

Session 22 gutgar@vet.ucm.es

First results from a divergent selection experiment for environmental variability of birth weight in *mus musculus*

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Research Group 920332
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Introduction

- Genetics of variability is becoming important
- Modifying environmental variability by selection is possible?
- Yes under simulated data
- And in real populations?

Objective

- Carry out a divergent selection experiment for environmental variability of birth weight in mice

Experimental Design

Nucleus

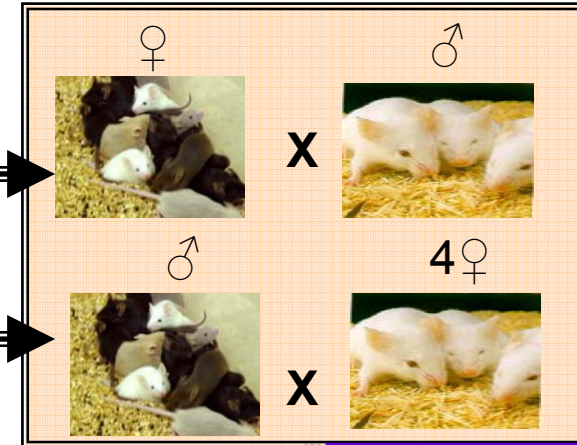
Evaluation with inbred line

Evaluation I



Evaluation 66 ♀

Evaluation 30 ♂

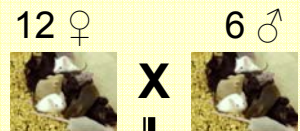


Genetic Evaluation

Best 6 ♂ and 12 ♀

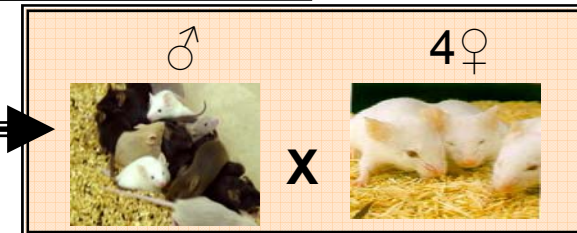
Setting up lines or Generation I

Evaluation II



12 ♀ + 30 ♂

Evaluation 30 ♂

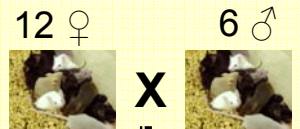


Genetic Evaluation

Best 6 ♂

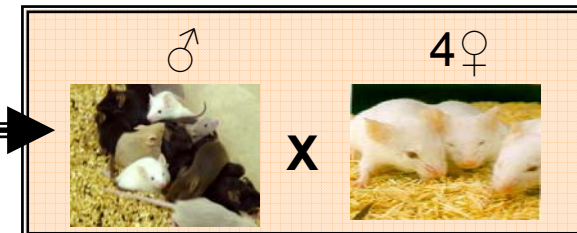
Generation II

Evaluation III

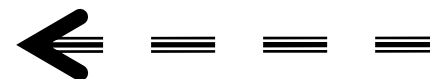


12 ♀ + 30 ♂

Evaluation 30 ♂



Genetic Evaluation



Genetic Evaluation

- Trait: Birth Weight
- All available records and 10 generations back of pedigree
- Fixed effects: sex and litter size (16 levels from second generation and covariate in the first), batch of litter
- Random effect: litter
- GSEVM v2.0 (N. Ibáñez-Escriche, M. García, D. Sorensen)

$$y_{ijk} = b_i + u_j + p_k + e^{1/2 (b_i^* + u_j^* + p_k^*)} \varepsilon_{ijk}$$

$$\rho = 0$$

Experimental Design: Mating in nucleus

INITIAL APPROACH:

- **Standard solution:**
 - 30 males (sons from the best 6)
 - 12 females (daughters from the best 3)

Male	Female	Sons or Daughters
1	1	3
1	2	2
2	3	3
2	4	2
.....		
1	1	2
1	2	2
2	3	2
2	4	2
3	5	2
3	6	2

Experimental Design: Mating in nucleus

IMPROVING THE DESIGN: WEIGHTED SELECTION

- **Standard coancestry**: average of those coancestries among the 42 offspring of the **Standard solution**.
- **Standard response**: Average breeding values of the Standard solution computed as the mean of their parents.
- Optimal solution searched by: “**simulated annealing**”:
 - Each male mated to ≤ 3 females
 - Maximizing response to selection
 - Restriction: **Weighted coancestry** $\leq$ **Standard coancestry**
 - Assuming: 4 males and 2 females born from each mate

