

## A Branching Process in Varying Environments- A Mixed Mating Model

S.D. Batra and S.C. Gupta  
CCS Haryana Agricultural University, Hisar  
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### SUMMARY

Considering the importance of mixed mating system over the single mating system in genetic improvement programmes, a model of branching process in varying environment has been developed. The model has been applied to a system where genotypic assortative and random matings operate alternately and where the complete selection against homozygote recessives and partial selection against heterozygotes is allowed. The ultimate genetic structure of the population in terms of superior genotype leaving aside the inferior ones has been studied.

*Key words* : Branching process, Genetic improvement programme, Mixed mating, Culling.

### 1. INTRODUCTION

Generally plant and animal breeders are interested to develop a new technology for genetic improvement. The genetic improvement in animals and plants is possible through suitable breeding methodology based upon effective mating systems and by culling (selection) of genotypes preventing undesirable characters. Random mating is one such mating system which is commonly used in genetic improvement programme as it restores the genetic variability in the population but certainly not after selection. Another more useful mating system over random mating system in genetic improvement programme is genotypic assortative mating and was studied through branching process with emigration (Gupta *et al.* 1992). This mating system allows mating between individuals of same genotypes which helps in increasing the genotypic variance and thus increases the selection response (Mebride and Robertson 1963, Baker 1973). However, assortative mating is likely to create inbreeding depression which lowers down the fitness of population (Saccheri *et al.* 1998). Thus, the assortative mating has its own beneficial effects in terms of increased variance and selection response but has its determinantal effect in terms of inbreeding depression. Thus, to make the genetic improvement programme more vibrant and successful, it is advantageous to combine the two or more mating systems and allow culling of undesirable

genotypes in different generations. Keeping in view the above fact here a model of branching process in varying environments (BPVE) with emigration has been discussed. The model has been applied to a genetic improvement programme under a mixed mating system where genotyping assortative and random mating operate alternately and there is complete selection against homozygote recessive and partial selection against heterozygote.

### 2. MATERIAL AND METHODS

Consider a branching process in varying environment  $\{X_n\}$  as per Jagers (1974)

$$\begin{aligned} X_{n+1} &= \sum_{k=1}^{\infty} \xi_{n,k} && \text{for } X_n \geq 1 \\ &= 0 && \text{for } X_n = 0 \end{aligned} \quad (2.1)$$

where  $X_n$  denotes the  $n$ th generation population size and  $\xi_{n,k}$  denotes the number of offsprings produced by the  $k$ th individual of  $n$ th generation. For fixed  $n$ ,  $\xi$  's are independently and identically distributed (i.i.d) random variables with p.g.f.

$$F_n(s) = \sum_{j=0}^{\infty} P(\xi_{n,1} = j) s^j \quad (2.2)$$

and is called as offspring generating function at the  $n$ th generation.

Let  $F_n'(1) = \mu_n$  denotes the  $n$ th generation reproduction mean. The offspring in the population may emigrate outside with probability  $p_n$  (say) at the  $n$ th generation and accordingly we define a new random variable  $\eta$  as follows.

$$\eta_{nk} = \begin{cases} 1 & \text{if the } k\text{th offspring of } n\text{th} \\ & \text{generation emigrates} \\ 0 & \text{otherwise} \end{cases} \quad (2.3)$$

and accordingly the p.g.f. of  $(1 - \eta_{nk})$  becomes

$$p_n + q_n s \quad (2.4)$$

where  $q_n = 1 - p_n$ . For simplicity we suppose that  $X_0 = 1$

**Theorem :** For a BPVE with generation dependent emigration distribution  $\{X_n\}$  the following is true

- (i) The expected population size of the  $n$ th generation is given by

$$E(X_n) = \prod_{k=0}^{n-1} (1 - p_k) \mu_k$$

- (ii) The expected number of total emigrants will be

$$E = \sum_{i=0}^{\infty} p_i \prod_{k=0}^{i-1} (1 - p_k) \mu_k$$

**Proof :** Let  $G_n(s)$  be the p.g.f of  $X_n$ . Therefore, we have

$$\begin{aligned} G_n(s) &= \sum_{j=0}^{\infty} P(X_{n+1} = j) s^j \\ &= \sum_{i=0}^{\infty} P(X_n = i) \sum_{j=0}^{\infty} P(X_{n+1} = j / X_n = i) s^j \end{aligned} \quad (2.5)$$

