FABRE-TP 2016

DECIPHERING INBREEDING AND ITS LINK TO LIVESTOCK PERFORMANCE

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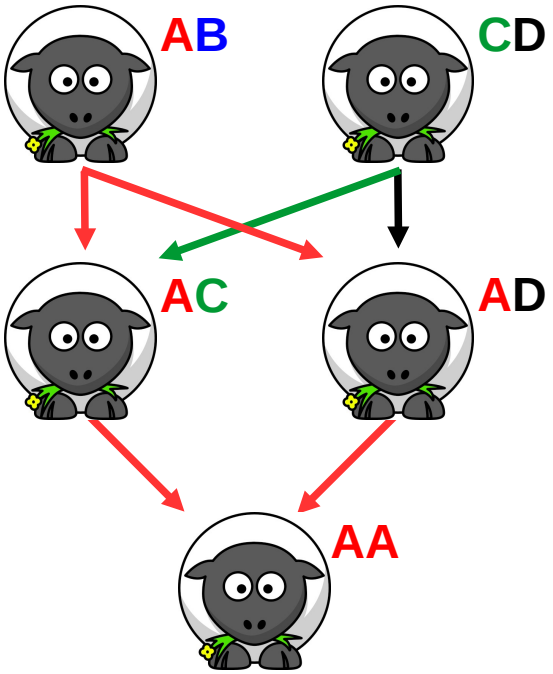
BACKGROUND

INBREEDING

Probability → two alleles at a given locus are identical by descent



INBREEDING DEPRESSION

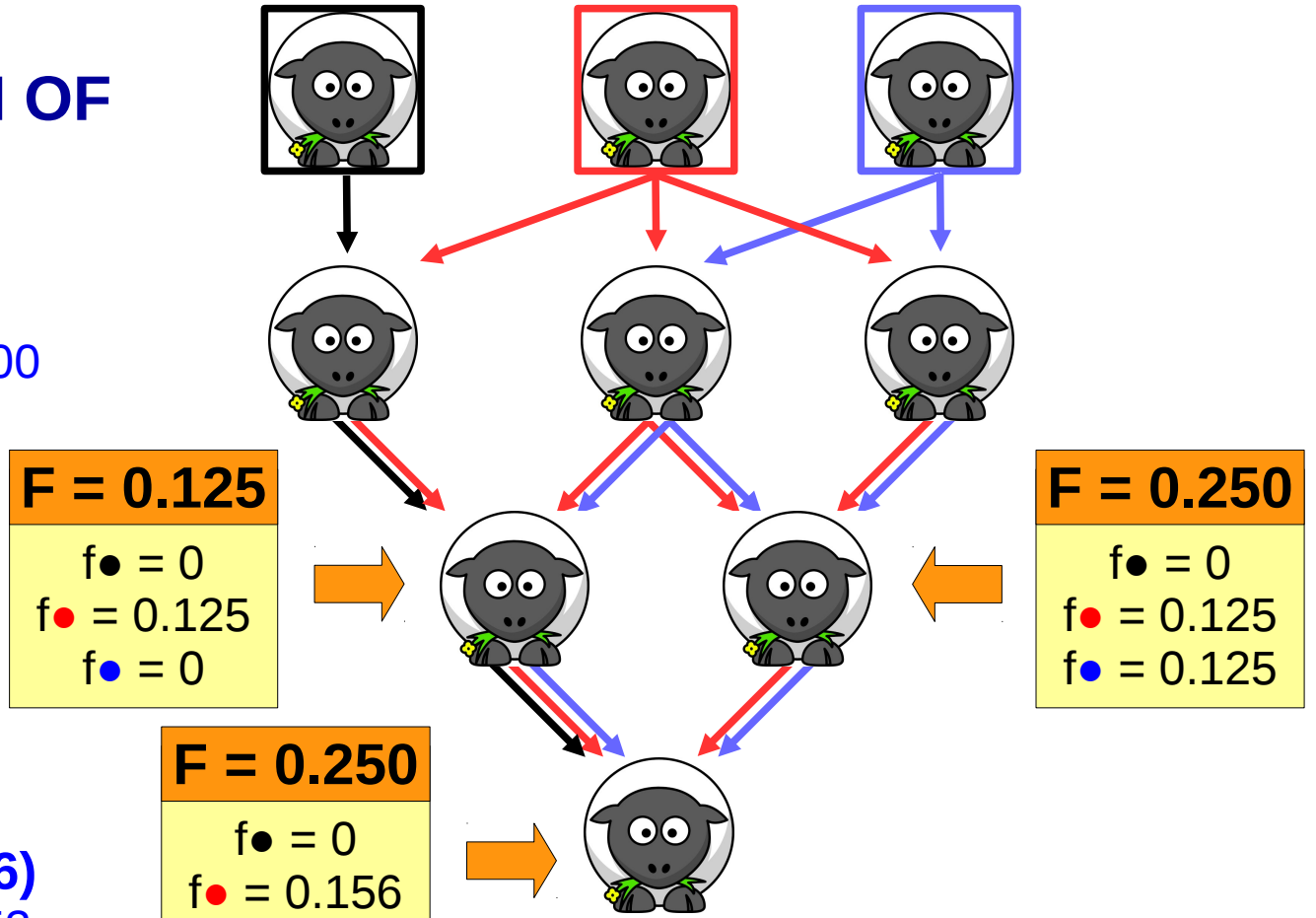
Impact of inbreeding on *fitness* traits