2 ANNEALING after births with real offspring

The “good” results



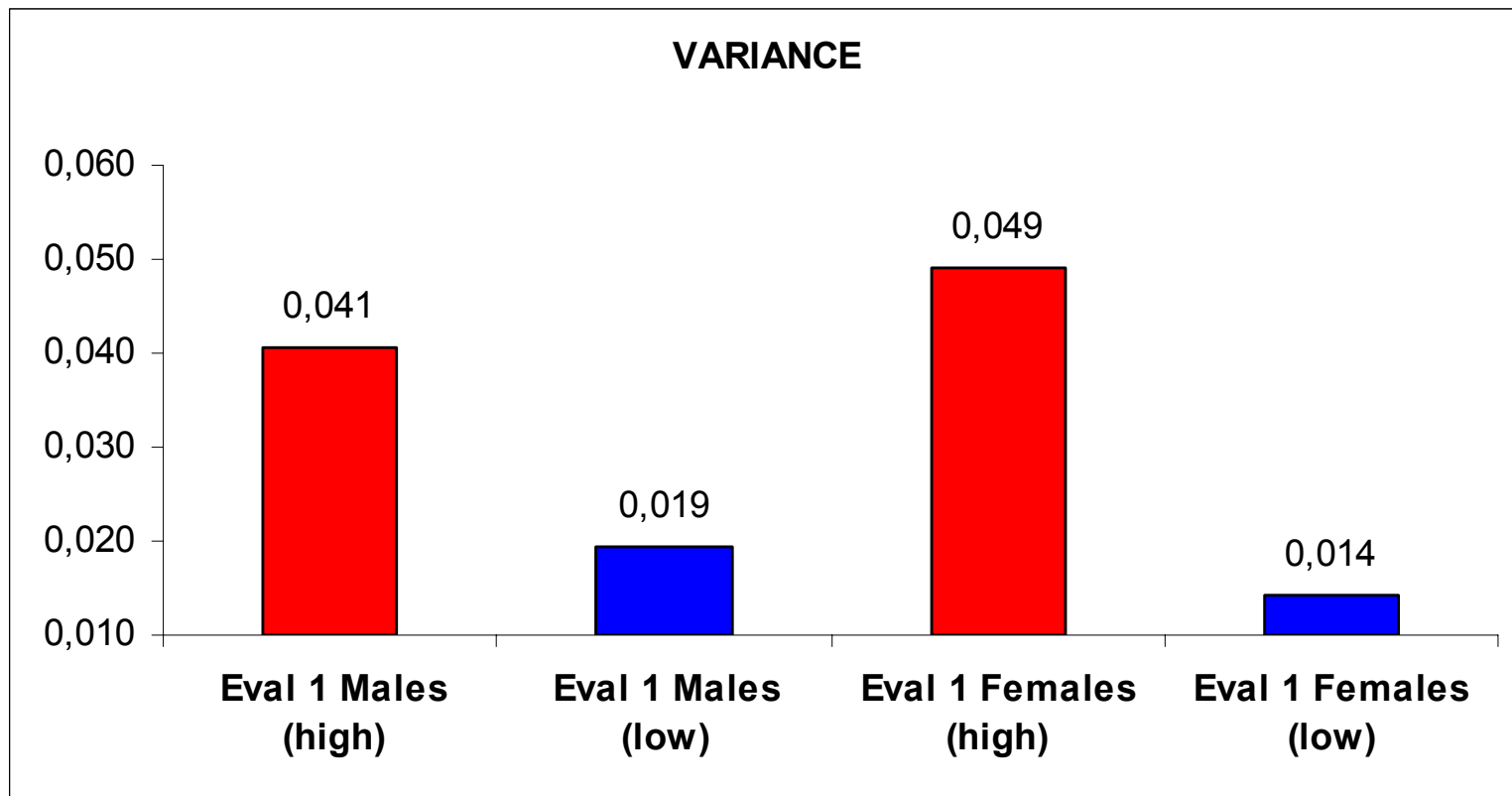
First results: Phenotypic Data

66 evaluated females x inbred males

Evaluation I

30 evaluated males x inbred females