In view of (2.1) and (2.3), we get

$$G_{n+1}(s) = \sum_{i=0}^{\infty} P(X_n = i) \sum_{j=0}^{\infty} P\left(\sum_{k=1}^{\xi_{n1} + \xi_{n2} + \dots + \xi_{ni}} (1 - \eta_{nk})\right) s^j \quad (2.6)$$

and by using (2.2) and (2.4) we have

$$G_{n+1}(s) = \sum_{i=0}^{\infty} P(X_n = i) |F_n(p_n^{-1} q_n s)|^i$$

$$= G_n [F_n(p_n + q_n s)] \quad (2.7)$$

By using the identity  $G_n'(1) = E(X_n)$ , we get

$$E(X_{n+1}) = q_n \mu_n E(X_n) \quad (2.8)$$

Using  $E(X_0) = 1$  the above recurrence relation yields

$$E(X_n) = \prod_{k=0}^{n-1} (1 - p_k) \mu_k \quad (2.9)$$

- (i) The expected number of emigrants ( $E$ ) throughout the process may be obtained by adding the number of individuals excluded out in different generations and is given by

$$\begin{aligned} E &= p_0 + (1 - p_0) p_1 \mu_0 \\ &\quad + (1 - p_0)(1 - p_1) p_2 \mu_0 \mu_1 + \dots \infty \\ &= \sum_{i=0}^{\infty} p_i \prod_{k=0}^{i-1} (1 - p_k) \mu_k \end{aligned} \quad (2.10)$$

### 3. RESULTS AND DISCUSSIONS

The model developed in Section-2 has been applied to study the genetic structure of populations developing in mixed mating system i.e. genotypic assortative and random mating alternately in different generations with culling of homozygote recessives and half of the heterozygotes.

Consider a population of diploid individuals with two alleles  $G$  and  $g$  at a single locus with respective probabilities 'p' and 'q'. So initially there will be three genotypes  $GG$ ,  $Gg$  and  $gg$  with probability of occurrence  $p^2$ ,  $2pq$  and  $q^2$  respectively. Since initially mating is allowed between the individuals of same genotypes after completely culling the homozygote recessives and half of heterozygotes, so only two crosses  $GG \times GG$  and  $\frac{1}{2}Gg \times \frac{1}{2}Gg$  will contribute to the next generation. In the beginning the probability of culling the homozygote recessives is  $q^2$ . In the first generation the genotype 'gg' will appear as a result of mating between  $\frac{1}{2}Gg \times \frac{1}{2}Gg$  and probability of occurrence of genotype 'gg' will be  $q^2/4(p^2 + q^2)$  and these are culled along with half of heterozygotes ( $Gg$ ). Since in the first generation random mating is allowed after culling of genotype 'gg' so only three crosses namely  $GG \times GG$ ,  $GG \times Gg$  and  $Gg \times Gg$  will contribute to the next generation. This process of mixed mating with culling of homozygote recessives and half of heterozygotes is repeated for say 'n'

generations. An outline of the technique for obtaining the probability of culling (selection) 'p<sub>n</sub>' against the

genotype 'gg' is as shown in Table 1. Looking at the table we see that the probability of culling (selection)

**Table 1.** Genotypic assortative and Random mating with complete selection against recessive genotype (gg) and half of heterozygotes (Gg)