Founder approach

FOUNDER DECOMPOSITION OF INBREEDING

Lacy *et al*. (1996)
Evolution 50:2187-2200

Gulisija *et al*. (2006)
Livest Sci 104:244-253



Founder approach

Sow longevity

Breed:	Landrace
Records:	4,226
Pedigree:	6,355
Founders (f):	18 + 1[13]

Model: Proportional hazards

$$h_i(t;\ \mathbf{x}_{1i}, \mathbf{x}_{2i}(t), \mathbf{z}_{1i}(t), \mathbf{z}_{2i}, \mathbf{z}_{3i}) = h_0(t)\exp(\mathbf{x}'_{1i}\mathbf{b}_1 + \mathbf{x}'_{2i}(t)\mathbf{b}_2 + \mathbf{z}'_{1i}(t)\mathbf{p} + \mathbf{z}'_{2i}\mathbf{d} + \mathbf{z}'_{3i}\mathbf{a}),$$

$N(\mathbf{0}, \mathbf{I}\sigma_d^2, \alpha)$

Lamb birth weight

Breed:	Ripollesa
Records:	2,459
Pedigree:	3,079
Founders (f):	9 (+18)

Model: Linear

$$\mathbf{y} = \mathbf{Fd} + \mathbf{Xb} + \mathbf{Z}_1\mathbf{p} + \mathbf{Z}_2\mathbf{a} + \mathbf{e},$$

Systematic

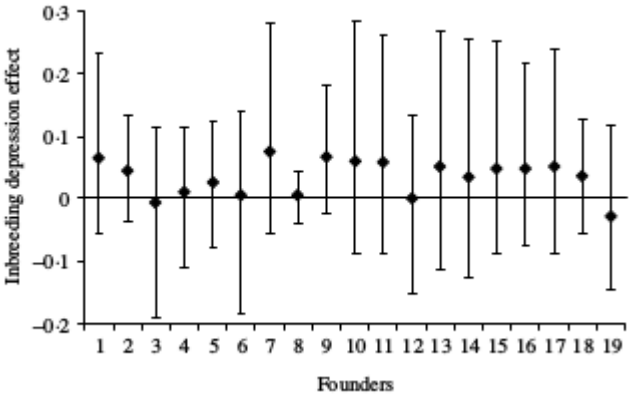
Founder approach

Skew distribution of founder-specific inbreeding depression effects on the longevity of Landrace sows

J. CASELLAS*, L. VARONA†, N. IBÁÑEZ-ESCRICHE, R. QUINTANILLA AND J. L. NOGUERA
Genètica i Millora Animal, IRTA-Lleida, Alcalde Rovira Roure, 191, 25198 Lleida, Spain
(*Received 16 May 2008 and in revised form 26 September 2008*)

***Genet Res* (2008) 90:499-508.**

Sow longevity



Analysis of founder-specific inbreeding depression on birth weight in Ripollesa lambs[1]