ONLY SELECTED ANIMALS



JPG1

JPG2

Diapositiva 8

JPG1 JP; 27/04/2010

JPG2 ojo
JP; 27/04/2010

First results: Phenotypic Data

First
Generation

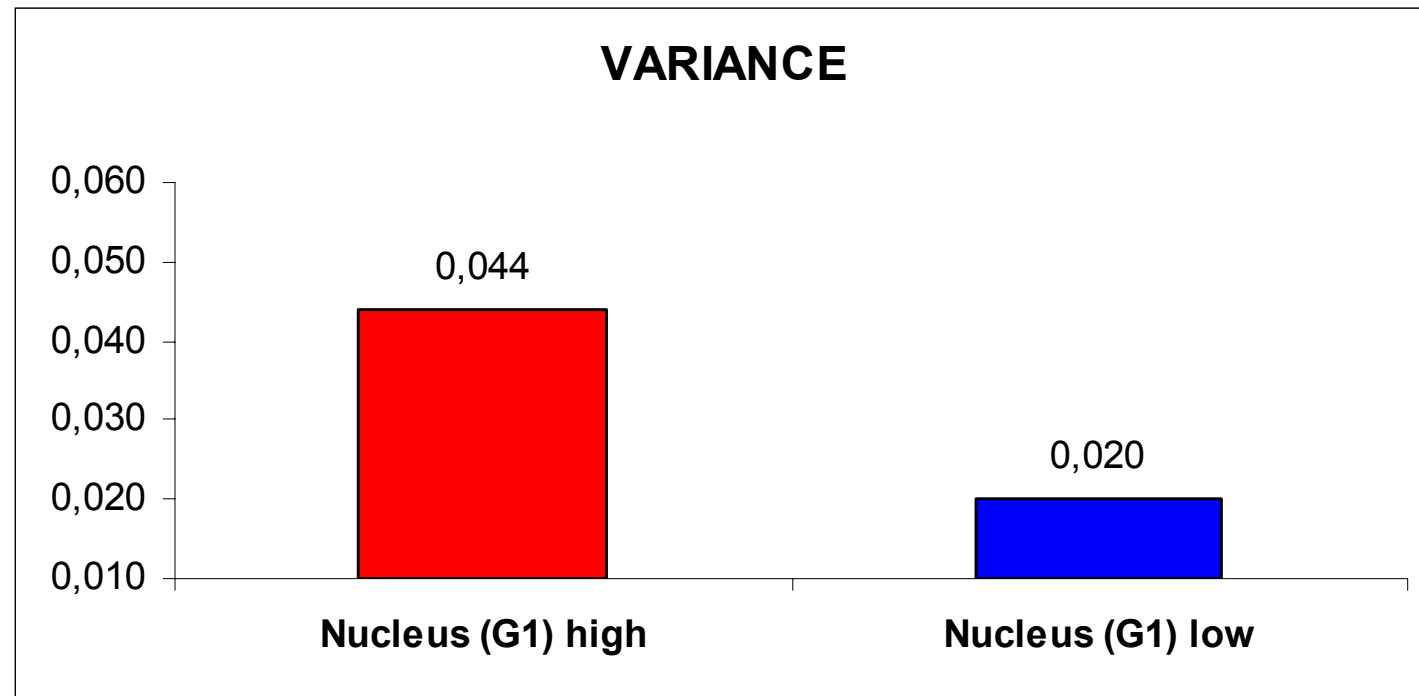
HIGH variability

Best 6 males x Best 12