Genotype	GG	Gg	gg	Probability of Selection against (gg)
Probability of occurrence in the zeroth generation	p <sup>2</sup>	2pq	q <sup>2</sup>	
Relative fitness	1	1/2	0	p <sub>0</sub> = q <sup>2</sup>
Genotypic ratio after selection	p <sup>2</sup>	pq	0	
<b>Mating type</b>				
GG × GG	p <sup>4</sup>	0	0	
Gg × Gg	$\frac{p^2q^2}{4}$	$\frac{p^2q^2}{2}$	$\frac{p^2q^2}{4}$	
Genotypic ratio in 1st generation	$p^2(p^2 + q^2 / 4)$	$\frac{p^2q^2}{2}$	$\frac{p^2q^2}{4}$	
Prob. of occurrence in 1st generation	$\frac{p^2 + 1/4q^2}{p^2 + q^2}$	$\frac{q^2}{2(p^2 + q^2)}$	$\frac{q^2}{4(p^2 + q^2)}$	
Relative fitness	1	1/2	0	p <sub>1</sub> = q <sup>2</sup> / 4(p <sup>2</sup> + q <sup>2</sup> )
Genotypic ratio after selection	$\frac{4p^2 + q^2}{4(p^2 + q^2)}$	$\frac{q^2}{4(p^2 + q^2)}$	0	
<b>Mating type</b>				
GG × GG	$\frac{(4p^2 + q^2)^2}{16(p^2 + q^2)^2}$	0	0	
GG × Gg	$\frac{q^2(4p^2 + q^2)}{16(p^2 + q^2)^2}$	$\frac{q^2(4p^2 + q^2)}{16(p^2 + q^2)^2}$	0	
Gg × Gg	$\frac{q^4}{64(p^2 + q^2)^2}$	$\frac{q^4}{32(p^2 + q^2)^2}$	$\frac{q^4}{64(p^2 + q^2)^2}$	
Genotypic ratio in 2nd generation	$\frac{(8p^2 + 3q^2)^2}{64(p^2 + q^2)^2}$	$\frac{q^2(8p^2 + 3q^2)}{32(p^2 + q^2)^2}$	$\frac{q^2}{64(p^2 + q^2)^2}$	
Prob. of occurrence	$\frac{(8p^2 + 3q^2)^2}{4(4p^2 + 2q^2)^2}$	$\frac{q^2(8p^2 + 3q^2)}{2(4p^2 + 2q^2)^2}$	$\frac{q^4}{2(4p^2 + 2q^2)^2}$	
Relative fitness	1	1/2	0	p <sub>2</sub> = q <sup>4</sup> / 4(4p <sup>2</sup> + 2q <sup>2</sup> ) <sup>2</sup>
Genotypic ratio after selection	$\frac{(8p^2 + 3q^2)^2}{4(4p^2 + 2q^2)^2}$	$\frac{q^2(8p^2 + 3q^2)}{4(4p^2 + 2q^2)^2}$	0	

against undesirable recessive genotypes in successive generations comes in decreasing order as given below

$$P_0 = q^2$$

$$P_1 = q^2 / 4(p^2 + q^2)$$

$$P_2 = q^4 / 4(4p^2 + 2q^2)^2$$

$$P_3$$

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Since the expressions obtained are not in closed form, therefore these probabilities have been computed for various values of gene frequency (p) and are given in Table 2. If the culling of the genotype 'gg' is considered as emigration, then the present situation of reproduction may be explained by the model developed in Section 2. The expected population size after culling the undesirable genotypes 'gg' and the expected number of culled individuals upto any generation can be obtained from (2.9) and (2.10) respectively after substituting the probability of culling given in Table 2.

**Table 2.** Probability of selection against recessive genotype

$p/p_n$	$P_0$	$P_1$	$P_2$	$P_3$
0.05	0.9025	0.2493	0.2473	0.0018
0.10	0.8100	0.2470	0.2381	0.0016
0.15	0.7225	0.2425	0.2215	0.0015
0.20	0.6400	0.2353	0.1975	0.0013
0.25	0.5625	0.2250	0.1674	0.0011
0.30	0.4900	0.2112	0.1337	0.0010
0.35	0.4225	0.1938	0.1002	0.0019
0.40	0.3600	0.1731	0.0701	0.0007
0.45	0.3025	0.1498	0.0457	0.0006
0.50	0.2500	0.1250	0.0278	0.0005
0.55	0.2025	0.1003	0.0157	0.0004
0.60	0.1600	0.0769	0.0083	0.0003
0.65	0.1225	0.0562	0.0040	0.0003
0.70	0.0900	0.0388	0.0018	0.0002
0.75	0.0625	0.0250	0.0007	0.0001
0.80	0.0400	0.0147	0.0002	0.0001
0.85	0.0225	0.0076	0.0001	0.0000
0.90	0.0100	0.0031	0.0000	0.0000
0.95	0.0025	0.0007	0.0000	0.0000

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