Proceedings 4th World Rabbit Congress, 10-14 October 1988, Budapest Hungary, Vol. 2, 254-260.

PARENTAGE CONTROL IN THE RABBIT

L., Varga and Á., Pálovics

Research Institute for Animal Production
2053 Herceghalom, Hungary

Introduction

Biochemical polymorphisms, which generally show codominant inheritance, can be efficiently used in parentage control. The pedigree errors can be better detected when more loci, more alleles per locus and more offspring are included. As the same probability can be attained by a variety of combinations, an attempt was made to develop an optimal one from a breeding and economic point of view.

Materials and methods

The following polymorphic systems were examined pretransferrin /Prt/, hemopexin /Hpx/, 6-phosphogluconate dehydrogenase /6-Pgd/, adenosine deaminase /Ada/, red blood cell esterase-1 and -3 /Es-1, Es-3/. The number of alleles and their frequencies are shown in table 1. Allele frequencyes were calculated on the basis of typing 233 individuals from a New Zealand White breeding stock. Calculations were made according to Oishi et al. /1970/, Oishi and Abe /1970/: Probability of phenotype difference between two randomly chosen individuals:

$$P_D = 1 - /\sum_{i=1}^{n} P_i^4 + 4 \sum P_i^2 \; P_j^2/$$

$$P_{D_t} = 1 - /1 - P_{D_1}/ \; /1 - P_{D_2}/ \; . \; . \; . \; . \; /1 - P_{D_n}/$$

where i, j : 1, 2 ..... n
n: number of alleles

P_i, P_j: frequencies of alleles

P_D : probability of distinguishing two animals by examining one locus

P_{D_t} : probability of distinguishing two animals by examining 6 loci.

Probability of detection pedigree errors:

$$P = \sum_{i \neq j} P_i P_j / 1 - P_i P_j / + 3 \cdot \sum_{i \neq j \neq k} P_i P_j P_k / 1 - P_i P_j - P_i P_k - P_j P_k /$$

$$P_t = 1 - /1 - P_1/ /1 - P_2/ \ldots . /1 - P_n/$$

P : probability of excluding paternity by examining one locus

P_t : probability of excluding paternity by examining six loci.

Probability of detection pedigree errors depending on the number of offspring per litter:

$$P_{t,s} = 1 - /1 - P_t/^s$$

S : number of offspring examined from the same litter

Results

The probability of demonstrating phenotype difference between two randomly chosen individuals on the basis of one locus is the highest with the Prt system, and the lowest with the 6-Pgd system. Taking all the six systems into account P_{D_t} is 99.87 % /table 2./. In the case when the phenotype of only one offspring is known beside those of the parents, probabilities of detecting pedigree errors /P/ by each systems and probabilities combining the two highest, three highest... and so on, at last all the six P values /P_t/, were calculated /table 3./. The table shows that the value of 80,6 %, calculated from the four systems having the highest probabilities increases by about 3 % with the addition of the E-1 system and only by 0.15 % with the addi-

tion of the 6-Pgd system.

Probability values will be higher when the phenotypes of an increasing number of offspring are known beside the parental phenotypes /table 4./. Pedigree errors can be detected with a probability of 99.04 % when the Prt types of seven offspring and the parents are known. The same probability can be attained with the six systems, in the case of two offspring and the parents.

Discussion

As the detection of pedigree errors in various species depends on the number of systems, the number of alleles in the systems, as well as the allele frequencies and the number of offspring available per litter, different methods must be chosen. In the case of multiparous species - if blood sampling is simple - it is worth while to type as many offspring per litter as possible. In this way the number of systems can be reduced with maintaining the same probability. Using only the Prt system in the parentage control of the rabbit, to achieve 98 % probability in the detection of pedigree errors, six offspring per litter are needed. Since there is not so many offspring in each litter, it is advisable to type less animals for more systems. Typing Prt and Hpx systems of 4 offspring per litter provides a probality of 98 %, which seems to be optimal in the parentage control of the rabbit.

References

Oishi, T. - Abe, T. /1970/ Usefulness of blood groups and serum protein types for parentage test. Jap. J. Zootech. Sci. 41. 495-500.