females

LOW variability

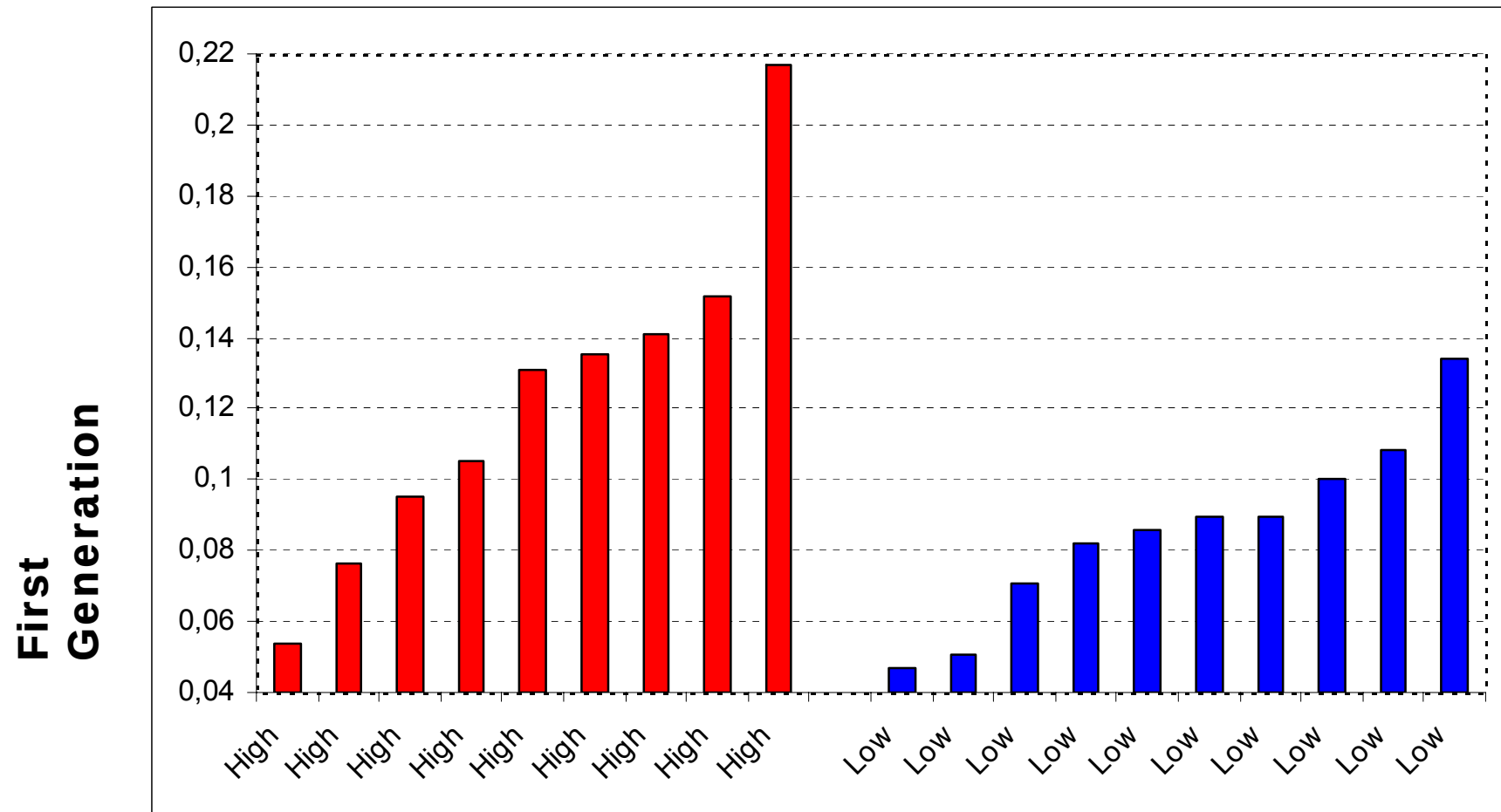
Best 6 males x Best 12
females

NUCLEUS

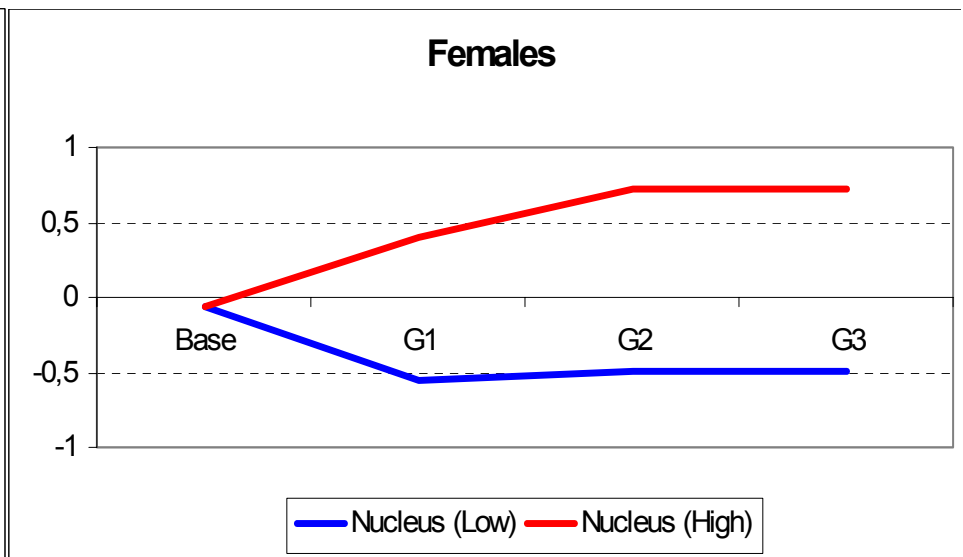
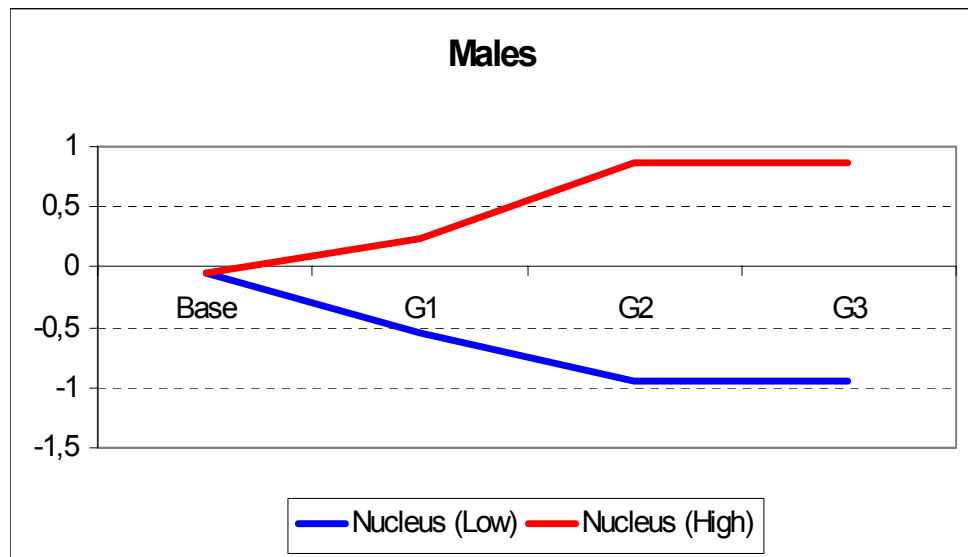
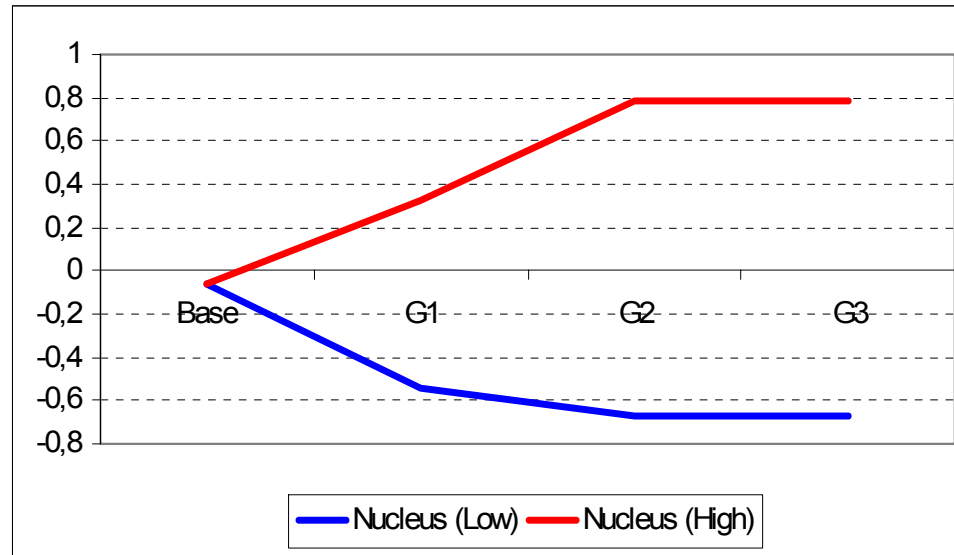