J. Casellas,*[2] J. Piedrafita,† G. Caja,† and L. Varona*‡

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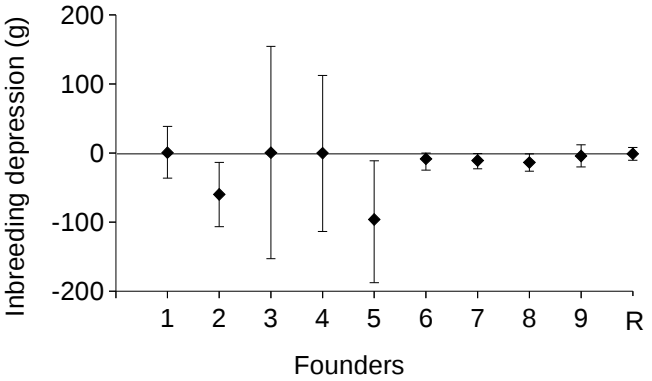
***J Anim Sci* (2009) 87:72-79.**

Lamb birth weight

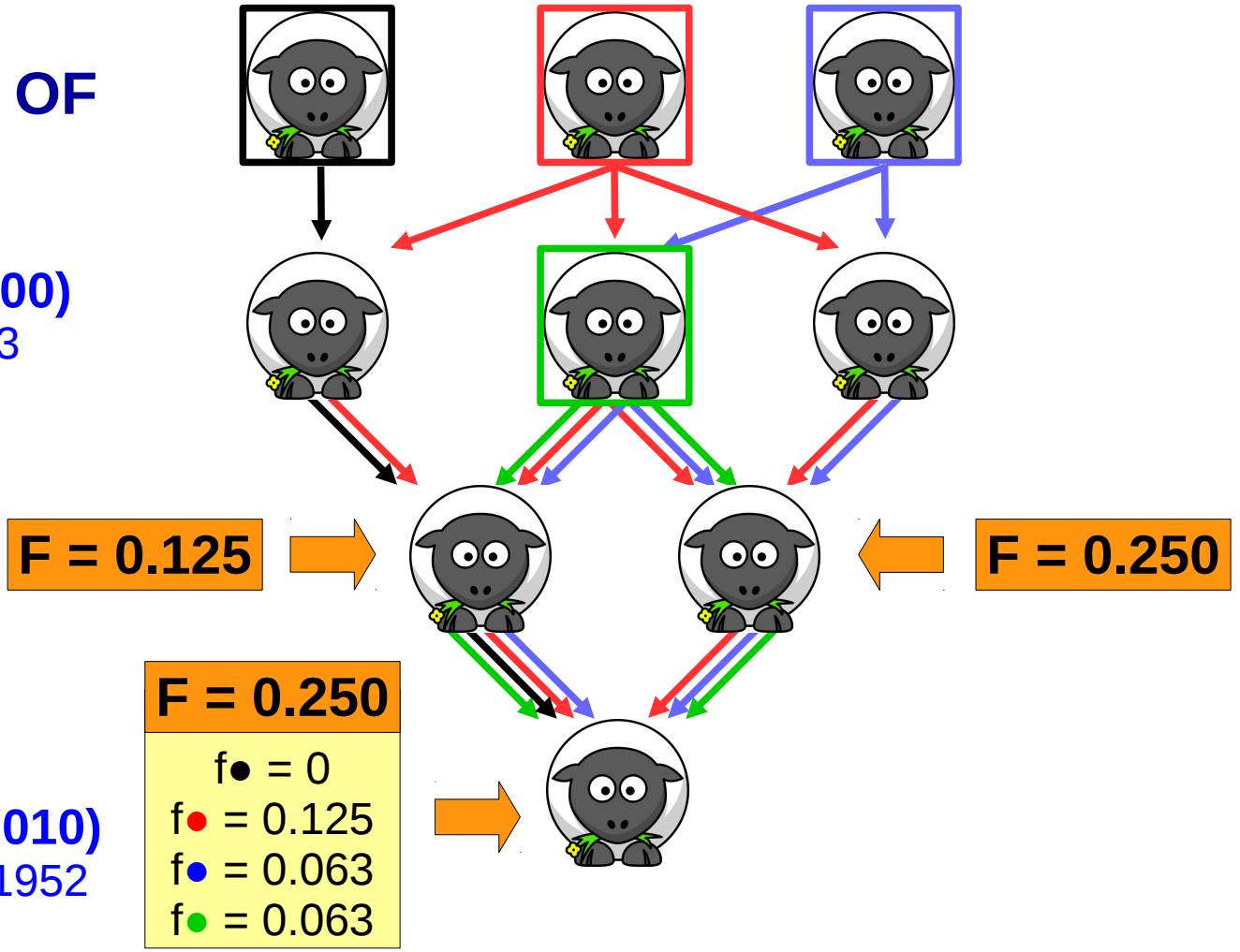


(Non)-founder approach

MENDELIAN DECOMPOSITION OF INBREEDING

Caballero & Toro (2000)
Genet Res 75:331-343

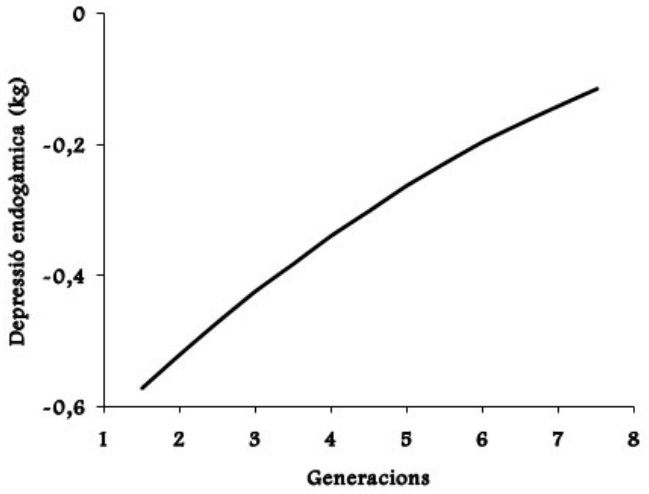
García-Cortés *et al*. (2010)
Conserv Genet 11:1945-1952



(Non)-founder approach

UAB
Universitat Autònoma de Barcelona
DEPARTAMENT DE CIÈNCIA ANIMAL I DELS ALIMENTS
OPTIMITZACIÓ DE L'AVALUACIÓ GENÈTICA DE LA RAÇA BOVINA BRUNA DELS PIRINEUS
MARTA FINA I PLA
TESI DOCTORAL
Programa de Doctorat en Producció Animal
Bellaterra (Barcelona)
2013

***Fina* (2013)**
Ph.D. dissertation



Calf birth weight

Breed:	Bruna dels Pirineus
Records:	8,130
Pedigree:	10,266

Model: Linear

$$\mathbf{y} = \mathbf{Xb} + \mathbf{f}\delta + \mathbf{Z}_1\mathbf{h} + \mathbf{Z}_2\mathbf{p} + \mathbf{Z}_3\mathbf{a} + \mathbf{e}$$

