Genetic Diversity Within and Among Feral Populations and Domesticated Strains of the Guppy (*Poecilia reticulata*) in Singapore

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**Abstract:** Genetic variability within and among feral populations and cultured strains of the guppy (*Poecilia reticulata*) was investigated by random amplification of polymorphic DNA (RAPD) fingerprinting. Feral guppies were collected from 6 isolated populations (BT, Bukit Timah; NS, Nee Soon; TS, Tuas; MF, Mount Faber; KR, Kranji; LI, laboratory-inbred feral line), while the Tuxedo and Green Variegated strains were sampled from 2 guppy farms in Singapore. Pairwise genetic distances analyzed by unweighted pair-group method with arithmetic means revealed distinct clustering of guppy individuals into their respective populations and strains. Percentage polymorphic loci ranged from 54.96% (TS) to 68.70% (KR), while average heterozygosity ranged from 0.220 (GV) to 0.271 (KR). In contrast, TS guppies had the highest (0.850) intrapopulation genetic similarity (S), whereas KR had the lowest (0.781). Among populations and strains, S ranged from 0.703 (between GV and LI) to 0.809 (between NS and MB). The GV strain S was closer to TX (0.784) than to the feral guppies. Bootstrapped genetic distance trees depicted 3 major nodes comprising BT-TS, NS-MF, and TX-GV. Principal coordinate analysis also differentiated the 6 feral populations from the 2 cultured strains.

**Key words:** guppy, *Poecilia reticulata*, RAPD-PCR, cluster analysis, genetic differentiation.

**INTRODUCTION**

The effects of natural and artificial introductions of populations or species into previously uncolonized territories on genetic diversity and population structure of local populations have been the concern of biologists for decades (Endler, 1983; Magurran et al., 1992; Carvalho et al., 1996). Attention has mainly focused on the formation of new “local” populations in apparently vacant ecologic niches. There are 3 types of wild populations: original natural populations, introduced wild (feral) populations that have adapted to a new environment and domesticated populations that have reverted to a “wild” state (Barinova et al., 1998). Comparison of genetic variability and differentiation between natural and cultured populations of the same species is important as such studies may shed light on the rates of evolutionary change and natural selection.
The history of the guppy *Poecilia reticulata* in Singapore is almost unknown. However, Herre (1940) documented that this small but hardy fish was introduced into Singapore and other parts of South-East Asia in the late 1930s to control mosquito breeding. From these artificial introductions, feral guppies proliferated in fresh and brackish waters throughout the island although their geographic distribution remains largely uncharted. The 1980s and 1990s saw a reduction of natural habitats for feral guppy populations owing to rapid urbanization and development of land-scarce Singapore. Consequently, the remaining feral guppy populations have become fragmented and isolated. Commercial culture of guppy strains in Singapore began in the 1950s (Fernando and Phang, 1985). The rich choice of colors as well as the shape and size of the body and fins of domesticated strains result from selective breeding and development of mutants over several decades from feral guppies. At present, about 40 to 50 guppy strains are reared in monoculture farms (Chen, 1999).

Since the early 1980s, natural populations of the guppy have been the subject of studies on morphology, behavior, predation, sexual selection, evolution, and ecology (Endler, 1983; Magurran et al., 1992; Houde, 1997; Reznick et al., 1997). In addition, Shaw et al., (1991, 1992, 1994) and Carvalho et al., (1991, 1996) examined allozymic diversity and genetic divergence of natural and artificially introduced guppy populations at different geographic locations in Trinidad. Genetic variability within and among introduced wild populations and cultured strains was also monitored by Macaranas and Fujio (1987) and Barinova et al. (1998) using isozyme and allozyme frequencies.

Random amplified polymorphic DNA (RAPD) fingerprinting is a simple and rapid molecular technique for generating genetic markers without prior knowledge of genomic DNA sequences (Welsh and McClelland, 1990; Williams et al., 1990). In this approach, arbitrary oligonucleotide primers are used to amplify random segments of genomic DNA by polymerase chain reaction (PCR). RAPD markers have been successfully employed for phylogenetic reconstruction and to assess genetic diversity and population structure in several teleost species: for example, tilapia, *Oreochromis* spp. (Bardakci arid Skibinski, 1994; Dinesh et al., 1995b); European sea bass *Dicentrarchus labrax* (Caccione et al., 1997); flyingfish *Hirundichthys affinis* (Gomes et al., 1998); guppies (Dinesh, 1995; Foo et al., 1995; Chen, 1999); catfishes, *Ictalurus punctatus* and *I. furcatus* (Liu et al., 1998, 1999); and discus *Symphysodon* spp. (Koh et al., 1999).

The main objective of this study was to determine the level of genetic diversity of 6 geographically isolated populations of feral guppies, *P. reticulata*, in Singapore by RAPD Fingerprinting. Two domesticated strains were used for comparisons with the feral guppies. Population differentiation among the wild-caught feral populations and farm-bred strains was also evaluated using this approach.

**Materials and Methods**

**Sources and Description of Guppies**

Feral guppies were sampled from Bukit Timah (BT), Nee Soon (NS), Tuas (TS), Mount Faber (MF), Kranji (KR), and Genetics Lab., Dept. of Biological Sciences, National University of Singapore (Table 1, Figure 1). Feral guppies from the latter, designated as LI, were collected from Kranji in the late 1980s and have been inbred for at least 25 generations. The Tuxedo (TX) and Green Variegated (GV) strains, used for comparisons with the feral guppies, were purchased from Chin Lam Brothers Tropical Fish Farm and Swee Hing & Brothers Aquarium Co., respectively (Table 1, Figure 1). The TX strain carries the black caudal-peduncle (*Bcp*) and red tail (*Rdt*) color pattern genes that are expressed in males as black pigmentation on the caudal-peduncle region and a red caudal fin, respectively (Khoo et al., 1999b,c). The TX females have olive-brown body coloration and gray caudal-peduncle with red tinges on an opaque white tail. The GV males display wild-type male body coloration, which comprises polymorphic patches of various colors that are overlaid by a green metallic sheen (Khoo et al., 1999a,c). The GV males also have an orange

![Figure 1. Geographic locations (▲) of the 6 feral populations and 2 guppy farms in Singapore (BT, Bukit Timah; NS, Nee Soon; TS, Tuas; MF, Mount Faber; KR, Kranji; LI, Lab.-Inbred; TX, Tuxedo strain; GV, Green Variegated strain) Scale bar = 10 km.](image-url)