First results: Phenotypic Data

Coefficient of Variation for each litter within lines **HIGH** and **LOW**



First results: Genetic Trends

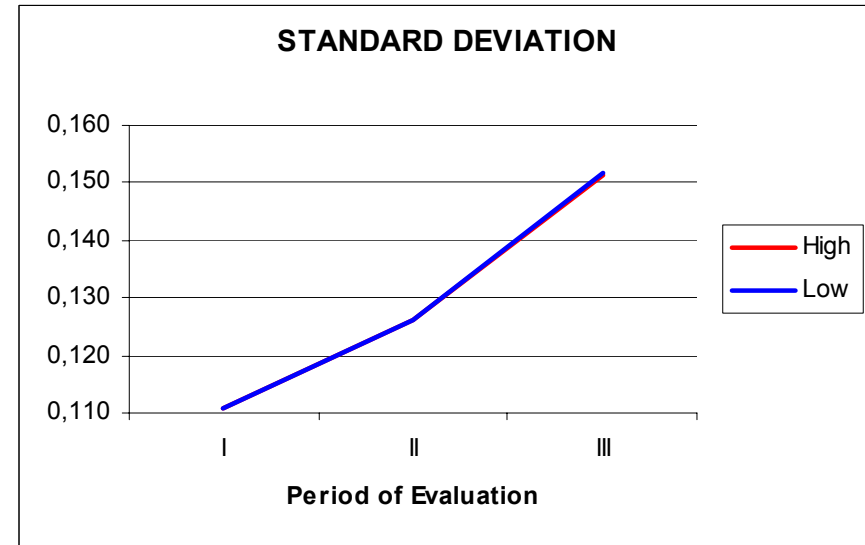
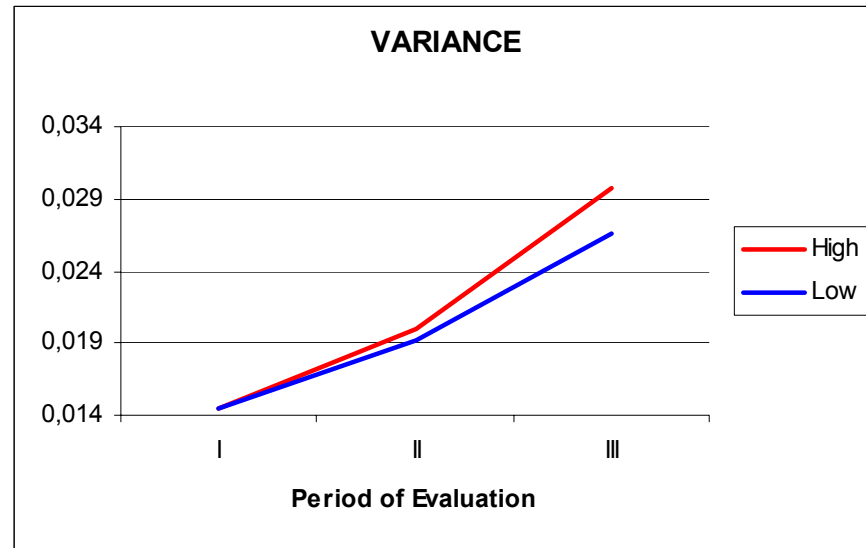


