

RESEARCH CONCERNING THE ESTABLISHMENT OF THE BEST SIZE OF RACES POPULATIONS FROM THE GENE STOCK SP. BOMBYX MORI L.

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Abstract

The present technique utilized in sericultural genetic resources conservation, provides "in situ" silkworm conservation with the maintenance of small effectives as part of races using the selection based on mainly qualitative criteria (layings aspect and colour, larvae colour, cocoon shape and colour). Paper's aim is establishing the best size of gene stock populations based on quantitative parameters achieved in the conditions of different populations size, and on the other hand the estimation of an actual population size taking as criteria the increase of consanguinization by generation and the real number of males and females. As biological material 6 silkworm races were used: AC 29/T, AB, B1, AC/T, RG 90 si IBV. Adult free pairing was practiced. In the case of populations small actual size utilization, small values of quantitative parameters, conglomerate layings deposit, appearance of malformations at adults, are achieved. Minimum actual size of populations gene stock that allows a distant consanguinization ($Df=0.50\%$) is of 100 individuals (50 females +50 males).

Key words: Bombyx mori L., population size, prolificacy, silk cocoons

INTRODUCTION

The size of silkworm population is represented by families number as part of a population and individuals number as part of a family [2], [3].

The two elements influence the conservation degree, genetic fin and selection effect.

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What differentiate the methods utilized in different sericultural is in fact populations size taken into conservation.

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of consanguinization by generation and the real number of males and females [4], [5].

MATERIAL AND METHODS

6 silkworm breeds were taken in study, AC 29/T, AB, B1, AC/T, RG 90 and IBV, for each being established different populations as actual size [1], as follows:

I st variant	5 males and 5 females
II nd variant	20 males and 20 females
III rd variant	50 males and 50 females

The effect of populations actual size (N_e) over the values of some quantitative characters, respectively prolificacy, hatching, raw cocoon weight and cocoon shell weight were followed.

Adults free pairing was practiced.

RESULTS AND DISCUSSIONS

The data presented in table 1 influence the effect of populations real size over the main quantitative characters for a number of 6 silkworm races.

From their analysis results that for small populations, of 5 individuals, for both sexes, the prolificacy is decreased, respectively 405-486 eggs/laying for all studied breeds.

As increases the number of females and males from which the offsprings were obtained, the respective parameter was improved, maximum values being obtained in the case of a population's actual size of 50 females and 50 males, when prolificacy achieves values situated between 498-614 eggs/laying.

The hatching rate registered a similar evolution, which in case of a small population size achieved, depending on the breed, values ranking between 70-84.9%, increasing with about 11.17 percent for the populations with a number of 50 males and 50 females.

Favourable influence of population's individuals number increase, was also noticed for raw cocoon weight which registered values situated between 1.534-1.918 g for small populations and between 1.974-2.861 g for populations with 50 females and 50 males.

A similar evolution registered cocoon shell weight which obtained maximum values, respectively 0.404-0.438 g, for populations with the highest number of individuals.

An estimation of populations actual size was attempted on the basis of consanguinization coefficient achieved by generations, beginning from the real number of males and females taking part to the obtaining of successive generations.

The results presented in table 2 shows that for small actual sizes of 6-20 individuals, an increase of the consanguinization coefficient by generations of 8.3-2.5%, which explains the small value of races quantitative parameters, achieved above, as well as some qualitative aspects concerning layings

conglomerate form, larvae slow evolution and adults malformations.

The increase of real size and implicitly those effectives of populations involves the decrease of consanguinization degree by generations which represents 0.50% for actual sizes of 100 individuals and 0.25% for 200 individuals, a distant consanguinization being achieved.

CONCLUSIONS

1. In the case of populations small actual size utilization, small values of quantitative parameters, conglomerate layings deposits appearance of malformations at adults, are achieved.

2. Concerning these small populations, consanguinization coefficient by generations is 8.3-2.5%, a close consanguinization, which induces negative effects as the ones reported previously.

3. The minimum actual population size is 100 individuals (50 females and 50 males), the gene stock allowing a distant consanguinization ($Df=0.50\%$).

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Table 1
 Evolution of quantitative characters by population's actual size (Ne)

Race	Prolificacy (eggs number/laying)			Hatching (%)			Raw cocoon weight (g)			Cocoon shell weight (g)			Aspect of layings and adults
	NeA*	NeB**	NeC***	NeA	NeB	NeC	NeA	NeB	NeC	NeA	NeB	NeC	
AC 29/T	463	499	510	80.7	93.9	95.7	1.578	1.535	2.041	0.317	0.317	0.404	In the case of populations small actual size (Ne=5-20), a decrease of the quantitative parameters, conglomerate layings deposit, appearance of malformations at adults, are noticed.
AB	408	508	498	78.5	91.9	97.8	1.772	1.646	2.148	0.347	0.339	0.438	
B1	407	504	578	70.0	90.7	92.8	1.534	1.548	1.974	0.296	0.334	0.434	
AC/T	405	510	523	71.4	96.5	87.2	1.605	1.482	2.861	0.299	0.295	0.425	
RG 90	429	583	614	84.9	95.0	95.4	1.589	1.783	2.007	0.320	0.363	0.407	
IBV	486	513	512	81.6	85.9	89.9	1.918	1.806	2.216	0.388	0.331	0.405	

*NeA=5M+5F **NeB=20M+20F ***NeC=50M+50F

Table 2
 Real and actual silkworm gene stock populations size

Real size			Free pairing- Paring selection
Male no	Female no	Actual size Ne ^{x)}	Rearing by generations of the consanguinization coefficient Df ^{xx)}
3	3	6	8.3%-close consanguinization
5	5	10	5.0%- close consanguinization
10	10	20	2.5%- close consanguinization
25	25	50	1.0%- close consanguinization
50	50	100	0.50%-distant consanguinization
50	100	150	0.37%- distant consanguinization
100	100	200	0.25%- distant consanguinization

^{x)} Ne=4Nm x Nf/Nm x Nf ^{xx)} Df=1/8 Nm x 1/8 Nf