Systematic

Weighting «f» by the number of elapsed generations

(Non)-founder approach

INBREEDING DEPRESSION LOAD

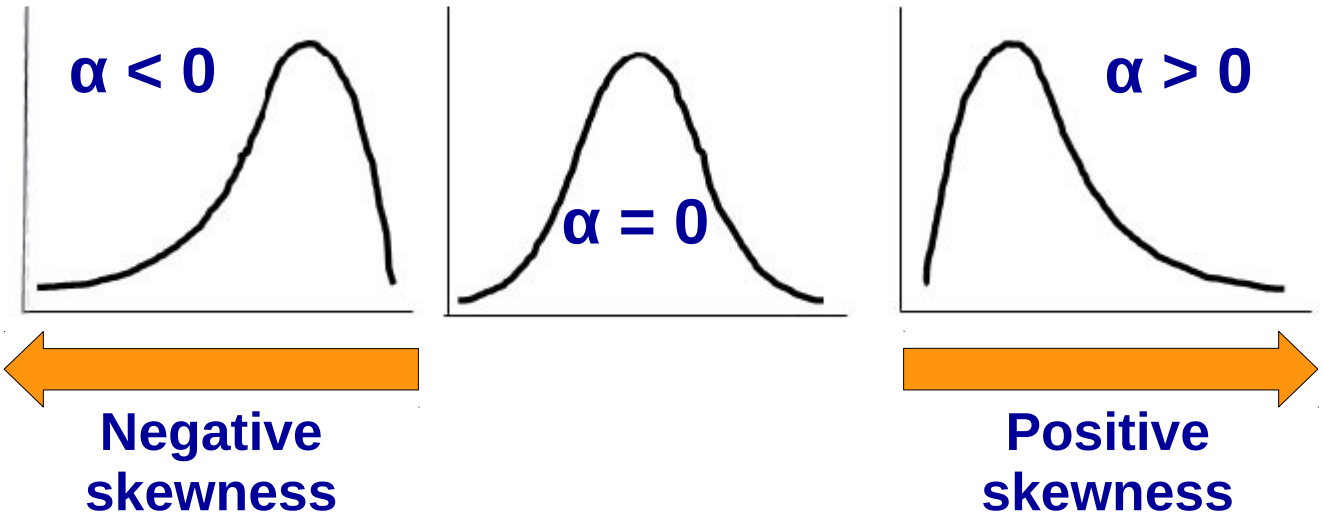
Recessive load
(or hybrid vigor)
in the genome of a given acestor that
will be expressed
(or will not be expressed)
in the phenotype of an inbred descendant

(Non)-founder approach

INBREEDING DEPRESSION LOAD

FOUNDERS ~ $N(0,\sigma_d^2,\alpha)$

Sahu *et al*. (2003)
Can J Stat 31:129-150



(Non)-founder approach

INBREEDING DEPRESSON LOAD

$$\text{OFFSPRING} \sim d_i = 0{,}5 \times (d_{\male} + d_{\female}) + \Phi$$

Mendelian sampling

Full sibs

Picston SHOTTLE

Tallent Mtoto CHARTREUSE

(Non)-founder approach

INBREEDING DEPRESSON LOAD

$$\text{OFFSPRING} \sim d_i = 0{,}5 \times (d_{\male} + d_{\female}) + \Phi_i$$

$$\Phi_i \sim N\left(\frac{-\alpha}{\sqrt{\pi}}, \frac{\sigma_d^2}{2}, \frac{\alpha}{\sqrt{2}}\right)$$

Mean = 0

50% genetic variance

(Non)-founder approach

DATA SET – MARET Rabbits

Weaning Weight

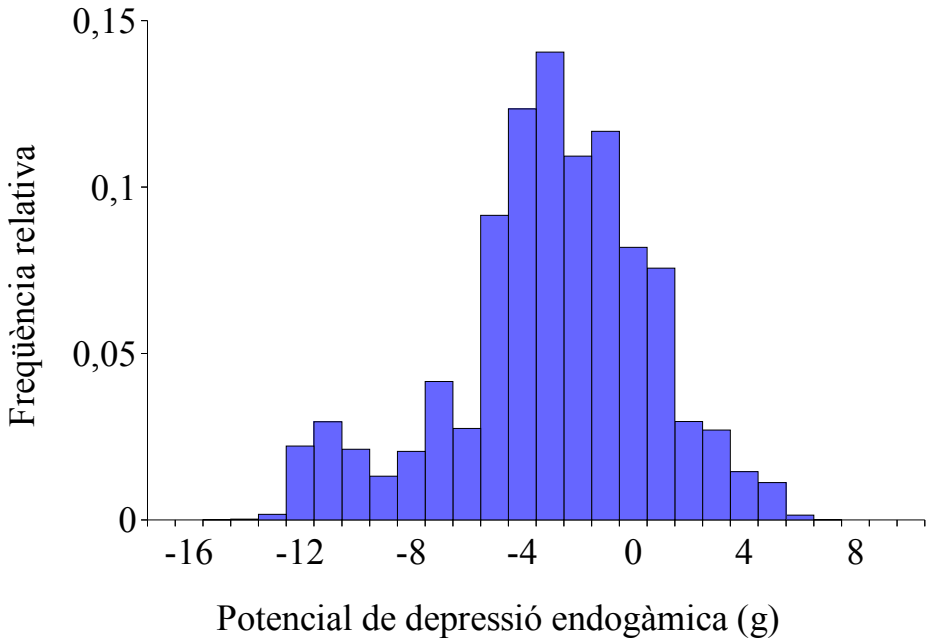
Records:	2,630
Years:	2002 a 2015
Mean:	608.0g
Pedigree:	2,657
Years:	1992 a 2015
Inbreeding:	
Individuals:	1,939 (73.0%)
Values:	4.5% a 68.1%
Descomp.:	1 to 42 components (43,634 comp.)
	0.0002 a 28.1%