The “bad” results

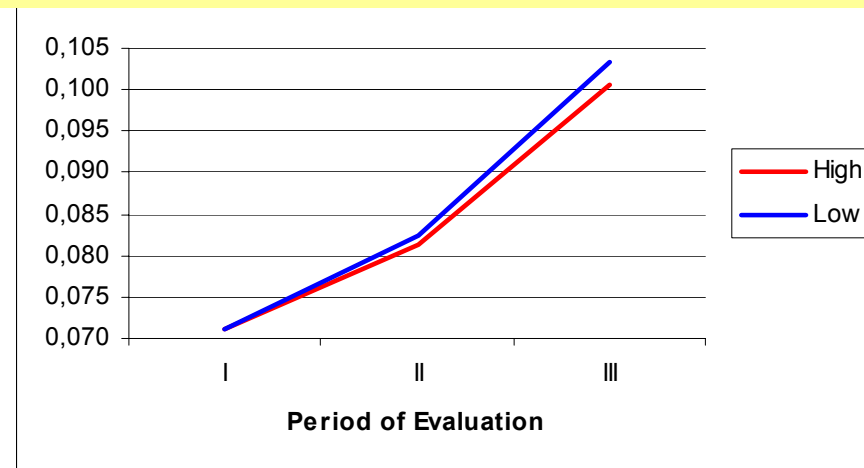


First results: Phenotypic Data

Birth weight variability in the litters for **Evaluation** step



Birth weight variability is essentially a maternal trait



First results: Phenotypic Data

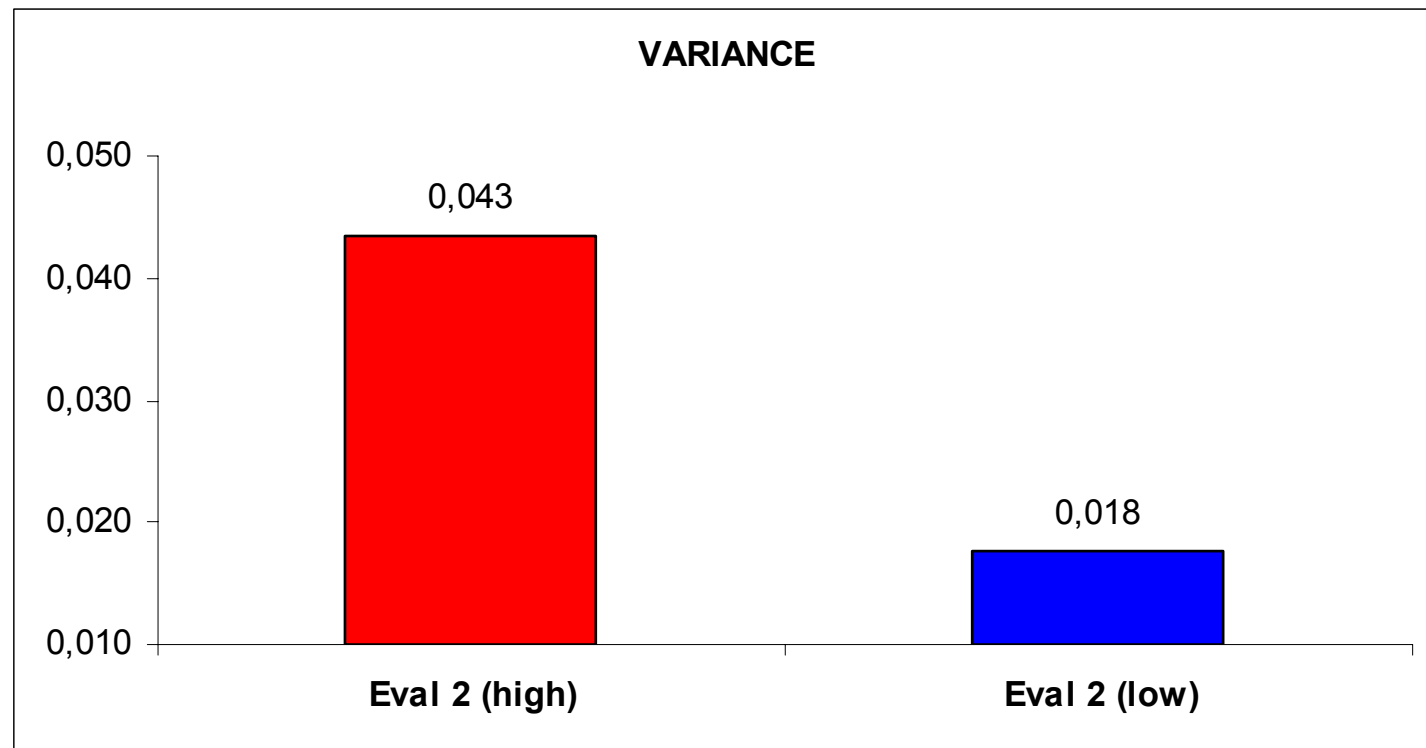
HIGH

LOW

30 males x inbred females:
Evaluation II

30 males x inbred females:
Evaluation II

