

# An interacting system in population genetics

By

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## 1. Introduction

The purpose of the present paper is to investigate an interacting system describing an evolution of gene frequencies in population genetics. In particular, we are interested in the effect of geographical structure in the process of evolution.

We shall first explain our interacting system. Let  $S$  be a countable set. Each element  $i$  of  $S$  is called "a colony". We assume that there are two alleles  $A$  and  $B$  at each colony and denote by  $x_i$  ( $1-x_i$ ) the gene frequency of the  $A$ -allele (resp. the  $B$ -allele) for the colony  $i \in S$ . A time evolution of gene frequencies is caused by the following three factors;

- (1) mutation in each colony,
- (2) migration among colonies, and
- (3) random sampling drift.

It is described by means of the following stochastic differential equation,

$$(1.1) \quad dx_i(t) = a(x_i(t))dB_i(t) + (v - (u+v)x_i(t) + \sum_{j \in S} q_{ij}x_j(t))dt$$

where

$$a(y) = \frac{1}{\sqrt{2N}} \sqrt{y(1-y)} \quad \text{if } 0 \leq y \leq 1$$
$$= 0 \quad \text{otherwise,}$$

with a positive constant  $N$ ,  $u$  and  $v$  are constants such that  $u \geq 0$  and  $v \geq 0$ ,  $q_{ij}$  ( $i, j \in S$ ) are constants such that  $q_{ij} \geq 0$  for  $i \neq j$  and  $\sum_{j \in S} q_{ij} = 0$  for every  $i$ , and  $\{B_i(t)\}_{i \in S}$  is an independent system of one-dimensional Brownian motions.  $N$  denotes the population size of each colony at random sampling,  $u$  and  $v$  denote mutation rates between  $A$  and  $B$ , and for  $i \neq j$ ,  $q_{ij}$  denotes the migration rate from  $j \in S$  to  $i \in S$ .

We assume

$$(1.2) \quad \sup_{i \in S} |q_{ii}| < +\infty.$$

Then it is known that if  $0 \leq x_i(0) \leq 1$  for all  $i \in S$ , (1.1) has a unique solution satisfying

$$(1.3) \quad 0 \leq x_i(t) \leq 1 \quad \text{for all } i \in S \text{ and } t \geq 0, \text{ a.s. (cf. Shiga-Shimizu [10])}$$