(Non)-founder approach

DATA SET – MARET Rabbits

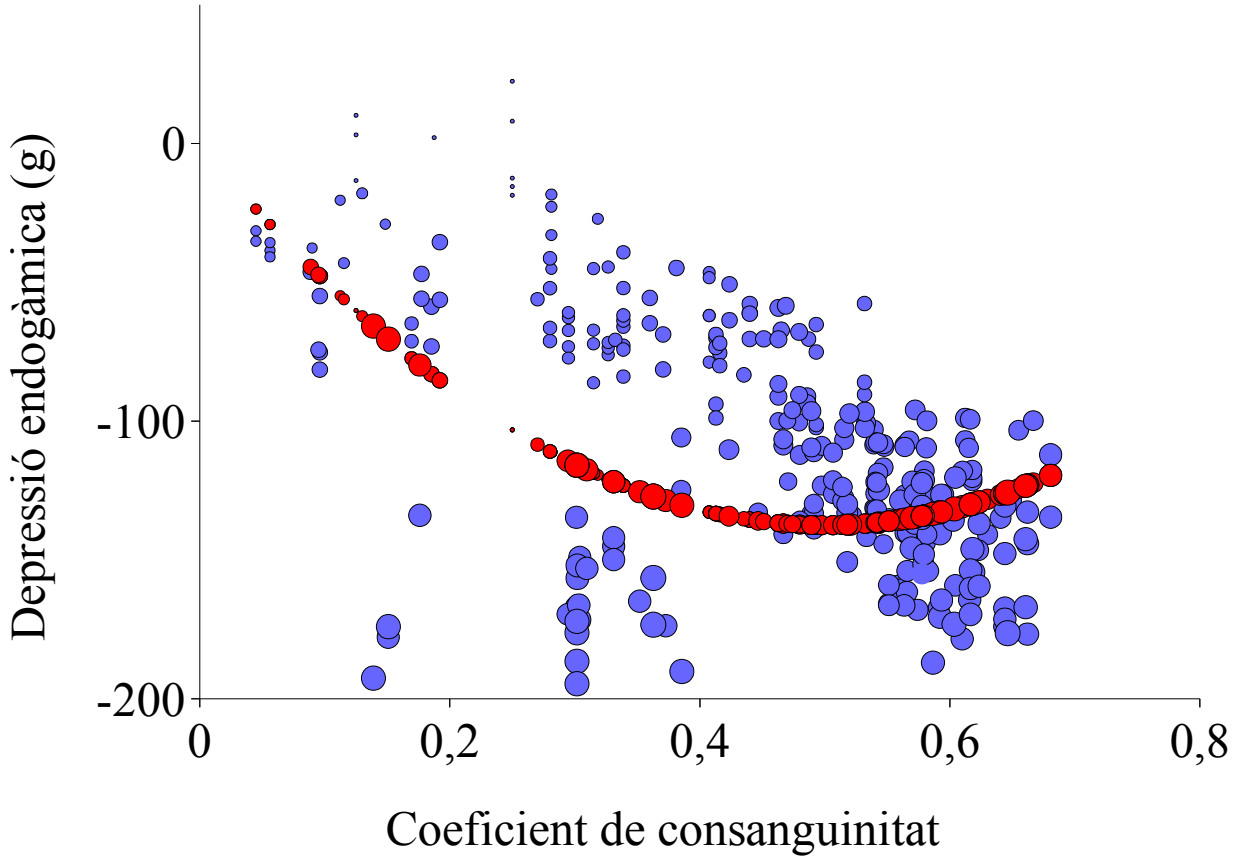
α = -4.29
(IC95% = -6.05 a -2.87)
σ_d^2 = 6.22
(IC95% = 3.72 a 8.87)

