivision in the guppy strains

Inbreeding tends to reduce the mean level of all characteristics closely connected with fitness in animals and to lead in consequence to a loss of general vigor and fertility. This phenomenon has been known as inbreeding depression. In the case of the guppy, the

most striking observed consequence of inbreeding is the reduction of the mean phenotypic value shown by characteristics connected with reproductive capacity, such as fertility ratio, offspring survival at birth and offspring size⁵⁾.

Fujio & Nakajima⁶⁾ estimated the frequency of the deleterious recessive allele as the lethal equivalent. Depression is considered to be dependent on the genetic load. The genetic load could be represented by the average number of lethal equivalents per individuals in a population of the offspring mortality at birth in F and S strains of the guppy, which were, maintained as closed colony. The offspring mortalities increased after single generation of full-sib mating, however, it decreased after second generation of full-sib mating. The frequencies of the lethal alleles were estimated from females for which mortality was expressed, and which were 0.267 in the S strain and 0.439 in the F strain at first generation of full-sib mating. In the F strain, the frequency of lethal allele decreased from 0.439 to 0.013 during 4 generations of full-sib mating, however, it takes 75 generations to change the frequency from 0.439 to 0.013 by random mating.

From the offspring mortalities at random mating and single full-sib mating generations, the amount of lethal gene were estimated by the methods suggested by Morton *et al.*⁷⁾. The estimated lethal gene per genome was 1.8 in the F strain and 0.8 in the S strain. These values were the same level as the values calculated in other domesticated animals, from 0 to 4.0 in a milch cow, 2.0 in a pig, 1.7 in a white leghorn, 5.7 in a Plymouth rock and 7.5 in a Japanese quail⁸⁾.

Table 1 Fluctuation of allele frequencies during the maintenance of strains of the guppy

S strain			S3 strain		
Collection date	<i>Aat-1</i> ^A	<i>Pgm-1</i> ^A	Collection date	<i>Aat-1</i> ^A	<i>Pgm-1</i> ^A
83.4	0.308	0.758	83.2	0.333	0.767
83.6	0.329	0.688	85	0.580	0.805
85	0.414	0.658	89	0.317	0.707
93	0.830	0.290	93	0.354	0.643
97	0.602	0.430	97	0.395	0.528

$$N_e = p(1-p) / (2 \cdot \sigma^2 \delta q^2)$$

Fujio *et al.* (1999)⁹⁾

Fig. 3 Fluctuation of fraction of genetic variance to total variance from maternal and paternal half according to the growth in the guppy.

Fujio *et al.*⁹⁾ suggested the decrease of effective population size (N_e) during the maintenance of the guppy population based on the magnitude of the random drift in the allele frequencies in the two isozymes loci, *Aat-1* and *Pgm-1* (Table 1). The estimated N_e was initially 623 in the S strain and 413 in the S3 strain, and these decreased to 18 in the S strain and 24 in the S3 strain over a period of 16 years, although the population size of strains were always maintained more than 500 individuals. Nakajima *et al.*¹⁰⁾ demonstrated that at least 14 pairs were needed to maintain the same allele frequency level as the original population in regard to two isozymic loci from the combination test of 16 sub-populations which were originated from one pair from same guppy strain. The number of individuals needed to maintain the population were simulated according to it, a founding population of, at least, 25 females and 25 males, is a reasonable absolute minimum^{11,12)}.

Genetic influence for the growth

Traits in which phenotypes are quantitative in nature and continuous in distribution are referred to as quantitative characters. Genetic control of variation in such traits is explained by the "multiple factor

hypothesis," which assumes that the quantitative character depends upon the cumulative action of multiple genes, each on a separate chromosome, and each producing a small cumulative effect. Most metric characters which are commercially important, such as body size, weight reproductive capacity and survival rate etc., are quantitative traits. Genetic influence on the trait is usually measured as heritability, which is the ratio of the total additive genetic variance to the phenotypic variance. Nakajima & Taniguchi¹³⁾ reported the fluctuation of variance component from maternal or paternal half during the stage of the growth.

The estimated fluctuations of fractions of variance component to total variance at various stages of the growth in sexes are represented in Fig. 2. Different patterns of fluctuations of the fractions of variance component from maternal and paternal half were observed between the females and the males. High fractions of variance component from maternal half were observed at 0 days old. The fractions of variance component in the females from maternal half were constantly high, except 60 days old. But, those from the paternal half had extremely low values. On the other hand, the males demonstrated a fluctuation in the fractions of variance component patterns in maternal and

paternal half with respect to those observed in the females. The fractions of variance component from maternal half had a indicated maximum value of 0.565, at 30 days old, and this decreased to 0.052 at 180 days old. In contrast, the fractions of variance component from paternal half increased from 0 at 60 days old to 0.831 with a maximum value at 180 days old. The variance component from paternal half increased after 60 days old which is the beginning of the maturation stage for male individuals, which suggest that the body size of matured male strongly detected the genetic factors from paternal half. And genetic factors from maternal half were separated to two stages, which are before 30 days old and after 90 days old, which suggest the maternal effect at the early stage of growth and genetic control which linked with sex. In the case of X-linked inheritance, the paternal parent is not a factor of variance, because there are no X chromosomes from paternal half in male offspring and female offspring have same X chromosomes from paternal parent. In the case of Y-linked inheritance, factor of variance is only Y chromosome in male offspring. Low variance component from paternal half and high variance component from maternal half in female offspring suggest X-linked determination, and high variance component from paternal half in male offspring suggest Y-linked determination of the growth in the guppy. In this case, the fractions of maternal and paternal half to total variance indicate minimum heritability estimates. These results suggest the existence of genes affecting the body size is located on the sex-chromosome. Especially, the gene, which controls the final body size of the male, which will be sex, linked thus located on the Y chromosome.

Future Development

From model experiment used guppy, useful information was obtained for fish genetics and breeding sciences. The obtained information about genetic drift and inbreeding depression in the guppy will be expound to the stock management and breeding methods in commercially important fishes. On the other hand, small number of gene was estimated for inbreeding depression and the control of the growth, however, could not identify the gene which influence the growth. The QTL analysis is powerful tool to settle this problem.

We need to develop DNA markers, because there is a little information about DNA markers in the guppy which are needed to analyze QTL. We believe that when QTL analyses are undertaken the model experiment will occupy an important position.

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