Oishi, T. - Abe, T. - Mogi, K. /1970/ Gene frequencies of blood groups and serum protein types and their usefulness as marker gene. Jap. J. Zootech. Sci. 41. 495-500.

table 1.: Allele frequencies of a breeding stock, consisting of 233 individuals

Prt /6 alleles/	A	= 0.1395
	B	= 0.0322
	C	= 0.4163
	D	= 0.2103
	E	= 0.0000
	F	= 0.2017
Hpx /4 alleles/	1F	= 0.0022
	1	= 0.2478
	2	= 0.5474
	3	= 0.2026
6Pgd /2 alleles/	A	= 0.9914
	B	= 0.0087
Ada /3 alleles/	A	= 0.3047
	B	= 0.6223
	C	= 0.0730
Es-1 /2 alleles/	A	= 0.2532
	B	= 0.7468
Es-3 /3 alleles/	A	= 0.6337
	B	= 0.3155
	C	= 0.0708

table 2.: Probabilities of distinguishing indivuduals on the basis of one locus /P_D/ and 6 loci /P_{D_t}/

P_{D_1} :	Prt	= 87.87 %
P_{D_2} :	Hpx	= 77.19 %
P_{D_3} :	6Pgd	= 3.36 %
P_{D_4} :	Ada	= 68.73 %
P_{D_5} :	Es-1	= 54.18 %
P_{D_6} :	Es-3	= 65.89 %
P_{D_t} :		= 99.87 %

table 3.: Probabilities of detecting pedigree errors by one system /P/ and different number of systems in the case of the two parents and one of their offspring

P_1: Prt = 48.5o %
P_2: Hpx = 32.54 %
P_3: Es-3 = 25.58 %
P_4: Ada = 24.96 %
P_5: Es-1 = 15.33 %
P_6: 6Pgd = o.86 %

Pt: Prt + Hpx	= 65.26 %
Prt + Hpx + Es-3	= 74.15 %
Prt + Hpx + Es-3 + Ada	= 8o.6o %
Prt + Hpx + Es-3 + Ada + Es-1	= 83.57 %
Prt + Hpx + Es-3 + Ada + Es-1 + 6Pgd	= 83.72 %

Proceedings 4th World Rabbit Congress, 10-14 October 1988, Budapest Hungary, Vol. 2, 254-260.

table 4.: Probabilities of detecting pedigree errors by the Prt system and all the six systems, in the case of the two parents and different number of their offspring

system	number of offspring	probability of detecting pedigree errors
Prt	1	48.5o %
	2	73.47 %
	3	86.34 %
	4	92.96 %
	5	96.38 %
	6	98.14 %
	7	99.o4 %
Prt + Hpx + Es-3 + Ada + Es-1 + 6Pgd	1	83.72 %

Proceedings 4th World Rabbit Congress, 10-14 October 1988, Budapest Hungary, Vol. 2, 254-260.

PARENTAGE CONTROL IN THE RABBIT

Varga L. - Pálovics Á.
Research Institute for Animal Husbandry Herceghalom, Hungary

Efficiency of six rabbit polymorphic loci in parentage control has been studied. Using these proteins two randomly chosen individuals can be distinguished by their biochemical phenotypes in 99.87 % of the cases. The pedigree errors can be better detected when more loci, more allels per locus and more offspring are included. On the basis of the six polymorphic loci examined the probability of detecting pedigree errors will be 83.72 % in the case of two parents and one offspring. This value is 99.93 % when phenotypes of four offspring are known. As some of the six polymorphic loci are less effective in exclusion of incorrectly alleged parentage, these can be omitted and the phenotypes of more littermates should be determined instead. In the rabbit it seems to be an optimal resolution to type pretransferrins and hemopexins of the parents and four of their offspring which gives a probability of 98.54 % in excluding incorrectly alleged parentage.

ABSTAMMUNGSNACHWEIS BEIM KANINCHEN

Es wurde die Effektivität der Verwendung von sechs polymorph Loci des Hauskaninchens im Bereich des Abstammungsnachweises untersucht. Mit der simultanen Verwendung dieser Loci können die biochemischen Phänotypen von zwei, aus der untersuchten Population zufallsgemäss ausgewählten Exemplaren mit einer Wahrscheinlichkeit von 99.87 % unterschieden werden. Die Wahrscheinlichkeit der Aufklärung der falsch registrierten Abstammungen ist am grössten, wenn bei den Untersuchungen möglichst viele Loci, innerhalb der Loci möglichst viele Allele, beziehungsweise möglichst viele Nachkommen verwendet werden. In dem Falle, wenn neben den Phänotypen der Elterntiere nur der Phänotyp von einem ihrer Nachkommen bekannt ist, können die falsch registrierten Abstammungen mit einer Wahrscheinlichkeit von 83.72 % aufgeklärt werden. Dieser Wert erhöht sich bis zu 99.93 %, wenn die Phänotypen von vier Nachkommen bekannt sind. Da es unter den sechs Systemen auch solche gibt, die die falsch registrierten Abstammungen mit einer sehr schlechten Effektivität nachweisen, ist es zweckmässiger, statt deren Verwendung die Phänotypen von mehreren Nachkommen aus dem gleichen Wurf zu bestimmen. Beim Hauskaninchen scheint es optimal zu sein, die Prätransferrin - und Hämopexin - Phänotypen der Elterntiere und von vier Nachkommen zu bestimmen. Mit dieser Methode kann die falsch registrierte Abstammung mit einer Wahrscheinlichkeit von 98.54% nachgewiesen werden.