$E(d_i) = -3.42$
$V(d_i) = 12.91$
$K(d_i) = -17.21$



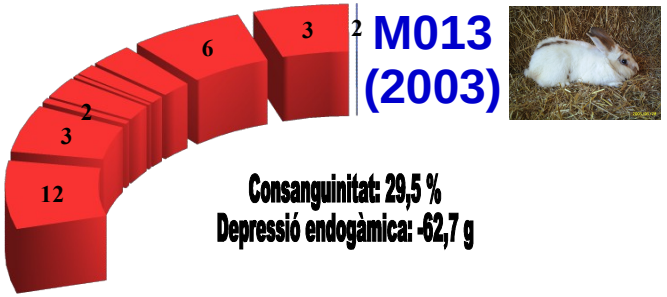
(Non)-founder approach

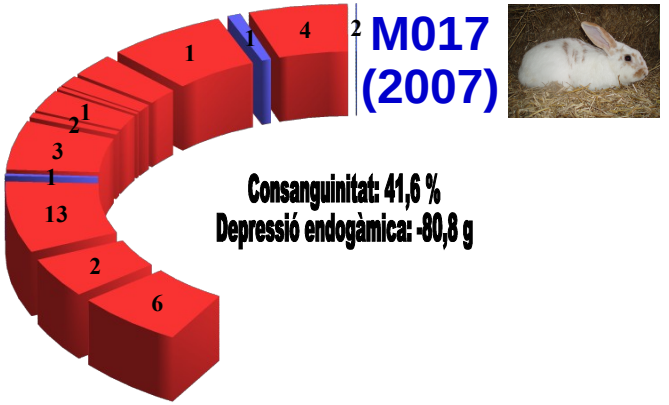
DATA SET – MARET Rabbits

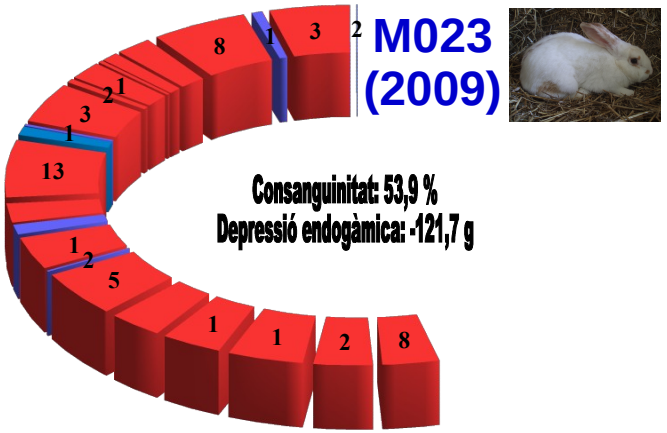


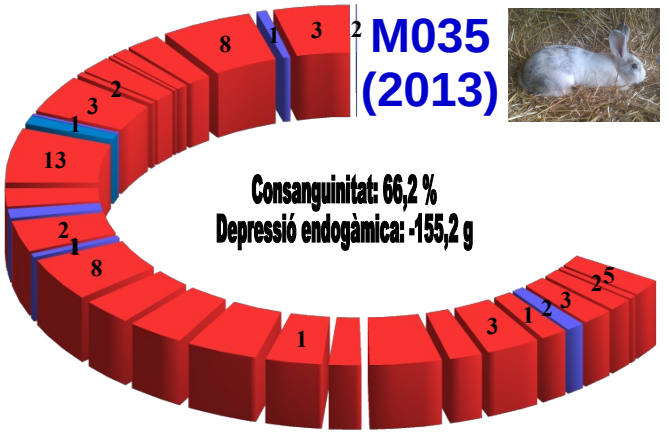
(Non)-founder approach

DATA SET – MARET Rabbits









(Non)-founder approach

CONCLUSIONS

Inbreeding depressions tends to be negative, although with a remarkable variability

Animals can be genetically evaluated by their «hidden» inbreeding depression load

The analytical approach (and its properties) is quite similar to standard genetic evaluation procedures (BLUP models).