Only litters of selected



First results: Phenotypic Data

Second
Generation

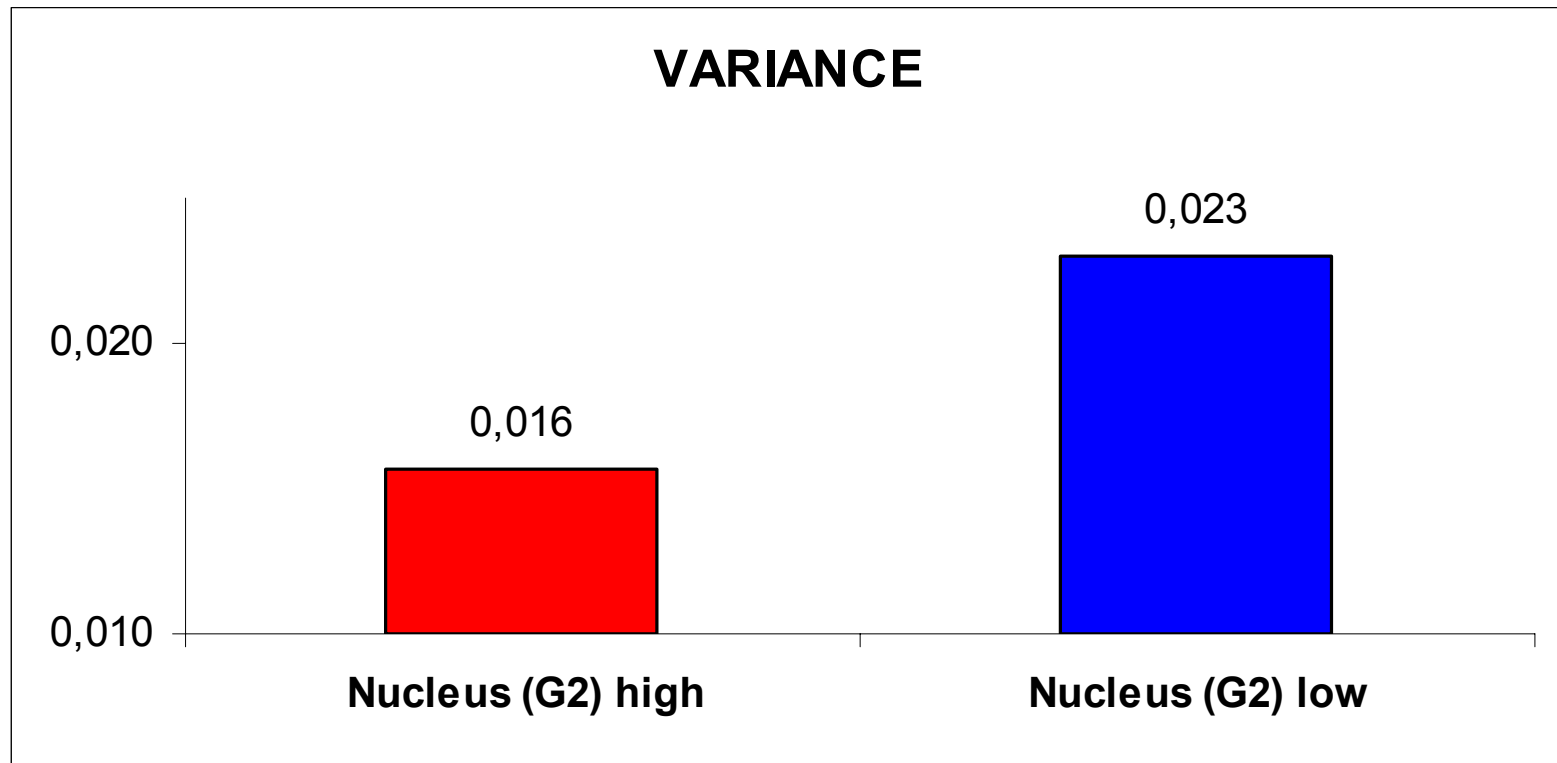
HIGH

LOW

Best 6 males x Best 12
females

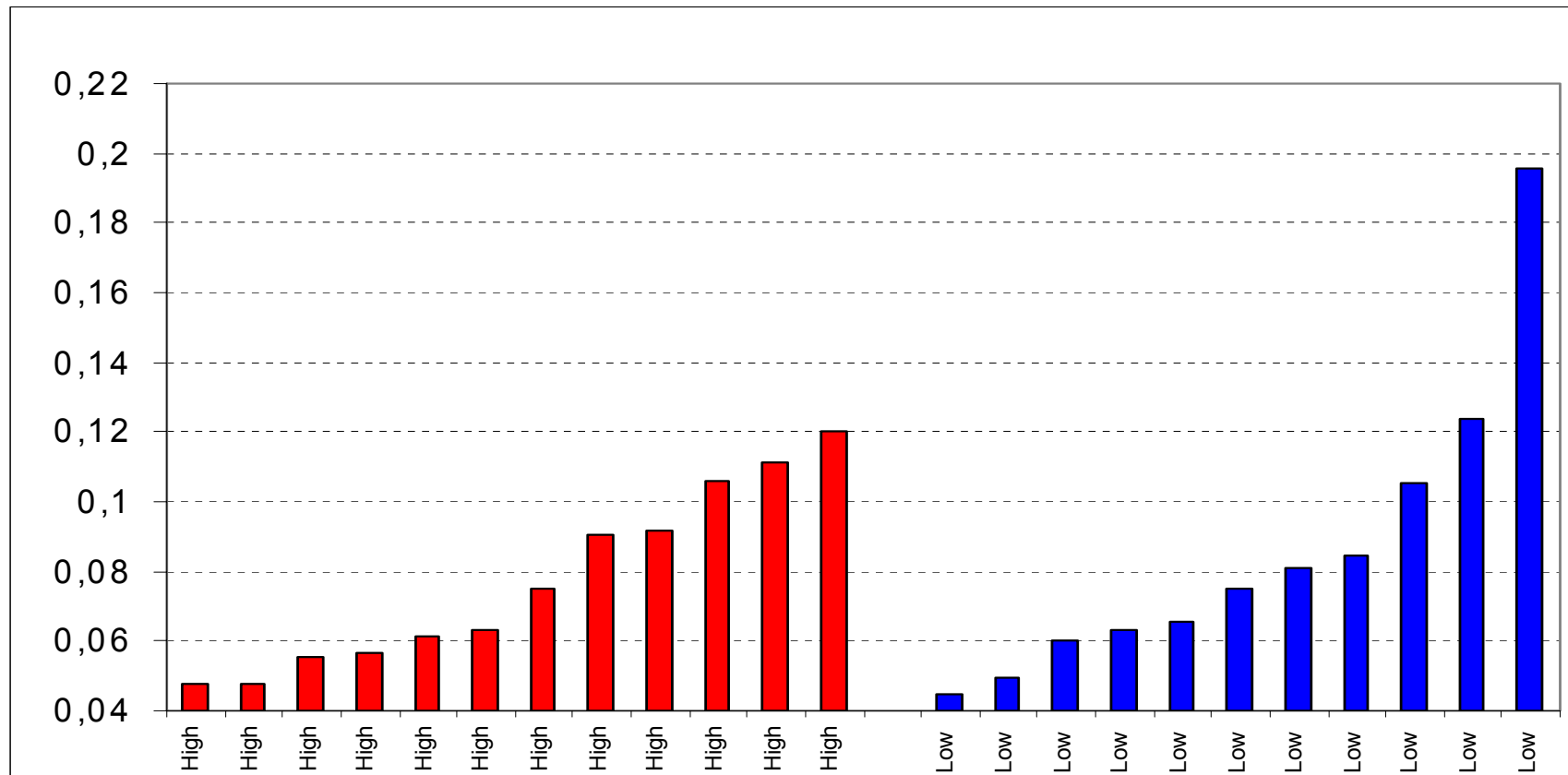
Best 6 males x Best 12
females

VARIANCE



First results: Phenotypic Data

CV for each litter withon lines **HIGH** and **LOW**

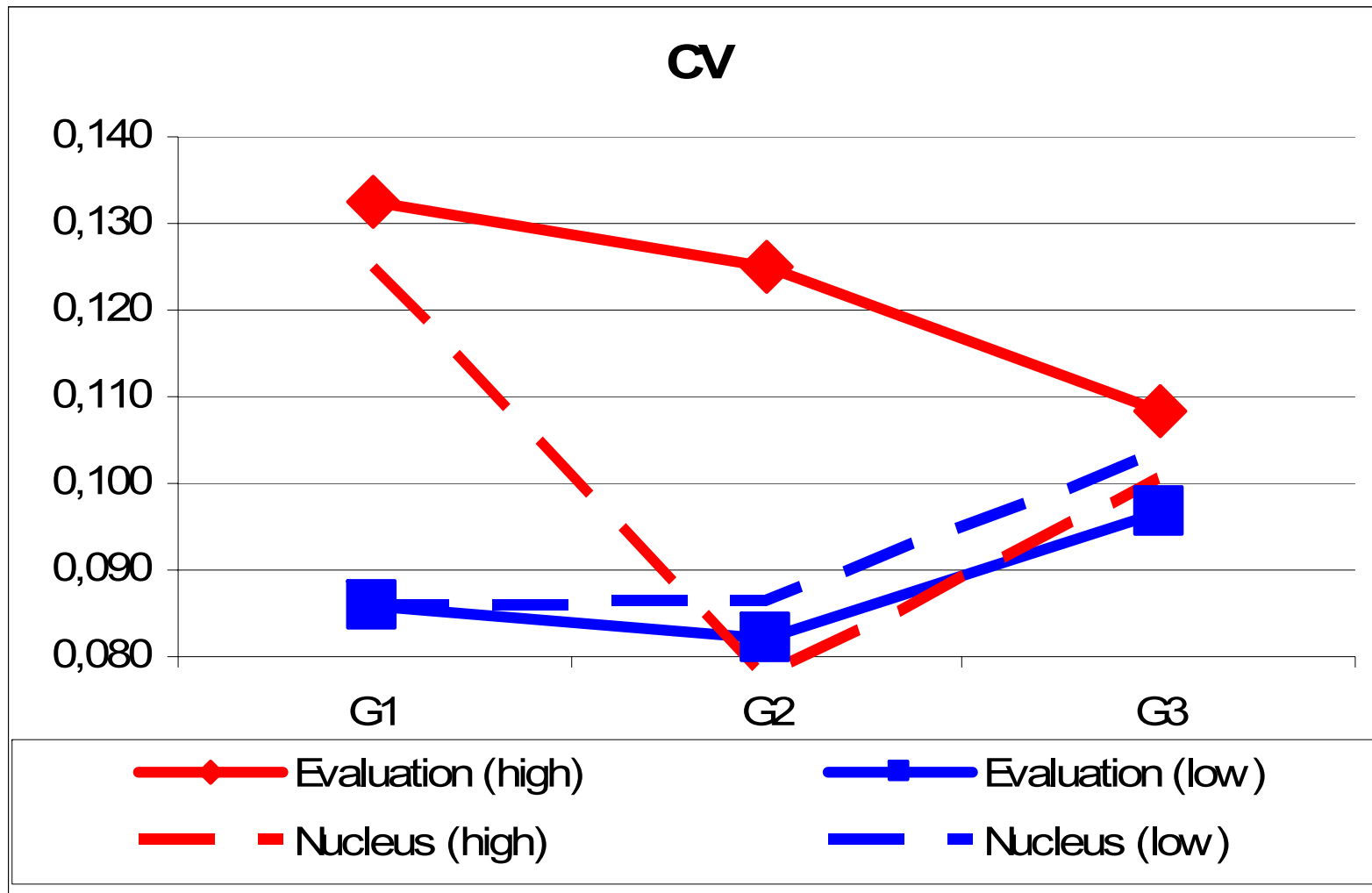


Second Generation

This has been very similar in the third generation

First results: Phenotypic Data

Evaluation + Nucleus Data



CONCLUSIONS

- Why have not we found phenotypic response to divergent selection?
- Is only a maternal trait?
- Has been lost of genetic variability?
- What will we find after some generations?

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